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From the editorial board

Dear readers, authors and reviewers!

The third issue of the journey presents the materials of the Second International Conference "Population Ecology of Animals", dedicated to the memory of Ivan Shilov.

Reviewing, editorial preparation and makeup were carried out by the organizing committee of the conference.

The correct link to the collection: II International scientific conference "Population Ecology of Animals", dedicated to the memory of Academician I.A. Shilov (Tomsk, October 10-14, 2016) // Principy èkologii. 2016. Vol. 5. № 3 P. 1–168.

With the constant willingness to work cooperatively,
Editorial board of electronic journal " Principles of Ecology"

FOREWORD

The second international conference “Population animal ecology” in the memory of Igor Aleksandrovich Shilov was initiated by the Biology Institute of Tomsk State University with the participation of RAS Theriology Society, department of vertebrae zoology of Lomonosov MSU School of Biology, “Vector” FBSC SSC of virus studies and biotechnology, Russian bird preservation union and EAS A.M. Nikolsky Herpetology Society. Such wide involvement of conference organizers illustrates fundamental value of I.A Shilov’s ideas, which Russian scientists develop consistently.

The conference is mainly focused on reports reflecting the main directions of population studies, including genetic and physiological basis of population and species stability, interacting with the environment, as well as ecological strategies of population and species adaptation in the dynamic environment, heterogeneity and population special and temporal variability of various species.

The presentations will uncover genetic, physiological and ethological aspects of population structures, physiological control of reproduction, animal metabolism, and population change with epidemic risk.

This conference will shed light not only to population ecology, but also to other research agenda and heritage of I.A. Shilov, including formation of communities, which are resistant to the modern civilization conditions. The issue of wildlife efficient use and preservation remains relevant, with new fundamental underpinnings as a result of phylogeography, genetics and ethology studies.

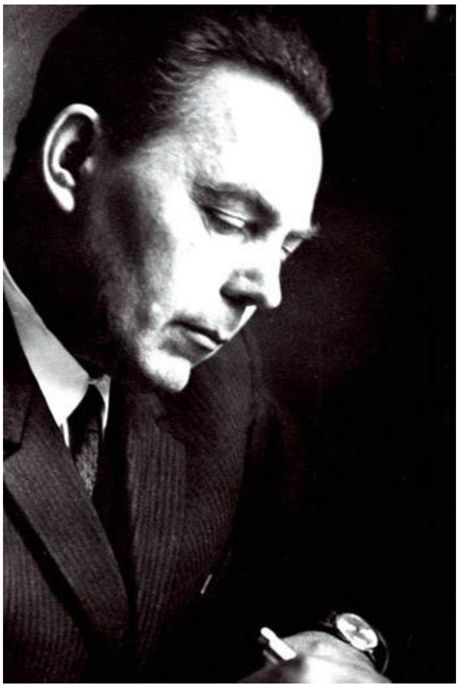
I.A. Shilov’s ideas developed into a combination of various approaches in population studies and new methods implementation. We pay much attention to modeling as a tool of natural populations’ analysis and a way to study areal and ecological niches. Few reports on species prevalence and their areas dynamics will reflect on climate change trends. We also highlighted the issues of populations change in the urban environment and the effect of human activity on the fauna. Presentations on kingdom of viruses’ biodiversity and related threat to humans are also very timely, as are the ones on the effect of nanoparticles on living organisms.

In general, the conference materials draw a large-scale picture of fundamental and applied topics of population ecology, addressed both by Russian researchers and by their colleagues from Germany, Austria, France, Poland, Moldova, Lithuania and other countries presented in these conference proceedings.

The conference was held with the support of Russian Foundation of Basic Research (grant № 16-04-20709) and state order №6.657.2014/K.

Prof. N.S. Moskvitina

IGOR ALEKSANDROVICH SHILOV



National Research Tomsk State University will host “Animal population ecology” international conference in the memory of Igor Aleksandrovich Shilov for the second time now. The first conference was organized in September 2006 and brought together 200 participants from the leading scientific institutions of Russia, Australia, Armenia, Belarus, Germany, Kazakhstan, Moldova and Ukraine.

I.A. Shilov (1921–2001) is a RAS member and one of the most prominent theoreticians of population ecology in Russia as well as one of the founders of ecological physiology, a concept of spatial-ethological organization and vertebrae population systems. Ecological physiology lab, which he founded at the MSU Zvenigorod biostation in 1950s, became a venue for field experimental studies on physiological mechanisms of animal adaptation. Series of studies on the mechanisms of thermoregulation in birds by Igor Aleksandrovich and his colleagues became a core of his Doctor of Science thesis and a “Thermoregulation in birds (ecological and physiological essay)” monograph, published after thesis’s defense in the USA.

I.A. Shilov published series of papers uncovering general trajectories and evolution of adaptive responses in the end of 60s. He concentrated on structural and functional organization of animal populations as complex biological systems, as well as on population homeostasis and ecological and physiological mechanisms supporting it, and evolution of ecological adaptation and animal behavior. His innovative approach and study results were published in the “Ecological and physiological bases of population associations in animals” monograph (1977), which later determined academic interests of many scientists and even the whole groups in Russia.

“Ecology” textbook is his fundamental work with its eight editions so far. Igor Aleksandrovich never separated scientific research from teaching ecology in Moscow University, which he was related to all his life. Creation and introduction of unique practical courses on ecological physiology of vertebrae as well as practical courses on ground vertebrae, coupled with “Animal physiological ecology” published training aid and a textbook on ecology altogether determined tremendous contribution of academician I.A. Shilov in setting fundamental educational basis of ecology science. He authored 177 publications, including 11 books.

Igor Aleksandrovich enormously influenced many generations of students and teachers as a model personality. This mostly relates to the alumni and scientists of Tomsk University, which he attended with lectures twice. Those lectures appeared to be true events attracting not only students as main target audience, but a wide range of lecturers of the School of Biology and Soil. No doubt that the ecological and physiological trajectories of studies in TSU were related to those visits, whereas further development was built upon close cooperation with him. With all the width of scientific, pedagogical and organizational interests, coupled with very busy work schedule, Igor Aleksandrovich was an amazingly open and easily approachable person, always eager to consult or review an academic piece of work.

This conference pays tribute to this outstanding scientist, who discovered new horizons in ecology.

LIST OF ABSTRACTS OF THE II INTERNATIONAL SCIENTIFIC CONFERENCE "POPULATION ECOLOGY OF ANIMALS" DEDICATED TO THE MEMORY OF ACADEMICIAN I.A. SHILOV

BENCHMARKING STUDY OF STRAY DOG POPULATION EXTERIOR CHARACTERISTICS FROM DIFFERENT REGIONS OF RUSSIA

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Stray dog population is increasing for last ten-fifteen years in Russia (Poyarkov, 2000). Stray dogs are the vectors of many diseases (such as canine rabies, leptospirosis, and different helminthoses), therefore, uncontrolled growth of stray dog population may dramatically worsen epidemiological and epizootological situation in human settlements and entail stray dog attacks. Humans try to regulate stray animal population throughout the entire history (Goriachev, 2001).

Stray dog survival depends not only on external conditions (shelter, food, etc.), but also on morphological, physiological and ethological animal characteristics which guide their adaptation. The identification of those is an important part of stray dog population structure monitoring (Rakhmanov, 2002).

We performed population assessment in all parts of Kemerovo in 2011–2015. Seventy five dogs were found via accounting method. We also used data from Kemerovo city animal protection society for the period from August 2, 2011 to September 20, 2015. The total amount of stray dogs was 235. We considered the following characteristics: height, ear shape, tail shape and hair structure. Mid-height dogs prevailed (48,9%), whereas small and large ones were equally prevalent (26,7% and 24%). In more than 50% cases hair type was average (“wild”). Stray dogs ears were predominantly half-flap and not long (60). “Ring” tail shape was the most prevalent one (63%). Therefore, the main stray dog morphotype of Kemerovo was the one of average height, average hair, half flap-eared, ring-like tail shape, when West Siberian laika was most likely to contribute to this type formation.

We conducted a comparative study of stray dog population exterior characteristics in Saint Petersburg (85 dogs, “Rzhevka” dog shelter population) and Voronezh (46 dogs “Pravo na Zhizn” dog shelter population). We elicited the main dog type of this region, such as shepherd-like mongrel of average height with “wild” hair type, stand-up ears and “billet”-tailed. That could be explained by the most popular breed in this region, Eastern European shepherd’ contribution in stray animal population formation. Moreover, breed and mongrel Eastern European shepherds were most likely to be admitted to the shelter.

The popularity of basic dog breeds in Voronezh and Saint Petersburg resulted in similar shepherd-like morphological type, which was different from Kemerovo laika-like stray dog. The most prevalent breeds in private possession mainly determined the regional stray animal morphological type. Living conditions were equally likely to make an impact and select the most physically fit breeds to survive in the severe climatic conditions.

THE COLLAPSE OF YAKUT POPULATION OF *SPERMOPHILUS UNDULATUS* PALLAS, 1778: CAUSES AND CONSEQUENCES

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For the first time Yakut suslik was described by P.Pallas in 1783. In 1937 S.Ognev determined this suslik as subspecies of an Long-tailed ground squirrel. Populations of this species spread from Eastern Kazakhstan to Amur region.

P. Larionov was the first, who determined limits of Yakut suslik natural habitat (1958). It was area between Lena and Viluy rivers estimated to be 60 000 square kilometers. Basing on amount of 3 creatures per hectare, he got the total amount about 1 200 000 overwintering susliks. Main areas, that had highest strenght of suslik, layed in three neighbouring valleys of Lena river: from Pokrovsk till Tabaga cape, than from Tabaga cape till Kangalassy cape (with centre in Yakutsk) and from Kangalassy cape till Tyubyatsy village in Namsky region in the North. This valleys have extension about 50–80 km long and 10 km wide. This territory covered only 25% of all inhabited area. Despite this, there they obtained about 95% of population.

In 1925 V. Bianki, who was the chief of biological squad at that time, wrote about suslik: «There is such a great amount of beasts around Yakutsk, that locals are sure, that they spawn twice». We should notice, that at that time those valleys had heavy crops of herbage, now it is barren steppe. In 1960s organized extermination of rodents began: mechanical, chemical and aerochemical. Nevertheless there still has been around 700 000 of susliks within all area of inhabitat in spring (Vinokurov, Akhremenko, 1982) and about 2,5–3 million – in summer. Further extension of development, including country-housing and garden co-op, conduced to population decrease. By 2000 population of suslik considered to be decreased (Anuriyev, Sedalishchev, 2002). Since that time no attempt to count the population was made. Further urbanization (urban population of Yakutsk has increased from 8 000 in 1924 to 350 000 in 2016) leaded to bigger population decrease. The result of it was total kite’s depopulation, whose ration is mostly suslik.

Population decrease may have also genetic reasons along with population consenescence. Considering Yakut suslik biocenotic role, we should track and analyze nascent soil-forming and trophic connections within this changing area. Analyzing snathes of information, we can see this tendency in other populations of *S. undulatus*.

FACTORS OF POPULATION DYNAMICS OF BIRDS IN THE MOUNTAINS

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We conducted quantitative analysis of birds on constant routes in mountain forest, sub rocky and rocky belts of the Western macroslope of Barguzin Range (460–1700 m) in 1984–2015. The total length of the pedestrian route was 18320 km, including 7660 km during the nesting period. We used Yu.S. Ravkin (Ravkin, 1967) method for bird abundance estimation.

The return ratio of earlier nesting adult birds in the conditions of the South-Eastern Siberian mountains was insignificant. It might have been the result of the regional effect of the nested area for the large part of species. The birds’ population of a particular area was formed of immigrant individuals again every year, which was also confirmed by rings data. That undermined intra-population mechanisms of quantity regulation and prioritized abiotic environmental factors and their permanent instability.

The population of birds can be seen as the result of individual selection of suitable conditions in a given year. Following return from places of wintering birds move a lot in search of territories for nesting during the prenested period. The following indicators are important for habitat selection: structures of vegetation, phenological state of vegetation, the presence of successful breeding markers in the previous year (existing old nests), presence of other individuals of the same species in the community of other individuals who occupied a habitat earlier and their acoustic signals.

Changes in the number of local populations are determined by the selection of favorable territories for nesting. This is confirmed by the analysis of the statistical association of the long-term changes in local quantity of bird species with various abiotic factors in mountain conditions.

Weather conditions of spring and the beginning of summer (heat supply and amount of precipitation) and spring phenological situation (time of snow cover termination and vegetation growth) influence existence and availability of fodder resources and suitable habitat for nesting. Variability of these parameters serves as the reason of annual population density of species distribution. Such redistributions occur between high-altitude lands and neighboring river valleys within one belt of vegetation.

Conditions of previous year, including heat balance and moisture, affect the formation of the nested population in mountains also. Formation of invertebrate biomass in the current year depends on balance of those indicators, including heat and moisture.

The quantity of individuals, who reached the area of nesting and settled in a particular habitat, is defined by conditions of duration and range of spring migrations. Changes of survival of birds in places of wintering are also important. Main forages productivity is important for specialized granivorous birds species. The population size of the victim-species in the previous and current year is important for prey birds. In many species, inconstancy of the local population is registered because of the nesting places change, depending on the environmental conditions of the migration period and the start of the breeding.

We found the association of nesting species abundance with the dates of the first registration in the spring breeding area. We also found nesting species density increase both in the earlier, and at a relatively late arrival. Time shift of spring birds’ arrival because of global climate change may have an impact on the formation of the breeding population and its dynamics. They are accompanied by directed transformations of the local abundance of nesting bird species.

IMPACT OF CLIMATE CHANGE IN THE NORTHERN BAIKAL REGION ON THE GROUND BEETLES (CARABIDAE, COLEOPTERA) POPULATION

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Investigation of the effect of climate change on the livelihoods of insects is pivotal. Long-term changes in air temperature observed in modern times can affect their numbers. Compared to eurytopic species, stenotopic species adapted to a particular set of conditions, and having low ecological valence, should be more responsive to the surrounding environment transformation (Chernov, 1975).

The aim was to study the effect of climate on the population ground beetles on the northeast coast of Baikal.

The key venue of constant research activities on herpetobiont insects is the central part of the Barguzin mountain range of the Barguzin State Biosphere Reserve. We commenced monitoring of the ground beetles by soil traps in 1988, and keep doing this until now (Ananina 2014). Sixteen stationary accounting areas are located on the 30-km transect stretching from the lakeshore to the highlands. Stenotopic species, including Pterostichus (Melanius) nigrita Payk, 1790 (short grass meadow on the shores of lake Baikal, 460 m above sea level), Carabus (Morphocarabus) henningi F.-W., 1817 (grassy meadow, low mountains, 518 m), Pterostichus (Steropus) orientalis Motsch., 1844 (aspen bergenia, Medium, 720 m), Carabus (Diocarabus) loschnikovi F-W., 1823 (tundra lichen, highlands, 1700 m) were used as model species for this study.

Studying the climate of the Barguzin range for the period 1955-2015 helped us identify general trend of the meteorological parameters. Positive trend the average annual air temperature ($R^2 = 0,443$) change with almost unchanged precipitation trend ($R^2 = 0,013$) were detected. The mean annual temperature increased by 1,1 °C. Because of extended warming in spring and summer and autumn months, there is a significant growth of the frost-free period ($r_\tau = 0,345$), a fall in summer precipitation ($r_\tau = -0,514$) and reduced Selyaninov’s hydrothermal coefficient ($r_\tau = -0,332$).

We examined the interaction of climatic parameters combination, providing the cumulative effect on the ground beetles quantity: the sum of active temperatures more than 0 °C, 5 °C; 10 °C; the average annual air temperature; the level of precipitation per year, over the summer period (June-August). We calculated the following indices: frost-free period duration (days); average monthly temperature (June-August); and hydrothermal Selyaninov’s coefficient in summer (June-August) and in autumn (September-October) in order to determine dry and wet periods of the year. We considered dates’ deviations from the mean annual values to estimate annual changes in climate: irreversible commencement of maximum temperatures more than 10 °C (spring), the stable transition of minimum temperatures more than 5 °C (summer) and stable transition temperature is less than the minimum 0 °C (autumn). We used rank correlation coefficient Kendall (r_τ) to test the presence and strength of “weather data - the number” correlation.

We found positive “quantity - the length the frost-free period” correlations for: *C. henningi* ($r_\tau = 0,372$), *C. loschnikovi* ($r_\tau = 0,361$), *Pt. orientalis* ($r_\tau = 0,324$), and a negative “number – hydrothermal Selyaninov’s conjugation coefficient” for: *C. henningi* ($r_\tau = -0,316$), *C. loschnikovi* ($r_\tau = -0,356$), *Pt. orientalis* ($r_\tau = -0,291$). Negative correlation with later spring commencement dates ($r_\tau = -0,287$) was found in *C. henningi*. No significant statistical associations were detected with regard to *Pt. nigrita*.

Over the past 60 years, the climate in the North Baikal became warmer with unchanged moisture, resulting in greater aridity. Increase in the length frost-free period along with the summer rainfall drop, affecting the developmental stages duration and breeding success ground of the beetles, altogether impacted the number of most stenotopic ground beetles species.

ECOLOGICAL AND GENETIC HETEROGENEITY OF NATURAL POPULATIONS OF THE «YELLOW» WAGTAILS (PASSERIFORMES, MOTACILLIDAE) IN THE MIDDLE VOLGA (ULYANOVSK AREA)

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During the field seasons of 2012–2015, we conducted a joint study of the nested settlement of yellow *Motacilla flava flava* Linnaeus, 1758 white-ear *Motacilla flava beema* (Sykes, 1832), white-headed *Motacilla flava leucocephala* (Przewalski, 1887) and yellow-frontal *Motacilla lutea* (S.G. Gmelin, 1774) wagtails in the surroundings of Peschanoe Lake of Ulyanovsk region (Middle Volga), which live sympatrically in the European part of Russia. For the molecular genetic analysis of masonry were studied types of eggs of the yellow-frontal wagtails (3 specimens) (20.05.2013); eggs of the yellow-frontal wagtails (3 specimens) (25.05.2013); eggs of the yellow-frontal wagtails (3 specimens) (23.05.2015); eggs of the yellow wagtails (4 specimens) (07.06.2015); and the eggs of the white-headed wagtail (4 specimens) (07.06.2015). The material was homogenized in the lytic solution for 10 minutes, followed by the addition of protease K and incubation at 56 °C for 6 hours. DNA extraction of silicon columns from the resulting supernatant was carried out. Mitochondrial cytochrome oxidase I (COI) gene was chosen as a genetic marker. Amplification was carried out using primers BirdF1: TTCTCCAACCACAAAGACATTGGCAC. Amplification was performed using a thermal cycler SpeedCycler 2 (Analytik Jena). Polymerase chain reaction (PCR) had the following conditions: 5 minutes at 94 °C, 30 seconds at 94 °C, 30 seconds at 52 °C and 40 seconds at 72 °C (35 cycles in total). Final elongation lasted for 5 minutes at 72 °C. To assess the quality of PCR, we did electrophoresis in 1% agarose gel. Purified amplification products were sequenced using capillary genetic analyzer ABI PRISM 3500 (Life Technologies) (conducting preliminary sequencing with fluorescently-labeled desoxyribonucleotides and subsequent purification of terminated fragments line). Sequences were equalized using ClustalW2 program, and phylogenetic dendrograms indicating the genetic distance were constructed using JalView program. As a result of molecular-genetic analysis we identified three clusters of individual broods in a joint nesting settlement of sympatric species, which correspond to white-ear wagtail *M. f. beema* (genetic distance 1,02) and net yellow-frontal wagtail *M. lutea* (genetic distance 0,72), as well as a large group of team (genetic distance 0,34), consisting of yellow wagtails nominative subspecies *M. f. flava* (genetic distance 0,13) and white-ear wagtail *M. f. beema* (genetic distance 0,39) and metis yellow-frontal wagtails *M. lutea* (genetic distances 0,13–0,18). This metis *M. lutea* were genetically quite homogenous group and clearly separated from the cluster, which was represented by white-headed wagtail *M. f. leucocephala* (0,21–0,26 genetic distance). The existence of hybridization between subspecies of yellow wagtails *M. flava* and yellow-frontal wagtail *M. lutea* limits the spread and the number of the latter, and leads to further accumulation of individuals in a population of white-headed wagtail *M. f. leucocephala*. Intraspecific hybridization subspecies forms yellow wagtails *M. flava* – nominative *M. f. flava* and white-ear *M. f. beema* and leads to constantly occurring genotypic splitting that support intraspecific polymorphism of populations and provide the basis for further genetic divergence of these species and subspecies. A subspecies of white-headed wagtail *M. f. leucocephala* is characterized by the maximum genetic distance (1306,67–1375,67), which corresponds to a species rank. Modern polytypical complex of *M. flava*, was probably formed in historical times through fan hybridization between the original forms of *M. f. flava* and *M. lutea*, when genetic differentiation and divergence played a leading role in the formation of space-time and the genetic structure of the *Motacilla* genus.

CHROMOSOME INSTABILITY IN NATURAL POPULATIONS OF PYGMY WOOD MOUSE (*SYLVAEMYS URALENSIS* PAL., 1811) IN THE URAL REGION

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Chromosome instability in natural populations of pygmy wood mouse (*Sylvaemus uralensis* Pal., 1811) inhabiting the territories of Ural region, affected by the technogenic impact of different nature and levels, was studied. 226 individuals from 11 localities were analyzed. Two investigated localities are situated in the head zone of the Eastern Ural Radioactive Trace (EURT), one locality – in the impact zone of Karabash Copper Smelter (KCS). The levels of radioactive and chemical contamination in the other localities did not exceed the regional norms. The frequency of bone marrow cells with chromosome aberrations was used as an indicator of chromosome instability. 50 cells per animal were analyzed.

Significant differences among populations of *S. uralensis* from the studied Uralian localities were found (χ^2(df = 10) = 96,969; p < 0,001). The frequencies of cells with chromosome aberrations varied from 0,33% to 4,67%. We observed high levels of chromosome instability in *S. uralensis* in both localities in the head zone of EURT (3,19% and 3,14%). Soil contamination densities with 90Sr (the main dose-forming radionuclide in EURT) in those localities were 6740-16690 kBq/m² and 2322 kBq/m² respectively. High portion of chromosome type aberrations and significant positive correlation of the frequency of aberrant cells and the specific activity of ^{90}Sr in bone tissue (R_S(N = 62) = 0,44; P = 0,0004) indicated that radiation pollution was the main reason of the increased frequency of chromosome aberrations. High level of chromosome instability (frequency of aberrant cells – 4,22%) comparable with those observed in the localities in the head zone of EURT was shown in *S. uralensis* in the impact zone of KCS (the territory of high chemical contamination). All mutations were of chromatid type. Correlations between frequencies of aberrant cells and heavy metal concentrations (Cu, Zn, Cd, Pb) in liver of *S. uralensis* were positive, and even significant in the case of Cu (R_S(N = 9) = 0,74; P = 0,024). Apparently, heavy metal contamination plays certain role in the increase of chromosome instability in *S. uralensis* in the impact zone of KCS, although the variety of chemical mutagens in the impact zone is much wider than studied at the moment. Unexpectedly high frequencies of aberrant cells in *S. uralensis* were revealed in two localities in the Southern Urals (3,00%) and in the Middle Urals (4,67%) despite no exceedance of technogenic contamination in those localities. No sex- or age-related variability was detected. The causes of high chromosome instability in those localities are still unclear and repeated sampling is necessary to overcome the effect of small sample size.

Thus, high variability of chromosome instability estimates was shown in populations of *S. uralensis* in the Ural region. The main role in the chromosome damage frequencies increase in certain localities is attributed to the mutagenic influence of environmental chemical and radioactive contamination, which is comparable with respect to the strength of the mutagenic effect. Inter-population variability of the level of spontaneous and induced chromosome instability in *S. uralensis* needs further elaboration.

The study was supported by Act 211 Government of the Russian Federation, contract №02.A03.21.0006.

GENETIC ANALYSIS OF BATS POPULATIONS IN WINTER AND SUMMER HABITATS

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Small mammals have been successfully used for a wide range of population ecology problems (Shilova, 1993; Lukyanov et al., 2002). One such problem is the study of the mechanism and phylopatry population variance among sedentary species. Bats are phylopatric animals, which is manifested in their quest to return to the same wintering sites up to particular locations in caves (Smirnov et al., 2007). Research in summer colonies is hampered by frequent changes of daytime resting places and the collapse of colonies (Metheny 2008, Kurt, 1998); however, this problem may be resolved using radio transmitters that allow tracking of colonies relocations. According to the data (Strelkov, Ilyin, 1990), summer bats colonies are mostly unisexual and mostly represented by females. As for males, they are either on the same territory with females (e.g., *E. nilssonii* (Keyserling, Blasius, 1839)), or fly over long distances and stay on a big distance from them (*M. daubentonii* (Kuhl, 1817)) (Smirnov, Vehnik, 2014). In summer habitat females form colonies in which they give birth to pups. After the collapse of the brood colonies born in summer, young animals live separately from adults and look for their own wintering sites later.

Radio telemetry studies and banding of individuals from different summer colonies and winter populations, which we carried out in 2012 to 2015 on the territory of the Samara Luka, indicated that summer colonies had all one wintering site. To determine the level of genetic variation between summer colonies, as well as between groups of individuals wintering in the different parts of a cave, we took genetic material from five groups of hibernating females living at a distance of 20 to 100 m from each other. One of these groups was ringed previously as part of summer brood colony. The analysis showed that the genetic structure of summer colonies remains in the wintering sites. Genetic distance between the groups of individuals wintering in the different parts of a cave, was way too small, indicating their genetic homogeneity. At the end of hibernation, individual groups wintering in one shelter, break apart, and obviously fly to different locations of summer habitat to breed. By the beginning of winter, they get together again under the same shelters, which is confirmed by ring tracking. Mating takes place in autumn during the “swarming”. However, induction of side genetic material at this time is more likely to by random mating with unrelated individuals from other wintering sites, as well as due to the population of wintering shelters with unrelated young animals.

This study was supported by RFFR (grant 15-04-01055-a).

THE DIFFERENCES IN THE CAROL OF PIED FLYCATCHER MALES (*FICEDULA HYPOLEUCA* PALL.) OF VARIOUS AGES

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For birds, singing is a biologically important behavior, firstly attributed to such vital functions as sex partner attraction, alert on the territory availability (Krebs, 1977), and settlement structure sustainability (Catchpole, Slater, 2008). Studying acoustic features is therefore quite informative as part of complex assessment of bird model species selected populations, such as pied flycatcher. The ongoing study of nest biology of this species on a particular territory lasts for 20 years, whereas the study of acoustic features began in 2014.

We studies frequency and structural and temporal features of male songs of various ages. The birds in this sample were divided into three groups: year-old (n = 20), two-year old (n = 10), three and more year old (n = 7). In total, we analyzed 923 songs.

The male song frequency analysis showed, that there was a significant difference between males of various age in maximal (Kruskal-Wallis test: H (2, N = 923) = 33,4; p < 0,001) and minimal (H (2, N = 923) = 27,3; p < 0,001) song frequencies, and therefore – in the song frequency range (H (2, N = 923) = 33,0; p < 0,001).

We found progressive drop of maximal song frequency in pied flycatcher males with age. Such reduction was most pronounced in two-year old birds compared to one-year olds (on average, by 393 Hz; H (1, N = 748) = 9,9 p < 0,001). Further reduction of maximal frequency with age was not so sound (on average, by 47,75 Гц), but still significant (H (1, N = 425) = 4,5; p < 0,03).

The rise of minimal song frequency was only noted in birds starting at year three. In those, it was significantly higher compared to birds reproducing the first (H (1, N = 673) = 23,3; p < 0,001) and the second (H (1, N = 425) = 21,2; p < 0,001) time. One- and two-year old birds did not differ between each other in this variable (H (1, N = 748) = 0,6; p > 0,05).

Summarizing this data, we conclude that pied flycatcher males exhibit changing frequency of songs with age, mainly narrowing the frequency range of attracting songs. The song frequency change occurs in two stages. At first stage, dramatic drop of maximal song frequency occurs in two-year old males compared to one-year olds, whereas the second stage is noted for rise in the song minimal frequency in birds three and more years old compared to the birds of one or two years old.

Singing structural and temporal analysis showed that males of different age had significantly different song duration (H (2, N = 923) = 30,0; p < 0,001) and a number of figures in it (H (2, N = 898) = 46,9; p < 0,001).

Song duration dropped with age. Group comparison showed that one-year old males sang significantly longer songs as compared to two-year olds (H (1, N = 748) = 10,9; p < 0,001) and three or more year old birds (H (1, N = 673) = 27,4; p < 0,001). There were no differences between the second and the third groups (H (1, N = 425) = 2,6 p > 0,05).

Three or more year old males demonstrated reduction in the figure count in theirs songs compared to one-year olds (H (1, N = 673) = 45,06126; p < 0,001) and two-year old males (H (1, N = 400) = 27,8; p < 0,001). We failed to find differences of this variable between the first and second year old males (H (1, N = 723) = 0,9; p > 0,05).

Thus, we demonstrated that the carol of pied flycatcher studied population had high variability of frequency and structural and temporal attributes with age.

MODERN METHODS OF TERRITORIES DEVELOPMENT GUARANTEE PRESERVATION OF SIBERIAN GROUSE *FALCIPENNIS FALCIPENNIS* (HARTLAUB, 1855) IN THE NATURE

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Siberian Grouse *Falcipennis falcipennis* (Hartlaub, 1855) is the bird included in Red Books of MSOP and Russian Federation. Siberian Grouse is almost universally considered a rare bird, but there are sufficient indications that in the optimal habitat Siberian Grouse may be quite prevalent or numerous (Nikanorov, 1977; Brunov et al., 1988; Biserov, 2011).

The main limiting factors for this bird species are deforestation, wildfires, uncontrolled hunting, and the presence of settlements. The proposed preservation measures are usually preservation of habitats via reserves organization, captive breeding, hunting regulation and promotion of protection (Nikanorov, 1977; Potapov, 1987; Nechaev, 1988; Isaev, 2011; Sandakova et al., 2015).

Long-term experience of these measures of protection utilization showed that shooting ban of a Siberian Grouse does not yield any results (Nikanorov, 1977) due to very poor control of its enforcement in sparsely populated areas. Protection promotion of this rare bird species is also ineffective. The organization of reserves promotes well-being of this species only on a very small part of an area and the most effective only in its southern part where industrial logging is done. Wildfires are known to be an integral cyclical factor in the life of forest ecosystems (Sannikov, 1992). Siberian grouse is quite adapted to them, and its areal includes territories of larch-fir forests and the larch of light forests. It was demonstrated that the Siberian Grouse is numerous in such woods with prevalence of trees of the IV-V site class (Biserov, 2011; Biserov, Medvedeva, 2016). Industrial logging in such woods is not profitable and therefore not done.

It is known that the most part of Siberian Grouse areal refers to one of the least developed and sparsely populated regions of the Far East of Russia. Economic activity there is presented by hunting, logging, a few sites of mining industry and hydropower generation to a lesser extent. Such enterprises were most often accompanied by human settlements.

The enterprises do not have a significant impact on Siberian Grouse, and a negative impact is mainly produced be so-called “excess population”, which is gradually formed in such settlements and not connected directly with production. The most part of these people are forced to make their living with hunting, often illegal, and they reduce Siberian Grouse population. Of note, considerable part of the fires in a taiga occurs because of local population. Siberian Grouse almost disappeared around Zeysky hydropower plant (Potapov, 1987), whereas negative changes in population of Siberian Grouse was not detected in much less populated region of the Bureya Reservoir (Zausaev et al., 2007).

In the conditions of market economy and accelerated urbanization new methods of territories development are formed. Shift-rotation methods with no permanent population may be such method in the northern and related territories of the country. Our studies in the surroundings of “Sakhalin-I” and “Sakhalin-II” camps and around gold mines in upper courses of river Niman (Khabarovsk territory) showed that Siberian Grouse in these parts is usual or numerous (Biserov, 2013). The presence of such vulnerable bird species population as a Siberian Grouse may serve on objective indication of effective nature protection of shift method of territories development.

Thus, modern methods of territories development can warrant preservation of a Siberian Grouse in the nature. At the same time such measure of Siberian Grouse protection as captive breeding, loses relevance, similar to the earlier made attempt of Capercaillie *Tetrao urogallus* cultivation (Nemtzev et al., 1973). Of note, social and economic transformations which began at a turn of the XX–XXI centuries in the country allowed to restore Capercaillie number in nature without creation of nurseries (Biserov, 2009).

SPECIFICS OF POPULATION DENSITY DYNAMICS IN CYCLIC POPULATIONS OF SMALL MAMMALS OF THE NORTH CIS-URALS

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Results of long-term survey of small mammals (1984–2015) were used for two landscape regions, i.e. at the plain (Russian plain) and at the foothills of Ural (North Ural), of the Pechora-Ilych reserve. The trapping was carried out simultaneously at trap-lines and in ditches. The trapping was carried out simultaneously at trap-lines and in 50-m ditches with 5 pitfalls per each ditch. Periodicity in time series of species abundance was estimated using autocorrelation and the spectral analysis.

Cyclic populations were common in the region. The periodicity of the cycles in various species ranges from 3 to 5, but most often 4-years. Two groups of populations could be distinguished depending on the range of variability of the population density. In the first group (*Sorex araneus, Sorex caecutiens, Myodes rutilus, Myodes glareolus*) the coefficient of variation (CV) is less than 100%. The second group includes *Sorex isodon, Microtus agrestis, Microtus oeconomus, Myopus schisticolor*, with variations in population density above 130%. Almost complete absence in capture in the years of population drop versus steep rise in the years of abundance is a characteristic feature of those species. *Myodes rutilus* ranged in capture index from 3,2 to 76,8, whereas in *Myopus schisticolor* it ranged from 0 to 133,0 individuals per 100 pitfall/day.

The summer decline in the years of depression is characteristic for cyclic populations of small mammals in Fennoscandia (Korpimaki, Krebs, 1996) and was considered “good quality attribute of a true cycle” (Henttonen et al., 1985), but in the Pechora-Ilych reserve is a very rare phenomenon. The phenomenon was found only in *Myodes rutilus* in the plain region once only for the entire period of observations. The index of abundance in various species normally rises from spring to autumn, at least slightly. Another specific attribute of cyclic populations of small mammals is prominent interspecific synchrony in the dynamics of their numbers (Korpimaki et al., 2004). In the foothills of the reserve, abundance of all of the cyclic species changed quite coherently: the phases of depressions and peaks usually coincided in time, some disparity were found in the phases of growth and decline only. Spearmen rank correlation coefficients were positive and ranged for these cases from 0,44 to 0,86. The most prominent coherence was found in the species of the second population group, *Microtus* voles, *Myopus schisticolor* and *Sorex isodon*.

The landscape diversity at a territory is of the great importance for shaping of population dynamics of small mammals (Ekerholm et al., 2001; Loman, 2008). The only 5 of the 14 species were found cyclic in the plain area of the Pechora-Ilych reserve, whereas this number increased up to 10 of cyclic species in the foothill region. As for example populations of *Sorex isodon* and *Myopus schisticolor* at the plain area were not cyclic, however in the foothill populations of those species fluctuations of population density were regular as a rule. The abundance indices in *Sorex isodon* ranged from 0 to 2,2 at the plain, versus 0–61,2 individuals per 100 pitfall/day at the foothills. In many ways, dynamics of small mammal populations are explained by changes in the ratio of the proportion of optimal and marginal habitats in a particular landscape (Lidicker, 1995). In this context, landscape at the plain area is highly fragmented. Habitats optimal for shrews and voles (spruce green moss and grass) are scarce (up to 11% of the territory), small, and isolated each from the other. Normally they represent local spots within vast areas of poor pine forests and bogs. That leads to low abundance of many species. In the dark coniferous taiga the optimal habitats predominate (90% of the area), this promotes the higher abundance of many species of small mammals, hence facilitate producing a greater number of cyclic populations.

FEATURES OF GENETIC STRUCTURE OF SMALL MAMMALS' POPULATIONS IN CONDITIONS OF TRANSFORMED ENVIRONMENT

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Studies of animals' population genetic structure are popular in ecological research. Fragmentation and isolation of populations usually lead to gene flow limitation, heterozygosity level decreasing, inbreeding level increasing and eventually genetic diversity loss.

Structure of small mammals' population was estimated based on the calculation of lines of Gero's traps. For molecular genetic analysis, ISSR-fragments (ISSR36 – $(AG)_8YT$ and ISSR6 – $(ACC)_6G$) and markers of microsatellite DNA (EU285408Mm D/R (GGAA-repeat), EU285402Mm D/R (CAT-repeat), EU285407Mm D/R (CAG-repeat) were used. Obtained genetic data were analyzed with *GenAlEx 6.5* (1/0 coding system) and *Arlequin ver. 3.5* (frequency analysis of alleles of microsatellite DNA)

The overall sample comprised 76 samples of seven murine and insectivores species, and also 68 individuals from 6 populations of bank vole captured in Penza and Ul'yanovsk Regions.

Features of the genetic polymorphism (ISSR) of murine's populations associated with different localities of the same natural landscape zone were revealed. We also showed genetic polymorphism range dependence from landscape-habitat level of considered murine's groups.

The analysis of three microsatellite DNA systems variability in bank vole's populations elucidated the following findings: 1) disparity of observed and expected heterozygosities almost in all populations (5 from 6) and quite high index of allelic losses per locus (G-W) – 0,802; 2) veraciously ($p = 0{,}052$) large genetic distances ($\delta\mu^2$) between populations from two geomorphological sites ($9{,}073 \pm 1{,}601$) compared to the distances between population within separate site ($4{,}410 \pm 1{,}120$). The latter indicates longer timescale divergence of populations from different geomorphological sites comparing with divergence time between populations within sites.

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COMMUNITIES OF SMALL MAMMALS IN THE URBAN ENVIRONMENT

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The urban environment for animals is a combination of multiple conditions, which determine species composition and count of various species. This is illustrated with a comparison of various cities in Russia (Starikov, 1987; Tikhonova et al. 1990; Moskvitina et al 1988). In this presentation, we report on the material we collected from the end of 80s of the last century until 2015 on the territory of Tomsk. Tomsk is an old city dating back 400 years. Its residential area comprises both traditional wooden construction and modern blocks with multi-storied buildings. This city is noted for the absence of large park territories with nice green zone in the outskirts.

On the one hand, species composition of urban communities includes adopted species, most often appearing in the city from the neighboring green zones (*Myodes rutilus*, *M glareolus*, *M. rufocanus, Apodemus agrarius, Ap. peninsulae, Mus musculus*, *Rattus norvegicus, Microtus rossiaemeridionalis*, *M. agrestis, M. gregalis, M. oeconomus, Sicista betulina, Sorex araneus*, *S. tundrensis, S. caecutiens, S. isodon, S. minutissimus*). Fixing permanent components is largely a predicted outcome, determined by the urban environmental structure as well as by the attributes of species, which help them benefit from those conditions.

These species may evolve different strategies, which is nicely illustrated in two most illustrative species of urban environment, field mouse and East European vole. Thus, field mouse is initially noted for insular type of population space structure (Flint, 1977), high mobility, euriphagia, huge reproductive potential, behavioral reactions lability, and potential for quick ecological structure rearrangement (Moskvitina, Suchkova, 1995; Karaseva et al., 1999; Agulova et al., 2008). On opposite, East European vole is a more sedentary species (Karaseva, 1960; Kluchnik, Starostina, 1963), showing inverted reproductive style in the urban environment, when winter reproduction is more effective than the one during the warm season (Moskvitina, Suchkova, 1995). Its ration includes juicy plants and roots in the vegetable stores, forms local groups in the cities with higher population density (2,0–13,0 animals per 100 days) compared to natural habitats (0,04–3,0). Such determinants as architectural transformation and disappearance of previously inhabited sites, most probably pushed this species dispersion all over the territory, and East European vole is also seen on streets in the last years. It was registered even on the territory of isolated park with full field mouse domination, and its count increases. Greenhouse complexes, present on this territory and making environment attractive for the vole, have probably created favorable conditions for the local group formation.

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ORGANIZATIONAL AND POPULATION RATIONALE FOR ANIMAL BREEDING AND USE IN THE ALTAI REGION IN 1970–1990

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In the 1970–1990s, Altai Region achieved significant results in hunting. Commercial hunting of moose increased 5,4-fold since 1976, 1,7-fold in Omsk Province, 2,2-fold in Novosibirsk Province, and remained unchanged in Kemerovo Province. In terms of moose hunted per forest area unit, in Altai Region they got 15 times more than in Kemerovo Province, 24,6 times more than in Omsk Province and 4,7 times more than in Novosibirsk Province (from 965 to 5159; from 511 to 530; from 140 to 234; from 591 to 1298, respectively). 58,4% (N = 37,700) of the total moose population was from Altai Region. With regard to roe deer, Altai Region increased hunting 113 times (up to 1700) during 15 years, whereas Kemerovo Province did not hunt roe deer at all. Omsk and Novosibirsk Provinces hunted about 100 heads each, or 15 times less than Altai Region. For the purpose of beaver re-acclimatization prior to 1964, 99 individuals were released inn Altai Region, 145 in Kemerovo Province; 232 in Novosibirsk Province; and 335 in Omsk Province. About 900 beavers were hunted in Altai Region, 3,8 times less in Kemerovo Province, 6 times less in Omsk and Novosibirsk Provinces in 1990. In 2008, the total moose population in the regions was 18,500, including 35% in Altai Region. Over the last 20 years, there occurred 1,7-fold drop in the proportion of Altai Region moose and 1,6-fold drop of roe-deer population.

Previously, that success occurred due to implementation of rich experience, work of qualified and honest professionals, their training, and supervision. Only non-demanded land holdings were used as lands available for hunting. At present, according to the law of 24.07.2009 No. 209-FZ “On Hunting...”, the entities of Russian Federation are required to have at least 20% of public or impersonal lands. Game managers and rangers independently monitored game resources by with the occurrence lists. From November to January, they used occurrence lists to monitor migration, structure and growth of ungulates populations; and based on that, they quickly changed hunting rate at the expense of hunting license reserves (Bondarev, 1978, 2010). The factors limiting fauna were identified and diminished. Many biotechnical measures were conducted (planting willow and aspen to cut back to stump, growing wild rice, making many nest boxes for common goldeneye, and yearly repair, making small ponds, etc.). The game was hunted based on assigning hunting areas to hunters on a long-term basis; beaver was selectively bred using Canadian and domestic techniques. Moose was shot selectively, and hunter labor was paid on carcass basis. The proportion of hunted young animals increased. Stud moose bulls and cows were kept for breeding. Hunting for ungulates was supervised. Hunters were given coupons to transport meat and skins, in which the date and place of delivery were indicated. Professional and amateur hunters were advised to be involved for free in biotechnical and animal protection activities; some of them were public hunt inspectors. The established and promoted public hunting inspection. More poachers were found in the Altai Region than in the Kemerovo and Novosibirsk Provinces each year; although those regions had twice as many hunters and potential violators of hunting rules. Mobile groups were most successful to combat poaching, acting independently of the local authorities and law enforcement agencies. Those mobile groups included 12 inter-district game managers and 3 state hunting farms. Game reserves and breeding grounds were important for the conservation and reproduction of game reserves. There were 70–77 rangers in the game reserves, leaving only 17 today! Hunting grounds belonging to hunting societies employed 90 gamekeepers. Some game reserves acted as “schools-workshops” of biotechnical activities, game protection, trapping roe deer, capercaillie and muskrat for acclimatization, and even outside the region. The work of state hunting inspection and hunting area users was evaluated based on the game population dynamics, game occurrence in the grounds, and the effectiveness of state hunting land protection. On the state hunting farms, the work was evaluated through integrated development of biological resources, their processing and sales on domestic and foreign markets. The state hunting farms were self-supporting and profitable.

THE IMPACT OF CLIMATE CHANGE ON SMALL MAMMAL POPULATION DYNAMICS: A LONG-TERM DEMOGRAPHIC STUDY ON ROOT VOLES

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Weather is known to be one of the most basic factors impacting animal populations, therefore climate changes should generate impacts on their population dynamics. In this study we analyzed long term data (1993–2016) from the root vole (*Microtus oeconomus*) population which lives in the valley of natural lowland European river Biebrza (Poland). We decompose the annual density-dependent and density-independent structures into their seasonal components. As density-independent factors we used local climate factors (mean, minimum and maximum values of ambient temperature, precipitation, number of days with precipitation, snow depth and number of days with snow cover, water level) and the North Atlantic Oscillation (NAO)

The partial rate correlation functions (PRCF) showed that the dynamics of the root vole population was dominated by first-order negative feedback, whereas second-order negative feedback was not significant. Direct density-dependent feedback process explained over 50% of variation in the data, while second-order negative feedback was less important.

During the entire study period, in autumn-to-autumn population changes of the studied populations second-order feedback was not significant and NAO alone explained 20,1% of total variation of population increase rates. For the period 1993–2007 second-order negative feedback explained highest proportion of variation of growth rates when compared with different time windows. For this period PRCF also showed that the dynamics was dominated by first-order negative feedback. Moreover, the effect of NAO was weaker and marginaly significant. Also the direction of the effect of NAO was opposite to the one observed during entire study period.

When analyzing seasonal population increase (autumn-spring and spring-autumn), we found that solely spring-to-autumn change of population density was positively affected by NAO. This variable explained 13,5% of population increase variation. Absolute value of summer population density increase was mainly affected by spring density and these two variables (NAO and spring density) explained 86,4% variation of population density change. However, autumn to spring population decline was marginally significantly affected by previous year autumn density of voles but not by NAO, whereas numerous climatic variables had significant effect on winter change of population density of voles. Additionally, none of these variables was significant when applied in the model separately, what indicates that most probably simultaneous effect of different factors affected winter decline of population density. All variables explained 84,5% of variation of this parameter. Overall population increase rate (autumn to autumn) was driven significantly by summer increase rate, NAO and autumn density of voles in previous year.

Our results illustrate that the vole cycles existed during the first part of the study (1993–2007) and then disappeared. In the same time effect of NAO on population dynamics was weak and insignificant. Whereas, in the next time window (2008–2016) the importance of changes in global weather (characterized by NAO) on root vole population dynamics was strong enough to collapse the cycles. These results indicate that recently observed global changes my by dampening vole cycles not only by snow shortage but also by more complex weather changes.

POPULATION VARIABILITY OF THE BONE MARROW ERYTHROID BLASTEMA IN THE CAUCASIAN SNOW VOLE (CRICETIDAE, RODENTIA) IN MIDDLE MOUNTAINS OF THE WESTERN AND CENTRAL CAUCASUS

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We first studied the bone marrow erythropoietic function in the Caucasian snow vole (*Chionomys gud* Satunin, 1909,) under sectoral mosaicity of the Caucasus at 1800–2000 m above sea level (MASL) during summer. *Ch. gud* is a typical mountain mammal species and the Caucasus endemic; it’s distribution is irregular, and embraces the alpine, subalpine belts and some areas in the forest belt of the Great Caucasus, from 600 to 3500 MASL (Gromov, Polyakov, 1977). We studied three populations: two populations were from the Central Caucasus – the Elbrus population (vicinity of Elbrus village, Elbrus vertical zonation) and the Bezengi population (vicinity of Bezengi village, Tersky vertical zonation); and the third population was from the Western Caucasus – the Lagonaki population (vicinity of Lagonaki plateau, Kuban vertical zonation) (Tembotov et al., 2001).

The cellular constitution of the bone marrow erythroid blastema in three *Ch. gud* populations was represented by erythroblasts, basophilic normoblasts, polychromatophilic normoblasts and oxyphilic normoblasts. Most cells include oxyphilic normoblasts – mature cells testifying to hematopoiesis normality.

In the comparative analysis, we found that the total number of erythroid cells was similar between groups and comprised 23,92% in males and 25,23% in females of the Elbrus population; 24,19% in males and 25,70% in females of the Bezengi population. There were approx. 75% leukoblasts. In the Western Caucasus, under conditions of warm and humid climate the bone marrow erythropoiesis function of the Caucasian snow vole was significantly suppressed, and the corresponding numbers were 19,26% in males, and 18,35% in females. Leucocyte counts increased to 80%. Partial erythrograms comparison showed similar differences. In arid and cold climate, in the animals of the Elbrus population the increase in total count of the bone marrow erythroid cells corresponded to a significant erythroblasts increase, unlike two other populations. Basophilic normoblasts count in all three groups did not differ. Most polychromatophilic normoblasts were found in Bezengi population, living under conditions of warm and arid climate. We also found larger quantities of mature cells, such as oxyphilic normoblasts in Lagonaki population. We could not identify sex dimorphism in this comparative analysis.

In summary, we recorded bone marrow erythropoietic variability in *Ch. gud* under different ecological and geographical conditions in middle mountains of the Western and Central Caucasus. The highest erythropoiesis activity was found in Central Caucasus, being indicative of stressed erythropoiesis under these conditions. Western Caucasus environmental conditions seems to be the most favorable for the Caucasian snow vole, because of the least stress.

A MATRIX MODEL OF AN ENDANGERED POPULATION OF THE ARCTIC FOX FROM MEDNYI ISLAND

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Mednyi Island (Commander Islands, Pacific Ocean) houses an island subspecies of the Arctic fox (*Vulpes lagopus semenovi*). This unique population occupies the most southern part of the species' range and has been isolated from other populations for tens of thousands years. It is included in the Red Book of the Russian Federation as an endangered subspecies. Conservation of the population requires a thorough assessment of its vital rates.

Up until the 1970s, the population number was maintained at up to 1000 animals, but an epizootic of ear mange that occurred among juveniles from 1976 to the mid-1980s, wiped out most of the population (Goltsman et al., 1996). Now the population number is about 150 adults only. A long-term population study has covered the southern part of the island where 60–90 marked Arctic foxes have regularly been found (Goltsman, Kruchenkova, 2001; Goltsman et al., 2005).

A demographic mechanism underlying population stability observed in the last 20 years is unclear. To reveal it, the one needs to estimate age-specific vital rates and then find out which of them affect the growth rate of our population most strongly. The idea behind this approach is that even small changes in those critical vital rates can destabilize the population and thus potentially lead to extinction. To this end, we build up a female-based Leslie-type population matrix model (Leslie, 1945). Each non-zero element of this matrix is either age-specific survival or fecundity. Age-specific survival is the probability of a female of a given age to survive to the next age class; age-specific fecundity is the average number of female offspring born to a mother of a certain age, accounted for non-breeding females.

We analyzed individual life histories of 220 females born in 1997–2010 and marked as juveniles. The study area covers about 26,2 km^2 in the southern part of Mednyi Island. We used a mark-recapture framework and registered marked animals every year to assess survival rates. We also conducted multi-day observations of dens to determine the number of juveniles. We excluded families with >1 lactating females as it was not clear how many offspring each female had.

We allocated all the animals to 7 age classes: juveniles, yearlings, two- to six-year-old adults. We omitted very few females older than 6 years old.

To date, we have obtained preliminary survival and fecundity rates which are, respectively: juveniles – 0,393 and 0 (n = 220); yearlings – 0,865 and 0,070 (n = 86); two-year-olds – 0,757 and 1,074 (n = 64); three-year-olds – 0,659 and 1,259 (n = 40); four-year-olds – 0,611 and 1,364 (n = 26); five-year-olds – 0,4 and 0,225 (n = 17); six-year-olds – 0,5 and 1,436 (n = 6). Population growth rate based on these vital statistics is $\lambda = 1{,}002$, which corresponds very well with count data according to which the population is stable.

In the future, we are going to refine the above vital rate estimates and conduct sensitivity analysis of the population growth rate. Sensitivity analysis is a tool to find out which vital rates most severely affect the population growth rate. This knowledge will help prevent extinction of the unique Mednyi Island population of the Arctic fox.

SPECTRAL ANALYSIS OF MULTI-YEAR VARIABILITY IN PARAMETERS OF REPRODUCTION OFG THE BLYTH'S REED WARBLER (*ACROCEPHALUS DUMETORUM*) IN THE BARABA FOREST-STEPPE

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Long-term dynamics of fertility and such an important reproductive parameter of birds as the size of eggs, in contradistinction with interannual population size fluctuations, are poorly described. By monitoring annual average reproduction parameters and putting results on time scale, we can assume that process of varying size of clutch and the size of eggs is stochastic. At the same time, this cannot be a purely probabilistic process, as breeding and all of its components are cyclical. If the processes are cyclical, they can be adjusted in accordance with the laws of chronobiology to the external and internal cycles and thus to get adapted to them. The purpose of our research was to find out whether there are any periodic components in the multi-year changes of clutch size and in the dynamics of the egg-morphological parameters of Blyth's Reed Warbler (*Acrocephalus dumetorum*) as one of numerous species of passerine birds of the Baraba forest-steppe (The South of Western Siberia**).**

We carried out the spectral analysis of long-term (1977–1999) data on reproductive indicators of Blyth's Reed Warbler in the population near the Lake Chany. In total, 942 clutches were surveyed, 4226 eggs were measured, 2606 nestlings were ringed, and 788 adult birds were captured in nests. Egg length L and maximum diameter (width) B were measured with calipers (scale division 0,1 mm). Egg volume V and shape (roundness) index S_{ph} were calculated as $V = 0{,}51 \times LB^2$ (Hoyt, 1979) and $S_{\text{ph}} = (B/L) \times 100$ (%) (Mänd, 1988). When studying the variability of egg-morphology parameters, arithmetic mean of all the eggs in each clutch was taken as the baseline data, as well as the coefficients of variation inside the clutch (CV). We used the programs possessed by institute for the spectral analysis.

Using spectral analysis of the long-term dynamics of clutch size, we identified four harmonic components of the process. The most powerful harmonics, which can be assumed, based on the chronogram analysis, was approximately two-year period. The 24-year periodic component appeared to be the second in power. Two nearly equally powerful harmonics (about 6 years rhythm and about 3 years rhythm) also performed well on the spectrum. These periods were likely related, as they were multiples of each other. The most powerful frequency is synchronized with the 2-years nature rhythm of that area, which is featured in fluctuations of the majority of climate characteristics and is also evident in the yield of herbaceous plants. This rhythm showed adaptability of clutch size to short-term environmental changes. There was also possible adjustment for changes inside the population, for example, it can be adjustment for the fluctuation in the age structure of breeding pairs, which largely depends on the reproduction success in the previous year. Concerning the 24-years cycle of clutch size, dynamics should be considered nor as a tactical, but as a strategic tool for long-term adaptation to changes in external conditions. Harmonic component with a 6-year period in this area is described as watering frequency (Bezmaternykh et al., 2009).

Long-term dynamics of egg diameter and egg volume changes have similar powerful periodic components in the medium frequencies (near 8-year rhythms) and low power in high frequencies (rhythms about 3 years long). These parameters directly depend on each other that also cause the synchronicity of their changes. With large similarity of chronograms changes of the eggs length and its roundness index, their spectra differ markedly. High-frequency fluctuations in the number of eggs in clutch are synchronous with egg-morphology characteristics. Noticeable differences were identified only in the low-frequency periodic components, which were absent for cyclical egg-morphology parameters (except for shape index).

GENETIC POLYMORPHISM AND DIFFERENTIATION OF RUSSET GROUND SQUIRREL POPULATIONS IN VOLGA REGION

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We conducted ML-analysis of Russet Squirrel's D-loop fragment's sequences ($n = 22$) with evolution model HKY. D-loop fragments' variability level was high (for intraspecific level) and varied from 0,0 to 11,8% (3,6%). The resulting cladogramm united geographically isolated populations in three groups (metapopulations) – G1 Left-banked, G2 – Right-banked (cutting Ul'yanovsk Region on Southern and Northern parts along the river Syzranka) and G3 – Volga. Sequences' variability inside metapopulations was low (G1 – 0,57%, G2 – 0,04% and G3 – 0,07%). Interpopulation differences were higher and overlapped the intrapopulation differences (0,2 – 11,4%).

The analysis of haplotypic and nucleotide diversity (D-loops) of Russet Ground squirrel's populations allowed distinguishing nine haplotypes ($Hd = 0{,}658$, $Pi = 0{,}0336$ and $k = 34{,}2$). D-test (Tajima) discovered intriguing features of population structure of the Right-banked part of Russet Ground squirrel's area. Although unreliable ($0{,}1 < p$) but close to zero (0,265), D-values possibly pointed to the genetic population equality and absent selection. Median net (NetWork 4.6.1.2) mostly confirmed data, which were obtained in the previous analysis. Median test results indicate the presence of two groups of genetically close populations living on the opposite banks of Syzranka.

The study of genetic structure of Russet Ground squirrel's populations using microsatellite markers by gamete fixation index found high level of genetic diversity of *S. major* local populations. Total F_{ST} of three loci was 0,477. When compared to similar data on the North American species of genus Spermophilus, it is obvious that populations of Russet Ground squirrels are isolated with insignificant level of gene flow between them. Gamete fixation indices confirm accuracy of Russet Ground squirrel metapopulation structure as of the mtDNA variability data. In the hierarchical row of fixation indices, we found insignificant trend to their approximated values increase. Therefore, proposed populations grouping has the right to exist but needs more evidence.

Genetic distance ($\delta\mu^2$) analysis based on stepwise mutation model between populations in distinguished groups (metapopulations) on microsatellite data (STR1) shows lower variability when comparing mean and max values only in G1-metapopulation (Left-banked Syzranka) (0,480, 4,000) compared to G2 (Right-banked Syzranka) (0,895, 2,983). It means that divergence of population from second group occurred later, and distribution of Russet Ground squirrel in the Left-banked Syzranka occurred recently.

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CORRELATION OF REPTILES BODY TEMPERATURE WITH MICROCLIMATIC ENVIRONMENTAL FACTORS

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It is well known that reptiles are ectothermic animals, their body temperature is variable, depending on the state of environment; however, it has been proved to not always coincide with it (Cherlin, 2012; Litvinov, Ganschuk, Chetanov, 2013). This partial independence is achieved by physiological and behavioral adaptations (Shilov, 1985). But the reptile's ability to regulate its own temperature is rather weak. Accordingly, the geographical spread and habitat distribution of certain species of reptiles are related to the microclimatic environmental factors (Cherlin, 2015). However, the degree of body temperature correlation with different microclimatic parameters is often not addressed.

The aim of our study was to estimate the correlation of reptiles body temperature with such microclimatic parameters as substrate temperature, surface air temperature, relative humidity, power density of ultraviolet radiation, visible light, heat flow, and total solar radiation.

Our own data on 5 species of reptiles was used for this analysis: steppe viper ($n = 52$), grass snake ($n = 59$), sand lizard ($n = 61$), steppe-runner ($n = 76$), spotted toadhead agama ($n = 193$). We collected the material in the Kamsky Predurale and the Lower Volga region from 2006 to 2014.

We considered temperature of the internal cavities (esophagus or cloaca), measured at the time of reptiles capture as body temperature. Microclimatic parameters were recorded at the site of an animal trapping, as we believe that finding the reptile in this or that point is not accidental, but is conditioned by behavioral responses to changes in external factors.

The analysis of body temperature distribution and microclimate parameters for the species studied showed that the distribution of the majority of samples significantly differed from normal. We used non-parametric Spearman's rank correlation coefficient at a later stage in this analysis.

We obtained the following results (we only present correlation coefficients with 1% significance or lower).

The steppe viper. There was a strong positive correlation with the temperature of the substrate (0,83) and the surface air (0,84), while correlation with a power density of the heat flux (0,52), UVB (0,39), visible light (0,56) and total solar radiation (0,54) was significantly weaker.

Grass snake. There was a positive correlation with only the temperature of the substrate (0,68) and the surface air (0,71).

Sand lizard. There was a positive correlation with only the temperature of the substrate (0,74) and the surface air (0,79).

Steppe-runner. There was a strong positive correlation with the temperature of the substrate (0,73) and the surface air (0,70), while the correlation with a power density of the heat flux (0,38), visible light (0,31) and the total solar radiation (0,31) was significantly weaker.

Spotted toadhead agama. There was a strong positive correlation with the temperature of the substrate (0,73) and the surface air (0,81), weak positive – with a power density of visible light (0,19).

In all cases strong positive correlation with body temperature and the temperature of the substrate surface air was noted, quite expected, but the most thermophilic species also had a significant correlation with different parts of the solar radiation spectrum. We hypothesize that the body temperature of less thermophilic species does not so strongly correlate with microclimatic factors of the environment.

SEXUAL DIMORPHISM OF METRIC AND MERISTIC CHARACTERS OF FLAT-TAILED HOUSE GECKO *HEMIDACTYLUS PLATYURUS* (SCHNEIDER, 1797) (REPTILIA, SAURIA, GEKKONIDAE) ON THE TERRITORY OF LARGE CITIES OF THE SOUTHEAST ASIA (BANGKOK, VIENTIANE, PHNOM PENH)

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Sexual dimorphism in metric and meristic characters of flat-tailed house gecko (*Hemidactylus platyurus* (SCHNEIDER, 1797)) was studied only generally. There are data on individual characteristics, obtained in the study of restricted areas and small material (Zug et al., 2007; Nerad, 2010). Mainly linear dimensions of the body were analyzed, and the signs of pholidosis were not considered at all. Meanwhile, stydying differences between males and females based on pholidosis has both theoretical and practical importance, in particular to determine the sex of juveniles (Peskov et al., 2010).

The aim of the study was to assess the sexual dimorphism *H. platyurus* using the range of metric and meristic characters on the territory of large cities of the Southeast Asia (Vientiane, Bangkok, and Phnom Penh).

Our material were 588 specimens of 3 localities: Bangkok (Thailand) = 154 females and 134 males; Vientiane (Laos) = 85 females and 68 males; and Phnom Penh (Cambodia) = 80 females and 67 males. We considered the following metrics: L – body length from the tip of the snout to the front edge of the cloacal slit; D. r.–o. – distance from the front edge of the eye to the end of the muzzle; D. tym.–o. – distance from the rear edge of the eye to the ear hole; L. f. – width of the forehead between the eyes; Sp. in. - width of the nostrils; Lt. c. so. – width of the head at the level of the junction of the second and third infralabial scales (on the outer edge); Sl. – number of supralabial scales; P. sl. – number of the next row of scales in contact with supralabial scales ; Il. – number of infralabial scales; G. il. – number of the next row of scales in contact with infralabial scales; Im. – amount of chin – shields scales; G. im. – number of the next row of scales for chin – shields scales; Ds – number of binate scales on the toe paws; Ads – number of non-binate scales on the toe paws; Sum. – amount of binate and non- binate scales on the toe paws. We considered bilateral metrics with no regard to the character of display from the right or left.

Data analysis was performed using stepwise discriminant analysis (“STATISTICA”, version 10.0 (StatSoft, Inc., 2010, USA)) with the successive inclusion of relevant variables in the model. After the analysis of the initial set of 42 attributes, only 12 were included in the model: D. tym.–o, G. il., G .im., L. f., Ds4, Sum10, Im., Ds7, Ads5, Ds3, Ds1, and L. The percentage of correct (true) assignments of males and females in their area of distribution for 298 females was 69%, 205 were identified as females and 93 as males. For 265 males, this ratio was 62%: 101 as females and 164 as males. The total percentage of success for inclusion in the group was 66%. In the next stage of the analysis, we cut the list of selected signs, whose contribution was more important in the intergroup differences. Of 12 signs, we removed the features, for which a statistically significant level of importance was equal to or greater than $p \geq 0.01$. The number of informative complex of signs included two morphometric features: D. tym.–o., L. f. and three meristic (G.il. G.im. Sum10) signs.

LONG-TERM FLUCTUATIONS AND STABILISATION OF NUMBER OF RODENTS: THE CAUSES AND FACTORS

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As a result of continuous stationary research from 1983 to 2015 in Middle Urals it was found, that the number of rodents dropped only once in 1984. Moreover, field experiments with additional food supply that year resulted in preservation of modeling species (bank vole) quantity at high level within experimental territory. Later on, from 1985 to 1993, the number of bank voles fluctuated in different directions around 50 ind./ha on average, reaching the peak of 112 and 160 ind./ha twice in 1989 and 1992 accordingly. After that, the number of rodents modeling species reached its peak level twice in 1994 and 1995. During the second year of very high animal quantity (156 ind./ha) in Middle Urals, a catastrophic mass windfall of forest because of squally wind strengthening occurred in spring. The number of bank voles decreased accordingly to 34 ind./ha in the following year of 1996. At this time, a year after the catastrophic mass windfall, parallel to substantial improvement of environment protection, food capacity of ecosystem did not improve because of significant deterioration of grass layer as typical wood vegetation. However, already in 1997, intensive cereal and motley grass vegetation began on the open windfall territories. As a result of that, in 1997 the number of a modeling species reached its peak of 162 ind./ha.

Subsequently from 1998 to 2004, the total number of voles in autumn regularly reached the peak counts. During the period of 2005 until 2015 in Middle Urals, the number of rodents modeling species in the end of reproduction season regularly reached the peak levels. This phenomenon was a consequence of synergetic (joint) effect of the trophic factor and the factor of protective conditions of rodents' environment after catastrophic mass windfall, when cereal and motley grass vegetation prevailed because of biotopes and seral processes clarification. In these conditions, the stationary large (from 1 to several hectares) population units of voles appeared with the abnormally high number of individuals on the places of numerous windfalls, as a result of natural processes of vole's population self-organization. Finally, a long and steadily functioning network of saturated and viable rodents' settlements was formed on the territories of mass windfall, which affected the biotopes surrounding windfalls.

APPEARANCE OF CHICK PERSONALITIES IN THE COLONIES OF CHARADRIIFORMES SPECIES

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The phenomenon of stable combinations of behavioral characteristics among animals has been known for about 20 years. In those cases, when it comes to the temporal stability of behavioral types, existence of personalities is suggested. Actual evolutionary explanations for the phenomenon of personalities are based on a rigid connection between individual behavioral characteristics within a single individual. However, from the classical view of the natural selection, the existence of a stable community of rigid behavioral “carcasses” within the population is unlikely to be the optimal being of the latter. Due to a gradual process of formation of behavior we should expect the most plasticity of personalities to occur just in the early stages of ontogeny, due to rapid changes in the environment of young individuals as its growth and development, in addition to the fact that the greatest selective pressure falls on the younger age classes. In recent years this led to a pronounced interest to ontogeny of personalities and distinguishing rapidly changing behavioral type (or profile) of the animal from the corresponding more stable inner matrix – personality.

Here we consider the role of the social environment of young individuals in the development of its individual behavioral characteristics. Charadriis colonial species, especially gulls and terns are best conform to this goal, due to the broad diversity of social interactions in their colonies and rapidly changing social environment of chicks before fledging. We’d present several examples of how social relations in the colony can interact with emerging behavioral type and affect the fitness of its carrier. In Black-headed Gull nest density facilitate chicks to contact each other earlier and more intense, but does not affect aggressive behavior. That is, the latter develops mainly influenced by inner, non-social factors. In this species we have found different and sustainable behavioral types of coping with mild stress (forced moving of the chicks to the familiar place near the colony), consisted of the more or less protracted exploring of the place where they were already moved. It is shown that chicks that are actively responding to the new environment, are less common to steal food from their neighbors, but consistently respond with aggression to the visits of the neighboring chicks on their nests. In Black Tern chicks increased frequency of inter-brood contacts does not affect aggressive behavior (in Black Tern aggressive contacts among the chicks are relatively rare), but usually is accompanied with a high rate of kleptoparasitism and also contributes to the greater mobility and exploratory rate in the new environment. In the Black-headed Gull the observed behavioral types varied in mass at hatching (so-called “Active” type was haevier), but later the differences disappeared. In those Black Tern chicks who had more inter-brood contacts, in contrary to the gull chicks, hatchlings did not differ in mass, but grew more slowly later on. We believe that a social environment of the nest colony influences the expression of individual behavioral traits, encouraging those that are most relevant to the chick needs at the given step of ontogeny.

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POPULATION STRUCTURE OF KILLER WHALES *ORCINUS ORCA* IN THE RUSSIAN FAR EAST SEAS

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Killer whales of the Russian Far East seas were traditionally considered a single population. However, in the last decades it was shown that many cetacean species consist of separate populations despite the lack of physical barriers in the sea and the ability to travel over large distances. This may be the result of ecological conditions heterogeneity as well as cultural traditions, because social learning plays an important role in cetacean behavior. In this study, we analyzed the population structure of killer whales from the Russian Far East seas.

We compared mitochondrial and nuclear markers in skin samples of killer whales from different regions, and analyzed re-sightings of individually identified killer whales in different regions. For genetic analysis, we used 100 killer whale biopsy samples from five regions: Avacha Gulf (50 samples) and Karaginsky Gulf (2 samples) of Kamchatka Peninsula, waters of the Commander Islands (13 samples), Kuril Islands (7 samples) and western Okhotsk Sea (28 samples). For photoidentification we used photographs obtained during ship and land-based surveys in these regions in 2000–2015.

Cluster analysis of microsatellite markers in Structure software divided the samples into two clusters: 75 samples belonged to the first cluster and 35 samples to the second. These clusters were rather sympatric: samples from both clusters were found in Avacha Gulf and the Commander Islands; nevertheless, we have never observed animals from different clusters in the same group or aggregation. Only samples from the first cluster were found in Karaginsky Gulf and Kuril Islands (probably due to small sample size), and only samples from the second cluster were found in the western Okhotsk Sea. Besides differences in allele frequencies, each cluster also had unique alleles that were not observed in another cluster.

No mitochondrial control region haplotypes were shared between these clusters. All killer whales from the first cluster had the same haplotype, while the second cluster had three haplotypes.

Comparison of photo-catalogs across regions showed high level mixing between different regions of Eastern Kamchatka and the Commander Islands. From 733 killer whales identified in Avacha Gulf, 51 animal was spotted in Karaginsky Gulf, and 143 – in the Commander Islands. However, we found no matches between Avacha Gulf and Northern Kuril Islands. Killer whales, identified in the western Okhotsk Sea, were not encountered in other regions, except for one winter sighting in Severo-Kurilsk town.

We found no genetic differences between killer whales from the first cluster from Avacha Gulf and Kuril Islands. We also found no genetic differences between killer whales from the second cluster from the western Okhotsk Sea, Avacha Gulf and the Commander Islands. Therefore, our results indicate the presence of two partially sympatric populations, and several local stocks within each population that have no observable genetic differentiation.

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TOTAL EVAPORATIVE WATER LOSS AT DIFFERENT AMBIENT TEMPERATURES IN BIRDS: ASSOCIATION WITH METABOLIC RATE AND BODY MASS

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Correlates of basal metabolic rate (*BMR*) and total evaporative water loss (*TEWL*) was studied in captive birds using literature data (Gavrilov, Dolnik, 1985, Gavrilov 1995, 1997, 2014, 2015; Williams, 1996; McNab, 2009, 2015) and original data from more than 60 species of Passerine birds and 30 species of Non-passerine birds during summer and winter seasons and in different ambient temperatures. We combined data for 102 species of birds from Table 1 from Williams (Williams 1996) and our data for 157 birds' species at thermally neutral temperatures (mostly 25 °C) to improve the statistical significance. The association of *TEWL* was body mass was as follows: *TEWL*25 °C Aves = $0{,}28\ m^{0{,}70}$, $R^2 = 0{,}92$, where *TEWL* is expressed as g H_2O/day and *m* is body mass (g). McNab (2009) showed that the power of body mass describing *BMR* in birds was 0,652 ± 0,007. The power of body mass describing *TEWL* in birds was 0,701 ± 0,007, which was 0,05 greater than in *BMR*. The relation in the equation between body size and *TEWL* is higher than between body size and *BMR*. If the dichotomy between passerines and non-passerines is added, the power describing *BMR* becomes 0,721 ± 0,009, or 0,705 ± 0,010 and the power of body mass describing *TEWL* in Passeriformes and Non-Passeriformes is 0,754, which is 0,05 greater than in *BMR*. The relationship between *TEWL* and body mass shows that the ratio of *TEWL* to body mass in passerine birds is higher than in non-passerine birds at all ambient temperatures (0 °C, T_{lc}, 25 °C, and T_{uc}). The dependence of water loss from the body mass at different T_{A} varies in a similar way as the correlation between evaporative and non-evaporative heat loss. In Passeriformes, *TEWL* is approximately 25–40% higher than in non-passerines (particularly at high T_{A}), which is consistent with the ratio of their *BMR* levels. Thus, a large expenditure of evaporative water determines the cost of the advantages of *BMR* increase and results in a higher energetic capability. This expenditure increased with the body size in Passeriformes due to the forced evaporative heat loss and showed virtually no increase in Non-Passeriformes. In Non-Passeriformes, there were nearly equal increases in the evaporative water loss and metabolic rate in summer and winter, suggesting that this group maintained heat balance even at the upper critical temperature, which is the ambient temperature at which additional mechanisms are insufficient to balance out the invariable *BMR* heat production. This requirement imposes strong limitations on the size range of Passeriformes. A high basal metabolic rate (*BMR*) in Passeriformes includes not only net benefits but also its maintenance that requires a definite cost. These findings suggest that the high level of basal metabolic rate in Passeriformes in comparison to Non-Passeriformes determines the necessity for them to utilize considerably greater amounts of water for evaporation to maintain a sufficient heat balance at high ambient temperatures. This requirement imposes strong limitations on the range of group size, and despite the considerable ecological and energy advantages of such high *BMR* levels, this pattern is not often found in other groups of endothermic animals. A considerable evaporative water loss reflects the cost of the higher *BMR* and energy capacities of Passerines in comparison with Non-passerines and other orders of endothermic animals. As shown in the previous study (Gavrilov, 1997, 2014), an increase in *BMR* resulted in an increase of the maximal existence metabolic rate and potential productive energy, which expanded the ecological capability. These changes confer many benefits but minimize the optimal size. The analysis of the allometric regressions for the energetic parameters shows that Passerines with a body mass ranging from 5–150 g have significantly higher productive energy than Non-Passeriformes (Gavrilov, 1997, 2014). About 80% of Passeriformes species have body mass in this range. Thus, a large expenditure of evaporative water is the cost of the higher *BMR* in Passeriformes than in Non-Passeriformes.

THE IMPACT OF FOREST MANAGEMENT ON A DIVERSITY OF SELECTED GROUPS OF INSECTS AND BIRDS

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One of the aim of “close to nature” forestry is to maintain forest biodiversity and vulnerability to disturbances. However, we cannot predict time, type and scale of future disturbances which may affect forest ecosystem. Additionally, forestry activities in themselves are a forces of artificial selection which create unknown pressure on forest ecosystem. Therefore it is necessary to conduct long-term observations of natural processes in commercial forests and to use this knowledge in forest practice. Such project, financed by Polish State Forest Enterprice, was started in Polish Forest Research Institute in 2012 and assumed the permanent exclusion of forest management practices from some areas of commercial forests as a reference for forestry. Such places have been selected in 12 forest complexes evenly distributed in the country, in the old stands representing the major types of forests and forest habitats in Poland. Observations and measurements were also carried out on the similar areas with forestry management activity.

Monitoring applied to the following elements of the forest ecosystem:

- stand spatial structure,
- dynamics of natural regeneration,
- amount of dead wood,
- the rate of decomposition of organic matter,
- biodiversity of the forest ecosystem measured by the various parameters (forest birds, fungi, beetles and flora).

Our presentation illustrates selected results of the observations and measurements conducted in the initial stage of the project. We not found any relationship between saproxylic beetles and analysed forests characteristics, among them – Coarse woody Debris (CWD) (amount, type and decay class) and forest tree basal area. Biodiversity of forest bird species (BSD) was not related with CWD, whereas it was slightly related with tree basal area. Our results show that in commercial forests probably there is no simple ratios between elements which are considered as a very important for the biodiversity and components of such biodiversity.

RACCOON IN NORTH CAUCASUS – POST-INTRODUCTION DEVELOPMENT AND PHENOMENON OF REPEATING “OUTBREAK” OF POPULATION

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Raccoon (*Procyon lotor*) history of introduction in fauna of the Western Europe and Russia is well described (Hohmann, Bartussek, 2001; Pavlov et al., 1973). Animals were released twice in the East Caucasus in riparian forests of Sulak and Terek rivers – in 1950 (N = 23) and 1965 (N = 30); three releases were accomplished in the Western part of the region in mountain woods: 1951 (28), 1957 (15), and 1958 (112). We initiated research on raccoon population ecology more than a half century ago. In 1979-1980, and 100 raccoons were caught by our technique for the needs of fur farming in Terek forest within a period of 11 days. We obtained data from 60 males (incl. 15 young) and 74 females (incl. 38 young).

In 1954, *P.lotor* population in Sulak River watershed was estimated to be 240 animals within the area of 320.0 km^2. By 1959, population grew up to 1,600, and in 1962 it was already 4,200–4,300 animals (Rukovsky, 1963, Pavlov et al., 1973). The beginning of 1960s may be considered the first “outbreak” of the East Caucasian raccoon population. Then artificial drying of Yangiyurt wetlands was done and resulted in decreased ecosystem feeding value for raccoons, and the population dropped to 1000 animals (1965), but later – even to 400 (1966) animals. Raccoons migrated to adjacent territories. Some of them moved to Terek forest even before the introduction in 1965. Total areal area in Terek-Sulak Basin reached 700 km^2, introduced population reached 2,500 individuals (Gineev, 1969, 1972). In 1980s, raccoons inhabited forest along Terek River from Kizlyar city to Staroshcherbinskaya Stanitsa. This period coincide with the second population outbreak, resulting in 7000 raccoons with the population density of 27 animals per 1000 ha. In 1990s, the east group border expanded to the junction of Sunzha with Terek, with is current line Terskoye – Grozny. Raccoons occupied inundated and island woods across Terek River, Chornaya Rechka, and partially in Chernogorye. Now the area inhabited by raccoons is more than 2,500 km^2 with population reaching 5,000 animals.

Western Caucasus raccoon population exists in less suitable habitats (Kotov, 1959; Yazan, 1967; Pavlov et al., 1973). In 1957, raccoons lived 90-100 km from places of release on the area of 5,000 km^2 (Kotov, Riabov 1963; Yazan, 1967). The core population (400 individuals) settled down on a 500 km^2 area with population density of 8 individuals per 1000 ha. Our later studies (Gineev, 1972) demonstrated considerable decrease in population density (1,2–6,0/1000 ha) and count (600 individuals). It took 19 years to reach a hunting level of this animal; population outbreak was recorded only 29 year after introduction (Gineev, 1989, 2016).

The current Western border of raccoon areal in Caucasus passes along the coast of Black Sea from Anapa to Sochi, northeast border – along the Kuban River up to a confluence with Urup River. Raccoons use river valleys as ecological corridors and penetrate high into the mountains. In the lowland, animals spread within the forest growing along small rivers, channels, and so-called Stalin forest belts. Nowadays (data for spring 2016) the total population of raccoon *P. lotor* in Krasnodar territory is more than 6,000 individuals, with its core in the forest district of Tuapse.

Development vectors point to habitats close to water-bodies and mountain woods as preferred territories for raccoons. The main factor defining explosive population growth is nutritive environment. Successful formation of East Caucasian population occurred thanks to rice fields system (network of channels and concrete trenches), leading to amphibians abundance; whereas adaptation to new plant food (chestnuts, acorns, fruits, etc.) fostered West Caucasian population occupying mountain-wood habitats. Development of the latter group took more time. Local distinctions in diets results in different physical condition of the animals: males from the East had a mean body weight of 6,3 ± 0,5 kg, in the West – 5,1 ± 0,2; females – 5,6 ± 0,5 and 4,0 ± 0,1 kg, accordingly.

THE MODERN CONDITION OF HERRING GULLS IN KEMEROVO REGION

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We report a multiyear population census of the gulls (1983–2015) on 50 water reserves the southeastern part of Western Siberia in the first (15.05.–15.07.) and second (16.07.–31.08.) halves of summer (Ravkin, 1967).

We describe the set of features (Ryabitsev, 2008, 2014; Firsova, 2013) of Baraba gull (*Larus heuglini barabensis* Iohansen, 1960) of the populations of large white–headed gulls, which were considered to be subspecies *Larus argentatus cachinnans* Pall. Sometimes animals with darker mantle, most probably West Siberian gull (*Larus h. heuglini* Bree., 1876) are also presents in the gulls colonies.

In the 30s of the last century, Khakhlov (1937) described herring gull in the Kuznetsk steppe only, and as rare species with unspecified nesting. Further industrialization of this region, ponds and reservoirs creation fostered fish growth in them with adjacent move of the species southeastwards. Nowadays, this species in nesting in the Novosibirsk reservoir (Andreenkov, 2015), the Zhuravlevskoe reservoir (Golovina, 1992, 2007), and in Belovskaya (Golovina, 2006) and Kara-Chumysh water reservoirs in summer. Thirty-seven Baraba gulls were counted on the lake Great Berchikul on July 15, 2009.

Depending on the nesting and feeding conditions seagulls nest in single pairs, in groups of 2–10 pairs of in colonies of over 100 pairs. Solitary nesting pairs of gulls are more common on small lakes in the floodplains of the rivers. Single breeding pairs can be seen as an adaptation to new territories and food resources. Larger numbers of gulls were observed at large lakes and reservoirs.

During the first decade of Zhuravlevskoe reservoir filling, the number of Baraba gulls increased from 43 breeding pairs (1984) to 130 pairs (1990), and the average count in summer was 95 and 294 individuals, respectively. After that, the number of nests dropped. Due to willow (*Salex* sp.) and cane (*Phragmites australis* Gav.) growth with adjacent nutrition worsening, gulls stopped nesting. There were only 17 nests and 63 gulls in 2008. Currently, there are no more than 20 pairs of gulls nesting there. Average count in summer of 2015 was 62 individuals. For the period 1984–2008, the number of adult baby birds per pair of gulls was 1,69 (1990) – 2,1 (2006), 1,97 on average. Quite many pairs of gulls had 2–3 adult baby birds. Single breeding pairs at the lakes of Kiya river had 3 adults baby birds quite often.

A certain part of the gulls colonies are not nesting individuals of different ages, forming separate clusters and migrating by the end of June. There were up to 50 not nesting gulls at Zhuravlevskoe reservoir. In summer, small nomadic flocks of gulls are always present the fishponds, rivers, and city landfills. In summer of 2007, there were 280 non-nesting individuals in the precipitation fields of Kemerovo Power Plant of river Tom’, which were wrongly classified as nesting flocks by Belyankin in 2007.

The population of Baraba gulls in Kemerovo region can be considered stable. The number of breeding pairs does not exceed 300. The number of migrating and non-nesting gulls in summer exceeds 500.

Baraba gull is tolerant the human activity and benefits from that. There is no tradition of collecting eggs of wild birds in the region. However, there were cases of shooting gulls at the aquaculture ponds. In the meantime, real threat to the nests of gulls are: *Mustela lutriola* L., *Milvus migrans lineatus* Gray, and *Circus aeruginosus* L. Migrating gulls in small water bodies can destroy the eggs and just born babies of ducks and other waterfowl.

THE ROLE OF LONG-TERM, INDIVIDUAL-BASED FIELD STUDIES IN BEHAVIOURAL ECOLOGY

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The long-term, individual-based field studies (LTIBS) are the studies of natural animal populations that last more than 10 years and based on individual recognition of the significant part of a population. They appeared in 1950s and now are considered not only as the most productive, but also as the most effective for scientific progress (Clutton-Brock, 2012). The individual recognition brought new opportunities to understand individual histories of animals and to measure, with a high accuracy, such population characteristics as survival and mortality rates, ageing, dynamic of reproductive activity, generative intervals, etc. The individual recognition also enabled to investigate intrapopulation variation of different parameters (for example, age-dependent variation of fertility and mortality, individual heterogeneity in life histories, behavior and reproductive strategies) (Clutton-Brock, 2001; Clutton-Brock, Sheldon, 2010). LTIBS allows to estimate costs and benefits of different behavioral tactics and social flexibility and to compare the reproductive success and survival rate of individuals with different phenotype and genotype. Finally, LTIBS is essential for analyzing social environment of individuals including the variations in the system of reproductive bonds and social structure (Silk, 2007). In the last decade, LTIBS started to play an important role in the identification of the effects of global changes of ecological conditions and their consequences in eco-evolutionary studies, i.e. in the investigations of rapid evolutionary processes going on the same time-scale as the actual ecological changes. Finally, most popular books and films on animal wildlife are based on LTIBS with animal personification.

However, there are relatively few existing LTIBS projects. According to T. Clutton-Brock (2012), who systematized the LTIBS data, there are now approximately 150 LTIBS projects for birds and mammals, and around 20–30% of them focus on primates. He considers it will take around 10 years to investigate species ecology, 10 to 30 years to investigate species demography and more than 30 years to understand animals’ reactions to long-term environmental changes. Many of the most important ecological and eco-evolutionary processes occur during a period of several tens of years and it is impossible to register them after weeks or months of observations. Long-term field projects with the individually recognizable animals are very costly, it is difficult to organize them and even more difficult to maintain, but it is the most perspective direction in modern population ecology.

THE INDIVIDUAL-BASED MODEL OF POPULATION DYNAMICS OF THE CRITICALLY ENDANGERED ARCTIC FOX (*VULPES LAGOPUS SEMENOVI*) ON MEDNYI ISLAND (NORTH PACIFIC, COMMANDER ISLANDS).

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The method of individual-based modeling rapidly gains new applications in ecology (Grimm, Railsback, 2005, 2012; DeAngelis, Mooij, 2005; McLaneetal, 2011). Several important advantages make this approach the most applicable for using in conservation biology. First, individual-based models (*IBM*) are the universal and powerful. They can work on ***ecological*** and evolutionary time-scales and describe systems containing thousands of unique entities (individuals or agents) that interact with each other and their environment. Second, *IBMs* are based on the logic of individual behavior of agents in the explicitly defined environment. System dynamics are formed by the interaction of autonomous components. These characteristics allow using *IBM* to study real demographical, population-genetic and evolutionary processes, since such models are less constrained technically than mathematical models.

We develop a spatially explicit IBM of population dynamics of the critically endangered Arctic Fox (*Vulpes lagopus semenovi*) on Mednyi Island (North Pacific, Commander Islands). Parameters of the model are derived from long-term (1994–2012) individual-based field study of behavioral ecology, diet, dispersal and demographic dynamics of the Mednyi fox population. We estimated the sex- and age-specific mortality rates and dispersal, life expectancy, sex ratio, family sizes and compositions, litter sizes, reproductive success depending on sex and age and mapped fox dens, home ranges and food patches. We parameterize the model with 47 input parameters representing resource distribution, behavioral strategies and life-history parameters of seven age classes of females and males. The ultimate purpose of the model is to explore the consequences of various environmental impacts (such as diseases, food source abundance, increase of mortality rate in different sex and age groups or artificial increase of survival and breeding rate due to human interferences) on the population structure and the dynamics of the main population characteristics. We describe the design and application of the model, and the processes of calibration, sensitivity analysis and validation with empirical field data. We test the model by comparing its predictions with field observations at the end of the 14-year period since the project's onset, i.e., 5 years beyond the time on which the parameters were based. The model matches closely the observed patterns of the Mednyi Arctic fox population, including population size, age structure, sex ratio, reproductive group number and spatial distribution.

EVOLUTION OF ONTOGENY TYPES AND ENERGETICS OF ADULT BIRDS DURING BREEDING

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A. Portman (1935, 1962), studying the development of birds and mammals, tried to create a system of the types of ontogeny based on morphological and behavioral complexity of the organization of adults. Portman thought that the main line of evolution of birds was an increase in the role of parents in raising chicks, and the altricial type of ontogeny came under regulatory control progressively developing an instinct of caring for offspring. Convincing picture of the development of parental care on the scale superprecocial – altricial drawn by D.N. Hoffman (1955, 1962). Hoffman believed that the evolutionary process of the origin of altricial birds aimed to reduce physiological stress of the female during reproductive period. Indeed, the energy value of eggs (q) changes in altricial Passerines with changing their mass (m) as the $q = 1{,}124\ m^{0{,}9438}$ kcal/egg, being $q = 1{,}910\ m^{0{,}9574}$ kcal/egg (Stark, Ricklefs, 1998; Kendeigh et al., 2012) in semiprecocial and precocial birds, which shows a greater energy price for eggs in precocial ones. However, the dependence of energy value of the eggs on species ecology is great: a greater energy contained in different precocial waterfowl and waders eggs, altricial and semialtricial penguins and Procellariiformes, semiprecocial guillemots and gulls (Nice, 1962; Dolnik, 1995). Energy consumption for the synthesis of one egg is well expressed in terms of day costs for the metabolism, in BMR (basal metabolic rate). So, the cost of altricial cuckoo egg is 0,35 BMR, and the egg of Procellariiformes costs 2,44 BMR. Of course, it is necessary to assess the number of eggs laid by a female in one season. There are usually 1–2 eggs in Procellariiformes (2,4–4,9 BMR), in the common cuckoo – about 10 eggs (3,5 BMR). The cost of feeding and heating the brood in precocial birds is less than feeding and heating nestlings and fledging in altricial birds. When feeding young, main energy costs of parents are associated with the distance from the point of prey capture to the nest. The energy cost of transporting food to the young determined by the price of pedal (1,6 *BMR*) or flight locomotion (16 *BMR* – Gavrilov, 2011). High values of energy expenditure (*DEE*) are established in the colonial sea divers (mainly altricial, semialtricial and semiprecocial) as about four *BMR* (Dolnik, 1995). Elevated energy consumption in precocial females for laying eggs are compensated with the lower energy consumption when driving the brood, while birds with altricial and semialtricial types of ontogeny have lower cost of eggs that is balanced by high energy consumption for feeding of nestlings and fledglings.

The selection for the birds that began to hunt in the air, nest in trees, rocks, holes, build complex nests, is possible only with a simultaneous increase of immaturity at birth. The immaturity at birth increases the training period of the perception and the training of coordination the sensory information and motor activity. In altricial birds, the critical imprinting periods for acoustic and visual communications are significantly stretched. Training of perception and memorization of complex signals are only possible after relative endothermy setting, the setting of effective thermoregulation – the moment when the chick is already able to keep its body temperature above 37 °C in the temperature range of adult thermoneutral zone. The critical period of imprinting of complex acoustic and visual signals coincides with the time of setting effective thermoregulation. The development of thermoregulation in precocial birds occurs very slowly inside the egg until pipping, then the speed of thermoregulation capacity grows fast, and achieved in one or several days after hatching the effective thermoregulation. In altricial birds, the thermoregulation, as well as hearing and vision, develop outside the egg under the influence of the external environment and species-specific signals. The critical periods of imprinting in precocial birds is short, being long in altricial ones. The long critical period is necessary, for example, to learn to catch prey in air, and to get capability to build a nest.

Palaeognathae do not fly and have precocial type of ontogenesis, most Neoaves are altricial, semialtricial or semiprecocial. Among Galloanseres, Anseriformes are precocial (waterfowl), Galliformes have a trend to be less precocial. The precocial type of onthogeny of waders is apparently secondary, and many waders are semiprecocial.

NOSEMA DISEASE SPREAD IN THE APIARIES OF TOMSK REGION

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Nosemosis is a threatening invasive disease of the honeybee. *Nosema* disease is widespread throughout the world and considered as one of the main causes of mass death of bees after wintering and significant economic losses in beekeeping (Bourgeois et al, 2010). Pathogens of nosemosis are two species of microsporidia *Nosema* (*N. apis* and *N. ceranae*), but microsporidia *N. ceranae* may lead to severe disease called nosemosis type C, and has higher levels of pathogenicity in comparison with *N. apis* (Higes et al, 2010; Botías et al, 2013).

One of the reasons for the rapid spread of nosemosis, including *Nosema* disease type C, on apiaries, both in Russia and around the world is the uncontrolled import of infected bee colonies to not infected areas (Mutinelli, 2011; Traver, Fell, 2011). Tomsk region is not an exception, and in recent years the bee import from the regions of Russia and CIS countries, infected with nosemosis, to the Tomsk territory quite active. On the one hand, lacking or absent quarantine measures contribute to the spread of infection; on the other hand, actively imported bees of southern origin (mainly Carpathian race) are less adaptable to the environmental conditions of Siberia and are more prone to the disease.

In Tomsk State University, a systematic study of infestation of bees by *Nosema* on the apiaries of Tomsk region using molecular genetic methods are conducted since 2012 (Ostroverkhova et al 2014, 2016; Golubeva et al, 2015). In 2012–2016, 132 bee colonies obtained from 68 apiaries of 47 settlements of 11 regions of Tomsk region were investigated. Nosemosis was detected in 40 out of 132 honeybee colonies (30,3%) and in 24 out of 68 studied apiaries (35,3%); and infestation as the bee colonies and apiaries by *Nosema* has grown significantly over the past three years. The maximal infestation rate of bee colonies and apiaries constituted more than 40% in 2014–2015, and in spring 2016, all studied bee colonies were infected with *Nosema*.

The reasons of different infestation of bee colonies and apiaries in different years can be the following: features of material collection, climatic conditions in different years, the import of infected bee colonies and other. In general, long-term studies indicate widespread nosemosis on apiaries of Tomsk region and a significant increase in the number of bee colonies and apiaries infected by *Nosema* in recent years.

Spread of nosemosis type C, caused by a highly pathogenic *N. ceranae*, on apiaries of Tomsk region is of particular concern. *N. apis* pathogen was registered in 82,5% (33 colonies) of infected bee colonies (18 apiaries, 75,0% of infected apiaries); *N. ceranae* was identified in 7,5 % (3 colonies) of infected bee colonies (2 apiaries, 8,3% of infected apiaries); and co-infection (*N. apis* and *N. ceranae*) was detected in 10,0% (4 colonies) of infected bee colonies (4 apiaries, 16,7% of infected apiaries).

The first case of detection of *N. ceranae* on apiaries of Tomsk region was described in 2013 (Ostroverkhova et al, 2014); the second case – in 2014; two cases were registered further in 2015. Finally, in spring of 2016, this pathogen was detected on two new apiaries, in which mass they described death of bee colonies (more than 50%) after winter.

The results indicate the relevance of further monitoring of morbidity of bees and apiaries of Tomsk region and Siberia as a whole, taking into account species composition of parasites for assessing and predicting of the epidemiological situation of nosemosis.

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MIGRATIONS AND GENETIC DIVERSITY OF CYCLOMORPHIC MAMMALS INHABITING THE ZONE OF LOCAL TECHNOGENIC CONTAMINATION

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The present study is focused on the comparison of the migrations of rodents, which inhabit the zone of radioactive contamination with complex configuration, and the parameters of genetic diversity based on the use of four microsatellite DNA loci (microsatellites). The research significance is stipulated by the ambiguity of views on the role of rodent migrations in the radioadaptation of animals in the zone of local incidents. The research was carried out in the Eastern Urals Radioactive Trace zone (EURT), being a consequence of the Kyshtym radiation accident at the Mayak Production Association in 1957 (Chelyabinsk oblast, Southern Urals). Nowadays, EURT zone is a unique test range for the studies of long-term consequences of chronic radiation effects in living organisms. The EURT zone is specific not only due to the spectrum of radionuclides and ecosystem structure, but also because of its configuration and dimensions. This is a narrow, extended (up to 300–350 km), heterogeneous (with the presence of “hot spots”) territory. The levels of soil pollution smoothly decrease along the axis of radiation trace with the highest levels observed at the source of radiation accident. However, the level of radiation falls quite sharply in both cross directions. Model species of rodents – mice and voles (pygmy wood mouse – *Sylvaemus uralensis*, field mouse – *Apodemus agrarius*, northern red-backed vole – *Myodes rutilus*) – possess a high migratory activity (Lukyanov, 1996; Shipanov, 2002; Grigorkina, Olenev, 2013; Tolkachev, 2016) and can overcome the distances comparable to the cross size of the EUTT zone. The results of a large-scale labeling of small mammals population with tetracyclini hydrochloridi label point to the high migration mobility of rodents, the presence of active animal migrations both in the pollution zone and outside the radiation reserve (Grigorkina, Olenev, 2011, 2013). It is logical to assume that the presence of animals in the EURT zone, even a short-term one, can affect the genomic profile of the organism.

To test this assumption, we compared the genetic diversity of samples of northern red-backed voles (*M. rutilus*) (67 individuals) from the EURT zone (initial density of soil pollution by ^{90}Sr – 18,5 MBq/m^2 = 500 Ci/km^2), the contiguous background site (10–12 km) and geographically distant (220 km) control (reference group) territories. The variability of four microsatellite loci was analyzed: MSCg4, MSCg9, MSCg15, LIST-3-003 (Gockel, 1997; Barker, 2005). We observed an increase in some indices of genetic diversity (the mean values observed and expected heterozygosity, an average number of alleles per locus, Garza-Williamson index) in the voles from the EURT zone in comparison to the rodents from the distant background site, subjected only to the global technogenic exposure. Of note, radionuclides, capable to induce the increased genome instability, were accumulated in bone tissue of voles from the EURT zone. On the basis of the variance of allele frequencies of microsatellite loci significant differences of the genetic structure between impact (EURT) and distant (reference) groups were shown (F*st = 0,015*; P = 0,010). However, the differences between the samples from the EURT zone and from the adjacent site were at the border of 5% level of significance. The background samples displayed no significant interpopulation differentiation, despite significant distance between them (Rakitin et al., 2016). Special attention should be payed to an increase in some indices of genetic diversity (allelic diversity, number of unique alleles) in animals from the contiguous to the EURT zone territories, the mutational pool of which was expanded owing to gene flows and the genetic instability inherited from migrants from the zone of local radioactive pollution (Gileva et al.; 1996; Rakitin et al., 2016).

Our research provided the following evidence: 1) the migrations and the configuration of pollution zone play important role in the formation of genetic diversity and animals’ radioadaptation; 2) the microevolutionary processes in cyclomorphic mammals populations in the zone of local radioactive pollution are very complex; 3) the use of microsatellite DNA loci as markers of radiation-induced effects in rodents was efficient.The work was partly supported by the Program of Basic Research of the Ural Branch of the Russian Academy of Science (the project no. 15-2-4-21).

SPACE UTILIZATION DURING SUMMER PERIOD IN THE COMMON GRASS FROG (*RANA TEMPORARIA*, L.) ACCORDING TO HOMING EXPERIMENTAL DATA

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The European Common Frog (*Rana temporaria*) is a widespread species but spatial orientation of this frog is partial. Characteristics of spatial usage are unknown too. Therefore, the aim of our investigation was to study orientation abilities of the common frog after artificial displacement from the capture site at different distances and to identify characteristics of space utilization during summer.

Our study was conducted at Zvenigorod Biological Station, Moscow region, Russia in summer 2013 and 2015. We measured length and weight of each captured adult frog. The main method of studying spatial behavior was tracking with a spool and line technique. Each tracking device consisted of spool with thread. Tracking devices were fixed on the frog's body with an elastic band. Overall weight of device was lower than 5% of frog's body mass. Distance of displacement ranged from 0 to 400 m. Capture points and releasing places were marked with GPS-navigator and sticks. We fixed thread end on the stick. Unreeled thread marked frog's movements. We checked frogs twice a day and map frog's route with environmental characteristics like shelters and borders.

We found that frogs could feel direction to capture sites after displacement to distances up to 300 m, but they were confused after displacement to 400 m and could not find the right direction (according to Rayleigh Test for circular data $p < 0{,}01$ for frogs displaced to 40 (16 frogs), 100 (20) и 200 m (13), $p = 0.03$ для 300 m (13), $p = 0.33$ для 400 m (24)). Larger distances of displacement correlated with longer periods needed to choose the right direction. Male's route length before choosing the certain direction was much smaller than that for female's ones.

We measured length of the route near logs, under them and above them, movements through brushwood and on open area and calculated the part of each characteristic in the whole route for each frog. Distance of displacement correlated with amount of movements on the open areas (Kruskal-Wallis test $p = 0{,}01$). Frogs moved more secretly at their capture sites and less secretly after displacement to 40 and 100 m. Nondisplaced frogs mainly used logs as shelters. Displaced frogs preferred fallen trees and branches as shelters, which could be observed distantly. These differences could probably be based on bigger frog's desire to come to their home sites faster if they could sense it nearness and ignore the risk to be eaten. Frogs displaced to bigger distances as 200 or 300 m were more cautious and often used shelters for rest and to avoid predators.

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COMPARISON OF MORPHOLOGICAL AND GENETIC VARIABILITY OF THE BROWN BEAR *URSUS ARCTOS* LINNAEUS, 1758 FROM FAR EAST

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Brown bear is a Holarctic species, and it has a significant areal covering the mountain-forest region of the Palaearctic and Nearctic. Studies of the intraspecific systematics of the bear continue up till now, due to the high individual and geographical variability of this species (Cherniavsky, 1986; Yudin, 1991; Baryshnikov, 2010). For the brown bear, were described 16 subspecies, differing in coloration and body size. For the Far East were substantiated 8 subspecies at different times and by different researchers, but they reached no consensus about brown bear intraspecific differentiation in this territory (Yudin, 1991; Baryshnikov, 2010). In the last years of wide use of molecular and genetic methods, discrepancies between morphological and genetic taxonomic schemes are widely discussed, which were constructed on morphological and genetic approach. Nowadays, only a few fruitful consensus in this direction exist (Baryshnikov et al., 2004; Abramson, 2013).

We examined variability of craniometrical and genetic parameters in brown bear population from the Russian Far East. For this study, we used 282 skulls from different museums of the country, as well as 54 tissue samples from four regions of the Far East: the Amur and Sakhalin oblast, Khabarovsk and Primorsky district. We studied the mtDNA fragment of 1257 BP, including cytochrome *b* and flanking sequences. Craniometrical analysis revealed two morphological clusters for skulls of brown bears older than six years old from North-East Asia. The clusters had a more significant statistical power in the analysis of males. The first cluster included specimens with smaller skull parameters than specimens of the second cluster. This analysis and the division into clusters were not based on the attribution of skulls to a subspecies or region. Comparison of clusters and distribution of subspecies in the Far East showed lack of correlation between them (by Aristov and Baryshnikov 2001; Baryshnikov, 2007). Only the prevalence of various clusters in a subspecies changed. Left-bank of Amur River (Amur oblast and Khabarovsk Krai) sample equally contained individuals from each cluster. Based on this distribution, we hypothesize transition from subspecies of the brown bear (*U. a. arctos*, *U. a. jeniseensis and U. a. lasiotus*) in this zone. This is confirmed with the presence of intersection of different faunas – the Amur, Daurian-Mongolian and East Siberian – in this territory (Kurentsov, 1959, 1965, 1974; Friman, etc., 2013). When we tested genetic structure of the Far Eastern brown bear population, most samples belonged to the basic type of halotype (3a), which was widespread in most parts of the area (Davison et al., 2011). A small part of samples was related to a rare sub-group 3b (Leonard et al., 2000). There was no correlation between our genetic data and the craniometrical study findings. There was no similar distribution of morphological samples when compared to mDNA samples. There were no monophyletic groups corresponding to one subspecies in the phylogenetic reconstructions.

Comparison of genetic data, which we obtained, with the current distribution of brown bear subspecies in the Russian Far East raises new questions. Should we agree that genetic traits for given species in this territory have a less variability compared to the morphological criteria, and, therefore, build brown bear systematic with genetic traits also, we then need to review the brown bear taxonomic system and add new diagnoses to already existing subspecies description.

PHYLOGEOGRAPHY AND HISTORICAL RANGE SHIFTS IN MAGPIE (*PICA PICA*): INSIGHTS FROM GENETIC AND BIOACOUSTIC DATA

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The Eurasian magpie *Pica pica* (Linnaeus, 1758) is a widely distributed, mostly Holarctic species occurring from Morocco and Spain to Western North America with several isolated occurrences. It lives in semi-open, semi-arid and often anthropogenic habitats. Here we present results on patterns of genetic variation in *P. pica*, particularly in its eastern Palearctic distribution, i.e., with special emphasis on populations from the Russian Far East, Japan, Korea and Taiwan. Moreover, own and published bio-acoustic data on the chatter calls of *P. pica* were compiled and the differences between populations discussed in comparison with the genetic results. Together with recent reports on the current range shifts and the spreading of the species we discuss possible ways of population expansion and settling.

The complete mitochondrial (mt) control region was sequences in 109 individuals representing nine subspecies. Deep genetic divergence between four lineages was found: (1) a European-Siberian group, (2) a South-Far-Eastern group, (3) *P. p. mauritanica* and (4) *P. pica hudsonia*. These lineages show a clear geographic pattern and clearly correspond to single subspecies or groups of subspecies. The differentiation within the European-Siberian group (clade West) covering a huge range is rather small implying fast recent expansion. A somewhat separated lineage was detected in Kamchatka. This population, which shows clear affinity to the European-Siberian group, is very homogeneous which indicates a bottleneck/founder effect. The South-Far-Eastern group (clade East) is subdivided into two subclades which, at first sight, could be explained by distinct Pleistocene refuges of the two subspecies *P. p. serica* and *P. p. jankowskii*. Yet there is no geographic pattern and the two subspecies are randomly distributed within these two clades. We assume that this is due to postglacial range shifts and admixing of populations.

The two other lineages are separated by 4,9–6,6% average p distances from each other and the other lineages, respectively. P. p. hudsonia represents the sister lineage to clade west, which is known already from earlier publications. The distinct position of P. p. mauritanica is reported here for the first time. Unfortunately, both lineages are represented by only single individuals in our data set.

Bioacoustic data mainly coincide with phylogeographic patterns as revealed by mt sequences and are in concordance with subspecific differentiation as well as with the major split of the four mt lineages. Yet several taxa remain to be analysed. Together with the phylogeographic patterns, historical and recent reports on distribution range shifts, e.g., the fast spreading of the P. p. jankowskii population towards the west in Transbaikalia, and that of P. p. leucoptera in the opposite direction leading to a new contact zone, are summarized and discussed. The homogeneity of the Kyushu population supports historical reports on the species´ introduction. The Hokkaido population originated only recently. Its unexpectedly high variation can be explained by ongoing introduction from the variable population of the South Russian Far East. In general, our data support the known scenario of divergence in geographic isolation, but ongoing expansion of distribution ranges may lead to dramatic changes in phylogeographic patterns as inferred from the mtDNA variation data presented.

HELMINTH INFECTION OF MOOR FROG *RANA ARVALIS* NILS., 1842 IN THE FLOODPLAINS OF THE OB RIVER IN THE CITY OF SURGUT

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Amphibian's helminthofauna has recently attracted attention of researchers (Chihlyaev, 2004; Malysheva, Zherdeva, 2008; Zaripova, 2012; Burakova, 2012; et al.), but still remains poorly studied. There exist only two known publications (Zhigileva and colleagues, 2002; Ibragimova, 2012) of studies from the territory of the Khanty-Mansiysk Autonomous District – Yugra.

Surgut is largest city of Khanty-Ugra, located on the right bank of the Ob River, the length of which within the city is 15 km. The floodplain of Ob River has the following objects built there: garage cooperatives, river docks, yacht club, hay meadows, hydraulic fill, Ugra path along which large buildings (ice stadium, shopping centers, car dealerships and gas stations). Combustibles and lubricants leak from the garage cooperatives every year into the regional water bodies. Therefore, we aimed to study helminth infection of moor frog from habitats within the city of Surgut.

We caught amphibians in 2011 in eight floodplain biotopes of Ob River. Fifty-two individuals of moor frog were subjected to the helminthological analysis of lung and gastrointestinal (GI) system. Collection of helminths was done via wet method (Anikanova et al., 2007). Attribution of helminths to species was done using the method of K.M. Ryzhikov et al. (1980). 696 helminths of five species and two classes (Trematoda (2) и Nematoda (3)) were identified. We calculated extensity of infestation (EI), intensity of infestation (II) and the abundance index (AI) for each species (Anikanova et al., 2007).

Trematoda class of moor frog of Ob River floodplain was represented by two species: *Dolichosaccus rastellus* and *Haplometra cylindracea*. Nematoda class – by *Cosmocerca ornata*, *Oswaldocruzia filiformis*, *Rhabdias bufonis*. The species composition of helminths of moor frog on this territory was similar to helminth fauna of this species in Saransk (Ruchin et al., 2008), Tyumen (Burakova, 2012), Ust-Kamenogorsk (Tarasovskaya, 2012) and other locations. In general, 73,1% frogs were infected with one or more helminth species. 15,4% of the individuals had clear lungs, and 21,2% did not exhibit helminths in the gastrointestinal tract. *Haplometra cylindracea* (EI = 39%; II = 4,86; AI = 0,27) and *Rhabdias bufonis* (EI = 64%; II = 13; AI = 0,44) parasitized in lungs. *Dolichosaccus rastellus* (EI = 25%; II = 5; AI = 0,17), *Cosmocerca ornata* (EI = 6%; II = 1; AI = 0,04) and *Oswaldocruzia filiformis* (EI = 86%; II = 9,1; AI = 0.6) were found in the gastrointestinal tract. Nematodes *Rhabdias bufonis* and *Oswaldocruzia filiformis* made the core of helminth fauna, which was typical for moor frog in Western Siberia (Zhigileva et al., 2002; Burakova, 2012; Zhigileva, Kirikina 2015; et al.). However, it was different from the hosts of the natural populations, for example in the floodplain of the Middle Ob (Tomsk region) (V.N. Kuranova (1988)), where trematodes prevailed. We found minor sex differences ($\chi^2 = 0{,}44$; df = 1) in the infestation of moor frog with helminths (61% males and 39% females).

Antagonistic relationship between trematodes and nematodes was well known, in particular between *Rhabdias bufonis* and *Haplometra cylindracea* (Markov, 1955; Tarasovskaya 2011; et al.) parasitizing in the lungs of the moor frog. In the floodplain of Ob within Surgut they registered low moor frog infestation with trematodes cohabitating with nematodes (10,1% and 89,9%, respectively), with significantly different EI of these helminth species ($\chi^2 = 5{,}64$; df = 1).

We conclude that human economic activity negatively affects parasitocenoses in the moor frog in the floodplain of Ob River. This is reflected in the poor diversity of trematodes, their low extensiveness of infestation and the abundance index, which we consider associated with the loss of intermediate hosts (mollusks) in the floodplain due to the systematic pollution.

MORPHOLOGICAL CHARACTERISTIC OF GRASS SNAKE *NATRIX NATRIX* (LINNAEUS, 1758) FROM VYSOKOGORSKY DISTRICT OF TATARSTAN

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Study of external morphology is an important part of research of reptiles associated with studies of variability and adaptation to environmental conditions. The grass snake is a species widespread in Tatarstan. We investigated external morphology of snakes from Zelenodolsky, Laishevsky and Spassky districts of Tatarstan Republic previously and found morphological differences of populations from each other. In this paper, we consider dimensions, pholidosis and coloration of grass snakes from Vysokogorsky district and compare them with other samples.

Material for this study was gathered in 2014–2015 in Vysokogorsky district of Tatarstan (Alan-Bekser village neighborhood). Eighty-two individuals in total were studied, including 30 males and 52 females. The standard technique (Pavlov, Zamaletdinov, 2002) of reptile handling was used so study morphology.

Females of grass snake were larger than males in the studied sample. Female head length was 30,0 mm (from 19 to 40) on average, male head length – 22,5 mm (17–27) ($t = -8{,}2$; $p < 0{,}0001$). The average snout-vent length was 676,8 mm (400–930) in females and 540,8 mm (410–760) in males ($t = -6{,}7$; $p = 0{,}0001$). The average tail length of females was 157,3 mm (100–190), males – 144,5 mm (113–180) ($t = -2{,}6$; $p = 0{,}096$). SVL to tail length ratio was 4,27 (3,40–4,94) in females and 3,69 (3,08–5,00) in males ($t = 6{,}76$; $p < 0{,}0001$). Females from Vysokogorsky district were larger than those from other districts we examined ($H = 11{,}98$; $p = 0{,}0175$). Differences in sizes can be explained by food resources abundance or by the prevalence of older animals in the sample. With regard to sex differences, we observed regularities consistent with those noted by other researchers (Pavlov, Pavlov, 2000; Trohimenko, 2004 et al.).

The number of supralabial, sublabial, preorbital, postorbital, loreal, temporal, ventral scales and mid-body scale row was on average equal in both sexes. We observed sex differences in the number of subcaudal scales: males had 70 pairs of scales (65–78) on average, females – 58 (52–70) ($t = 13{,}9$; $p < 0{,}0001$). Quantitative characteristics of pholidosis of individuals from Vysokogorsky district did not differ from the animals of other districts except for number of sublabial scales. On average females from Vysokogorsky district had less sublabial scales on the right ($U = 2{,}94$; $p = 0{,}032$) and left ($U = 3{,}19$; $p = 0{,}013$) side of the body than those from Laishevsky district.

We found sex-specific differences in color pattern in the studied sample: yellow-orange temporal spots ($\chi^2 = 5{,}28$; $p = 0{,}021$) and yellowish supralabial scales ($\chi^2 = 26{,}08$; $p < 0{,}0001$) were more common in males than in females. Some researchers also observed differences in the prevalence of signs in males and females of grass snake (Voronov et al., 2003), whereas others pointed out the lack of sex differences in coloration (Morozenko et al., 2003). Individuals with olive-grey dorsum prevail in Vysokogorsky district that is also typical for other districts. Only one melanistic individual without temporal spots (1,2% of all individuals) was observed, less than in other samples. We observed greatest prevalence of melanistic individuals in Spassky (10,5% of individuals) and Laishevsky (6,2% of individuals) districts.

In general, grass snakes from Vysokogorsky district of Tatarstan are similar to those from Zelenodolsky district in meristic and quality morphological features. Females from study sample are larger in size compared to the other (from Zelenodolsky, Laishevsky and Spassky) districts. Finally, we identified sex differences in dimensions (females are larger than males), quantitative characteristics (males have greater number of subcaudal scales) and color pattern.

ACOUSTIC DIFFERENTIATION OF BIRDS IN THE MODERN MEGALOPOLIS

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Many modern large cities represent a favorable, though a specific habitat for birds, especially for those that are not typical urban species. Most of them belong to the dendrophylous complex and are associated with distinct parkland, represent isolated fragments of habitat surrounded on all sides by the typical urban environment, unsuitable for habitation. Another manifestation of the big city specific environment is its considerable noise, which may be important for songbirds that actively use acoustic communication. In 2010–2016, we studied the effect of habitat fragmentation and high noise on intra – and inter-population differentiation of the song of the Thrush Nightingale and Chaffinch – numerous inhabitants of urban parks in the city of Moscow. For comparison, we used phonogram, made in the suburbs. We analyzed data using cluster analysis and multidimensional scaling. We found that populations of Nightingale and Chaffinch living on different parks within Moscow did not show bioacoustics differentiation, corresponding to the fragmented structure of their habitat. The data obtained confirm the hypothesis of the shift of birdsong frequency range in response to the urban noise.

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OOLOGICAL CHARACTERISTICS OF KENTISH PLOVER *CHARADRIUS ALEXANDRINUS* LINNAEUS, 1758 (CHARADRII, CHARADRIIDAE) FROM DIFFERENT PARTS OF THE AREAL

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We analyzed a number of oological indicators, including the quantity of masonry whose linear dimensions (length – L, mm, width – D, mm), shape (index of elongation – I, %), volume (V, ml) and egg weight (m, r), and the relative weight of the one and full clutch of Kentish plover *Charadrius alexandrinus* Linnaeus, 1758 from different parts of the areal (from Central Europe westwards all the way to Sakhalin Island in the East, and from Scandinavia in the North to the Southern Turkmenistan). We found that most of the indicators varied slightly depending on the geographical coordinates (latitude and longitude), however some association with altitude was detected. We conclude that the species adaptation to different environmental conditions occurs not only through the change of oological characteristics, but also due to changes in various reproductive attributes (breeding season prolixity, the possibility of dual breeding cycle, and the presence of polyandry and polygyny).

POSTMETAMORPHIC GROWTH OF *PELOPHYLAX RIDIBUNDUS* IN POPULATIONS OF COOLING RESERVOIRS IN THE MIDDLE URALS

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We investigated some features of biology of marsh frog – *Pelophylax ridibundus* (Pallas, 1771) – the invasive species accidentally introduced in the cooling reservoirs of Verkhnyi-Tagil (VT) and Reftinskaya (Re) power stations in the Middle Urals. These reservoirs have similar hydro-chemical parameters, but the VT has higher average temperatures by 4–6 °C, and does not freeze in winter. Distance between reservoirs is about 100 km. Marsh frog belongs to the European green frogs' complex and is characterized by semi-aquatic lifestyle. However, the species areal dramatically expanded during the rise of fish farming since mid-seventies of the last century and few populations on the Eastern slope of Middle Urals were found (Toporkova, 1977; Ivanova, 1995). The populations differed in the type of spawning, fecundity, larval period length, growth rate and development of larvae. The batch spawning is observed in VT, but simultaneous – in Re (Ivanova, 1995; 2002). The mean fecundity in Re is higher (Ivanova, Zigalski, 2011). The minimum larval period is 60 days. In VT, the tadpoles from latest clutches do not have enough time to complete its development, wintered in the late larval stages and metamorphosed in the next year.

We collected data in spring during breeding season and in summer after larval development completion. For age determination, we used bone-chronological method: the number of bonding lines was counted on the colored sections of the second phalanx of the right hind limb fourth toe, and the annual relative growth was measured. In total 456 (Re) and 918 (VT) individuals were sampled.

Age structure of studied populations was different: a three- (21,3–38,5%) and four-year (23,0–30,0%) animals dominated in Re, but older five- (10,6–26,0%) and six-year individuals (14,3–24,5%) – in VT.

In this study, our main objective was the assessment of the population- and sex- specificity in the growth rate. Usually, in amphibians the growth is defined as lifelong and infinite (Tanaka, 1982), but growth rate drops after puberty. It is convenient to use such nonlinear model, which can be linearized and allows for the desired ("difference in difference") parameterization for population and sex specificity. We used GRM, separate and homogeneity of slope models, best subset selection (Mallow's Cp criterion) technique. The best model contains common intercept (b_0), only main effect and couple of two-way interactions. The linear-logarithmic growth model gave convenient and simple interpretation of regression coefficients: the b_0 is expected value at the age of 1 year; the slope coefficient at the predictor lg(age) shows how it changes (in average) for every 10-times age increase. For example, for phalanx section (mm^2) area used as dependent variable, we obtained the next parameter estimates and standard errors [se] for best model: $Y = 0{,}09[0{,}007] + 0{,}97[0{,}014]*X + 0{,}20[0{,}006]*Population*X + 0{,}09[0{,}006]*Sex*X$, where the X is $lg(age)$. Thus, for an "average individual" we predicted 0,09 (95%CI 0,08–0,11) mm^2 area of phalanx section at the age of 1 year, the increase on 0,97 (0,95–1,0) mm^2 from 1 to 10 years. Re had 20% (19%–22%) higher rate. Finally, females had 9% (8%–10%) higher growth rate compared to males. The intraclass (within individual) correlation was estimated via mix-effect modelling and equaled 0,71 ($F_{730;\,1525} = 5{,}09$).

DISTRIBUTION AND ECOLOGY OF WILD BOAR (*SUS SCROFA L.*,1758) IN THE SOUTHEASTERN PART OF WESTERN SIBERIA (TOMSK PRIOBYE)

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The intensive process of fauna mixing, introduction of alien species into new regions are the main trends in regional faunas nowadays. This is indicative of the existence or rapid formation of new, previously missing conditions of life for mammals (Demidovich, 2016). At the same time, due to quantity increase a number of species reverts to its historic habitat restricted in the past because of human activity (Kirikov, 1966). In Western Siberia, last decade was noted for an expansion of wild boar habitat northwards (Pankov, Markov, 2016). However, both in the past and in the present there was no information about the habitat of this species in Tomsk region (Danilkin 2010). This study was conducted based on anonymous questionnaire survey of hunters and game managers in 13 districts of Tomsk region, as well as the analysis of skeletal remains of mammals from the 20 settlements of the late Holocene. 100 questionnaires in total were sent out, and only 31 were returned. Hunting lands for boar were evaluated to determine the capacity of habitat in a certain areal (Economov, 2016).

The bones of wild boar found in three archaeological sites in the South of Tomsk Priobye and at the border of Novosibirsk and Tomsk regions. In addition, copper image of a wild boar head was found in the basin of the river Chai (Myagkov, 1929).

Nowadays, wild boar in Tomsk region is recorded since 1991 and found in 13 districts in total, in five of those annually (Kozhevnikovskiy, Bakcharskiy, Chainskiy, Asinovskiy and Krivosheinskiy), and only in summer and autumn in other districts. The northernmost areal border of this species is the floodplain of river Tym in the middle taiga (v. Napas, Kargasok district).

Wild boar on the territory of Tomsk Priobye prefers mixed forests (35%), pine forests, fields (12%), forests with pine dominance (11%), and deciduous forests and floodplains (9%) to a lesser extent. It appears in hay meadows, in the marsh for feeding, in coniferous forest and overgrown valleys (3%). Animals were observed in forests of different types in 68% cases. Wintering of the species in the South and in the North of the region were also recorded. However, in most cases local population shot animals in the snowy period. No other causes of death other than anthropogenic were recorded.

Significant body mass, high fecundity (up to 12 individuals) and a small waste of young – 10–15% are typical for the wild boar in the study area. Data on the morphology, fertility and mortality confirm the southern districts of Tomsk region are favorable habitat for the wild boar. The evaluation of hunting lands for wild boar (Economov, 2016) showed II class of quality of locality in most areas of Tomsk region, with potential population of 10–15 individuals per 1000 ha.

Thus, wild boar in the southern part of Tomsk Ob region is not only a native mammal, but also has promising hunting potential. No historic facts of his stay in the Northern part (middle taiga) exist, and only sporadic arrivals were registered in present time.

GENETIC DIVERSITY OF OGNEV'S LONG-EARED BAT (*PLECOTUS OGNEVI*) IN SIBERIA AND FAR EAST

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Methods of molecular biology and population genetics enabled to identify huge cryptic diversity of chiropterans in Palaearctic during the last 15–20 years (Spitzenberger et. al, 2006; Benda et. al, 2000; Matveev et. al, 2005). Various groups of bats have undergone serious revision. The existence of at least four pairs of vicariate species was confirmed in the north-eastern Palaearctic (Kruskop et. al., 2012). The aim of the study was to ascertain genetic diversity of *P. ognevi* in Siberia and Far East.

Samples were collected on the territory of Irkutsk region, Buryatia and Zabaykalsky Krai: Upper and Lower Angara region, Eastern Sayan, Primorsky Range, Barguzin and Daursky reserves from June to September 2015. We extracted DNA from wing membrane fragments and mummified remains using modified method of Doyle and Dickson (Doyle, Dickson, 1987). PCR products were visualized in 1% agarose gel. The fragments of CO1 genes of mtDNA were used as genetic markers. The structure of primers and parameters of amplification of DNA were described by Ivanova N.V. (2006, 2012). Nucleotide sequences were aligned using BioEdit v. 7.2.5.0., and molecular genetic analysis was performed using DNA SP v.5.10.00 and TCS v. 1.2.1.

Forth-two CO1 sequences 607 bp long were produced for representatives of *P. ognevi* from various areas of Baikal region. Additionally, 23 CO1 sequences of *P. ognevi* from other areas of Siberia and Far East were retrieved from the GenBank (accession numbers: JX008089, JF443104, JF443108–JF443128). Within all aligned CO1 sequences, 18 variable sites were found and 15 of them were transitions, and 3 were transversions.

Analysis of mismatch distributions showed most pairwise comparisons had small genetic distances (D = 0,002), that confirmed low genetic polymorphism of mitochondrial molecular marker. Mismatch distribution graph had unimodal shape and exhibited relatively good fit to the expected mismatch distribution under the model of population growth. A set of neutrality tests (Tajima's D, Fu's Fs and H test with outgroup (*Plecotus kozlovi*)) demonstrated population expansion in Ognev's long-eared bat.

Haplotype network for species studied revealed 14 unique haplotypes (six of them were found in Baikal region) with "central" haplotype, including 70% of all nucleotide sequences and number of singleton haplotypes. Geographically "central" haplotype was found throughout entire areal of *P. ognevi* from Altai to Primorye. The highest genetic diversity was noted in the south of Zabaykalsky Krai – Daursky steppe that can be explained by the ecological features of this habitat. Climatic conditions in Daursky steppe sharply contrasted with those in the forest zone, where long-eared bats were more common. The climate was close to arid with temperature up to +49 °C and 150–350 mm rainfall per year. In Daursky steppe, long-eared bats were deprived of the opportunity to choose preferred wood shelters. Cracks in rocks and few human constructions can be used as shelters in the steppe.

Thus, the analysis of *P. ognevi* genetic diversity elicited single large population of this species on the territory of Siberia and Far East, the number of which was currently growing. The observed phylogeographic pattern indicated that *P. ognevi* easily developed new territories and habitats in ecosystems.

PERSONALITY STUDIES IN AVIAN POPULATION BIOLOGY

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According to Shilov's concept, intrapopulation heterogeneity is the basis for population homeostasis (Shilov, 1977, 1997). This notion was prevailed in studies of animal behaviour, which boosted in 1960–70, both in natural and artificial groups. One of the first studies using the experiments on house mouse showed the association of individual central nervous system characteristics with behavioural traits in a competition for social rank. It turned out that animals of high rank had stronger type of nervous system and weaker stress reaction. Variation in typological characteristics of central nervous system favoured faster formation of stable relationships in the groups under feebly pronounced aggression (Maslov et al., 1974; Shilov et al., 1974). The first behavioural ranking of free-living birds was done in series of tests on freshly-caught individuals of several species. It was discovered that birds that were more aggressive had lower level of anxiety (Burtt, Giltz, 1973). Further studies conducted by different researchers were mainly based on great tit (*Parus major*) as an object. They aimed to determine: 1) personality traits and their intercorrelation; 2) the causes of individual variations in behaviour; 3) the influence of behavioural context and the environment on personality performance; 4) the consequences of personality performance. Separation of personality types was based on the reaction of an animal to a novelty (new environment and objects). It was shown that such reaction, rested on different individual susceptibility to the environment (Koolhaas et al., 1999), was not related to sex, age and physical condition of an animal, but correlated with certain characteristics of its physiology, biochemistry, etc. (Drent, Marchetti, 1999; Drent et al., 2003; Dingemanse, Wolf, 2010; Ivankina et al., 2010; Cockrem, 2014; Matthysen et al., 2014). Characteristics of specific personality type were conjugated, e.g. so-called "fast" great tits (proactive type) made more movements than "slow" tits (reactive type) in the open field, and in the aviary with great number of various objects first ones coped with more resources than the latter (Ilyina et al., 2010). The heritable nature of behavioural heterogeneity was demonstrated using artificially selected lines of captive-bred great tits and natural populations (Dingemanse et al., 2002; Drent et al., 2003; van Oers, 2003). In addition, using great tits and coloured flycatchers (*Ficedula albicollis*), it was shown that individuals of different personality types had significant differences in dopamine-related gene DRD4 (Fidler et al., 2007; Garamzegi et al., 2014). Moreover, they demonstrated that two different intercorrelated behavioural features were associated with two different and certain SNP within this gene. It was the correlation between traits that created possibility to reveal the personality type using simple tests and to approximately predict other characteristics of this type. It is important to separate wide reaction norm from polymorphism (Dingemanse, Wolf, 2010). It turned out that not all tests were equally suitable for work with different species (Morand-Ferron, 2014), therefore developing species-specific complex of tests has a great potential.

SPECIES DIVERSITY, DISSEMINATION AND DISTRIBUTION OF SNAKES IN KAZAKHSTAN FOREST-STEPPE AND STEPPE ZONES

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The territory of Kazakhstan is located in the temperate zone and includes the forest-steppe, steppe, semi-desert areas, and mountains.

The forest-steppe area of about 1 million hectares (0,4%) of the territory is situated in the far north within the North-Kazakhstan plains and stretches from west to east with a band 150–250 km wide. The steppe zone occupies about 77 million hectares (30% of Kazakhstan). Band 600–700 km wide stretches from the northern part of the Caspian lowlands to the foothills of Altai. The southern boundary runs between 51 ° and 50 ° N (Vilesov et al., 2009).

Ofidiofauna of the Republic of Kazakhstan consists of 19 species, of which 8 are found in the forest-steppe and steppe zones, such as *Natrix natrix* (Linnaeus, 1758), *Natrix tessellata* (Laurenti, 1768), *Coronella austriasa* Laurentiis, 1768 *Elaphe dione* (Pallas, 1773), *Pelias berus* (Linnaeus, 1758), *Pelias renardi* (Christoph, 1861), *Pelias altaica* Tuniev, Nilson et Andren, 2010 *Gloydius halys* (Pallas, 1776) (Paraskiv, 1953, 1956; Tuniev, Ananiev, 2010). Information Data on the fauna and ecology of Kazakhstan snakes were reviewed in a number of publications (Kubykin 1994; Red Book of the Republic of Kazakhstan, 1996; Kubykin, Brushko, 1998; Brushko, Kubykin, 2000, 2002; Duysebaeva, 2005, 2010; Kolbintsev, 2006). This report is based on the literature data and author's observations in 2004, 2008 and 2011.

N. natrix and *P. berus* are prevalent in the forest-steppe zone. In Kazakhstan, *N. natrix* is found everywhere. The snake lives in damp places, and on the banks of various reservoirs (Paraschiv, 1953, 1956). In 2011, we observed *N. natrix* around Uzunkol village (Uzunkol District, Kostanai region). The southern boundary of *P. berus* areal passes in the Altai Mountains. The species is found in deciduous and mixed forests and mountains on the slopes with rich herbage and undergrowth (Paraskiv, 1953, 1956). In 2004, *P. berus* melanistic individual was found near the Kusmurin station (Aulekolsky district, Kostanay Province).

P. altaica has limited areal in the southern foothills of the Altai, where inhabits rocky slopes with steppe vegetation (Tuniev, Ananiev, 2010).

Peripheral borders of 3 species' areas are pass though steppe zone of Kazakhstan, including *E. dione*, *N. tessellata*, and *G. halys*. *N. natrix*, *E. dione*, and *P. renardi* are numerous species and ubiquitous in the steppe zone. *N. natrix* in the southern valleys comes deep into the desert and semi-desert areas. *E. dione* inhabits a variety of habitats, preferring trees and bushes, mountain slopes, and floodplains. *P. renardi* inhabits steppe, semidesert clay and salt meadows, riverbanks with reeds, sodded sands, and salt marshes (Paraschiv, 1953, 1956). In 2008, *N. natrix* and *E. dione* were found at a distance of 15 and 20 km northwestwards from the city of Semey along the road Semey – Pavlodar. In May 2008, *P. renardi* and three snakes of *N. natrix* were caught near the village Vishnevka (Akmola region).

Thus, data on the forest-steppe and steppe ofidiofauna are outdated and fragmented now. The occurrence, distribution and abundance issues remain open and require further study.

SMALL MAMMALS AND POTENTIALLY DANGEROUS INFECTIONS IN NORTHWEST VOLOGDA REGION

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Epidemic monitoring of potentially dangerous infections and related observations are carried out in the north-west of Vologda region, in Vytegra district since 2008. Favorable environment for many wild animals, including rodents – carriers of dangerous infectious diseases were formed in the forests of Vytegra district formed. Counts of small mammals and their trapping are held monthly in two main habitats: forest and meadow-field at stationary points in rural Anhimovskoye settlement. In addition to surveys at the stationary points, single surveys are also done in other places. Each year, prior to summer, we examine the territory of a country healthcare camp, and catch small mammals in the places where human infection is suspected.

39 species of small mammals exist in the north-west of Vologda region (Kolomiytsev, Poddubnaya, 2014). During the study period, we caught the following voles: the bank vole – *Myodes glareolus* (*Clethrionomys glareolus*), the northern red-backed vole – *Myodes rutilus* (*Cl. rutilus*), the field vole – *Microtus agrestis,* the common vole – *M. arvalis,* and the European water vole *Arvicola amphibius* (*A. terrestris*). We also caught mice: the striped field mouse – *Apodemus agrarius*, the wood mouse – *Ap. sylvaticus*, the harvest mouse – *Micromys minutus*, and shrews – *Sorex* sp. Agents of tularemia, leptospirosis, hemorrhagic fever with renal syndrome, tick-borne encephalitis and tick-borne borreliosis were found in the organs and tissues of the animals. The district has natural foci of these diseases. Their revitalization depends on different causes and occurs mostly during periods of high animal counts being reservoirs of infection. In the Prionega, animal population growth and the rise in their contamination rate does not occur simultaneously with the neighboring areas. High number of rodents occurred in 2008–2011 (reaching the peak in 2011), whereas high number of shrews was observed in 2008–2010 and 2013.

In Vytegra district, infection of small mammals with different serogroups of Leptospira depended on the year, such as *Grippotyphosa* – annually, *Javanica* – 2009–2012 and 2014, *Australis* – 2008–2011, 2014–2015, *Icterohaemorragiae* – 2008, 2012 and 2014, *Bataviae* – 2012, *Sejroe* – 2014, *Autumnalis* – 2008.

Tularemia DNA was detected by means of PCR in the water of Oshta river in 2010 only once. Tularemia antibodies were detected in four shrews in 2010 and 2013, in one bank vole in 2012, whereas tularemia registered in the pellets of prey birds annually (3 to 19%, 12,57% on average) and in the nests of small mammals (0 to 5% of nests, 3,13% on average).

Thus, almost a decade of observations, using the same methodology, helped identify stable foci of dangerous infections, which required early detection and localization.

GENETIC DIVERSITY OF mtDNA AND MICROSATELLITE LOCI OF HONEYBEES IN TOMSK REGION

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Genetic diversity of the honeybee is of considerable interest from both evolutional and applied perspectives. One of the important directions are gene-geographic population studies, emphasizing not only the bee race, but also climatic conditions (ecological factors) that influence specificity of gene pool structure of honeybees in different regions. The aim of this study was to ascertain genetic diversity of honeybees living in the harsh climatic conditions of Siberia using the example of Tomsk region.

To assess the ecological impact on the formation of gene pool structure, we studied genetic diversity of 100 honeybees from apiaries of different geographical locations. Honeybees obtained from two apiaries of the northern districts of Tomsk region (Molchanovsky, Kolpashevsky) and two apiaries of the southern district (Tomsky) were examined using mtDNA (the locus COI-COII) and microsatellite analyzes (lociA008, H110, Ap049, A043, A024, A113, AC117, AC216).

Three variants of COI-COII locus were found: PQQ, PQQQ (typical for the Middle Russian race *Apis mellifera mellifera*) and Q (specific for the races of southern origin – Carpathian race *A. m. carpatica* and Gray Mountain Caucasian race *A.m. caucasica*). Variants PQQ and Q of mtDNA were identified in the northern bees; whereas PQQQ and Q were found in the bees of the southern district.

Among eight microsatellite loci examined, the greatest genetic diversity was shown in loci A008, A113, Ap049 and A043 (10, 9, 7 and 6 alleles were registered, respectively), whereas the bees from the southern apiaries had higher genetic diversity. Thus, for the locus A008, nine alleles were registered, and the effective number of alleles was 3,34 (n_e), expected heterozygosity was 0,701 (h_e) in bees from the southern district, whereas five alleles were revealed $n_e = 1,23$ and $h_e = 0,187$ in the bees of the northern districts. Frequency of rare alleles as an indicator of the genetic diversity loss was higher in bees of the northern districts ($h_\mu = 0,52$) compared to the southern bees ($h_\mu = 0,31$). Similarly, locus A113 (7 alleles, $n_e = 1,72$ and $h_e = 0,417$ were registered in the bees of the southern district; 5 alleles, $n_e = 1,50$; $h_e = 0,333$ were registered in the bees of the northern districts); locus Ap049 (7 alleles, $n_e = 3,74$, $h_e = 0,732$ for southern bees; 2 alleles, $n_e = 1,37$; $h_e = 0,269$ for northern bees); locus A043 (6 alleles, $n_e = 2,97$, $h_e = 0,663$ for southern bees; 3 allele, $n_e = 1,47$; $h_e = 0,322$ for northern bees). However, h_μ value for bees of the southern district was higher than the northern bees.

For loci H110, A024 and AC117, the common allele spectrum and number of alleles were identified in bees of different locations, and for the locus AC216, only one allele was identified in all studied bees. At the same time, for the locus A024, the different calculated parameters for two bee groups have been set: for bees from the southern district – $n_e = 2,97$, $h_\mu = 0,002$ and $h_e = 0,663$; for bees from the northern districts – $n_e = 1,99$, $h_\mu = 0,16$ and $h_e = 0,498$. Only for locus AC117 the genetic diversity of bees of the northern districts ($n_e = 1,91$, $h_\mu = 0,13$, $h_e = 0,476$) was higher than in bees of the southern district ($n_e = 1,51$, $h_\mu = 0,23$, $h_e = 0,338$).

In general, we showed higher genetic diversity in bees from the southern district compared with bees of the northern districts in terms of majority of microsatellite loci studied. On the one hand, it may be associated with greater beekeeping development in the southern district of Tomsk region and an active importation of bee colonies of different origins to this territory. On the other hand, it may reflect the role of geographical and ecological factors (specific adaptation to local conditions).

The comparative analysis of genotyping data of Middle Russian bees (*A. m. mellifera*) of Siberian, Ural (loci A008, Ap243) and European (locus A008) populations confirms the existence of different ecotypes of *A. m. mellifera* as well as the influence of environmental factors on the formation of the honeybees genetic diversity (Ostroverkhovaet al., 2015).

CURRENT STATUS AND TRENDS IN THE POPULATION STRUCTURE CHANGE OF WILD REINDEER OF TAIMYR

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At present, Taimyr population of wild reindeer is exposed to technogenic, anthropogenic, pyrogenic, pastoral, zoogenic, uncontrolled poaching and other adverse factors. Uncontrolled withdrawal of highly productive animals from a population in autumn and selective large-scale poaching of the largest adult males for antlers altogether lead to dramatic changes in the reproductive traits of a population, altering sex and age structure. A decrease in the number of wild reindeer from 1 million to 400–450 thousand individuals is indicative of population changes, which are mainly caused by anthropogenic factors (uncontrolled large-scale fisheries, artificial barriers, technological impact). There have been significant changes in the population structure. Percent of calves of the year also dropped. In 2000, they accounted for 21,0%, being 19,9% in 2003, 18,4% in 2009, whereas the proportion of calves in different groups ranged from 11,2 to 13,6 per cent in 2014 as of the aerial survey (Kochkarev et al., 2014). Such a reduction is also indicative of increased mortality of calves and low reproductive capacity of animals.

Because of the population areal extension, spatial structure became more complicated, wintering areas and calving grounds changed, as did paths and timing of migrations, and their intensity rate across different regions. Number of wild deer increased first in Central and then in the Eastern Taimyr. Differentiation of the groups on pasture and increasing population density of animals are getting more apparent. Increasing isolation of the Western and Central-Eastern groups becomes clear. General trend of a shift of population to the Eastern part of the area has led to a noticeable change and areas of calving. Great number of female moved southwards for calving. Eventually, migration of retarded females with newborn is significantly delayed because of ice drifting, and that affects the distribution of deer during the calving season. The appearance of bloodsucking insects and gadflies makes females with immature calves migrate to the summer habitat, which entails death of calves when overcoming numerous water barriers and colds. In addition, increased migration rate of females in the last month of pregnancy apparently increases the rate of poor outcome calving.

No doubt, the changes in the spatial and temporal structure of Taimyr wild reindeer population demonstrate intrapopulation changes, also being response to anthropogenic factors. Undoubtedly, some negative impact increasing the rate of this process was produced by poaching on Pyasina River and anthropogenic factors associated with industrial activities, and the presence of insurmountable Messoyakha – Norilsk-Palatka pipeline. Artificial linear obstacles (oil and gas pipelines, roads, rails, fences for deer hunting, ice destruction for the navigation extension on Yenisei River) are the main anthropogenic factors that block migration routes of the herds to seasonal pastures and traditional calving venues. In the short term, artificial barriers may be the main threat to the wild reindeer survival of Taimyr. Further decline of the wild reindeer population on the northern Yenisei is predicted. Again, this confirms the need for regulation of wild reindeer population in an organized controlled fishery and better strategy and management. Environmental monitoring using modern aerospace vehicles (satellite telemetry) and GIS-technologies is required.

CERVIDS (*CERVIDAE*) POPULATION CHANGE IN THE LAZOVSKY RESERVE

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Lazovsky Nature Reserve was established in 1935 in the southeastern part of Primorsky Territory. There are six species of native ungulate in the reserve. The wild boar (*Sus scrofa)* and cervids: roe deer (*Capreolus pygargus tianschanicus*), Manchurian wapiti (*Cervus elaphus xanthopygus*) and sika deer (*Cervus nippon hortulorum*) are the most numerous and widespread ungulates both in the reserve and in the whole southern Primorye.

Since the reserve establishment, the focus was on the protection and restoration of the wild sika deer population whose number dropped to a few hundred individuals (Bromley, 1956) by the mid-twentieth century. Lazovsky Reserve was the largest habitat of the species.

Until the end 1970s, the average population density of all cervids in the reserve did not exceed 12–17 animals per 1000 ha. Free deer species’ contribution to the general population was quite equivalent. Sika deer concentrated in the coastal zone, whereas the Manchurian wapiti and roe deer populated protected area (within the inherent habitat) evenly, avoiding only the places of sika deer concentration on the coastal line. Roe was always less prevalent compared to Manchurian wapiti and sika deer due to limited suitable habitats and regular season migration of its population outside the reserve (Kon'kov, 2009).

Since mid-1970s, sika deer population was no more under pressure of regulation which resulted in population growth. That happened due to elimination of wolf (*Canis lupus*) general softening of climate in winter. Replenishment of wild populations with animals, which escaped from deer parks, also played role. Sika deer population growth was accompanied by its intense expansion both into the continental part of the reserve and outside the protected area. Since 1990s, sika deer prevailed among the ruminants in the great part of the southern Primorye.

Profound changes in the structure of ruminant guild occurred as a result of sika deer population growth. Expansion of sika deer was linked with the emigration of roe deer and Manchurian wapiti from sika habitats. Over the past 40 years, the population size of these species dropped manifold. In 2000s, population size exceeded 4,000 individuals with the mean density of 8,6 deer/km^2 (Voloshina and Myslenkov, 2009). At the same time, the average population density of roe deer and wapiti decreased to less than 0,1 deer/km^2. Until now, their total count remains at a consistently low level and does not exceed 100 individuals. Long-term data on the population monitoring of ungulates (results of snow track counts from 1961 to 2015) collected in some areas of the reserve confirm distinct competitive exclusion of roe deer and wapiti by sika deer.

Research on cervid winter-feeding elicited similarity of their browse diets along with high potential for food competition in species pairs including sika deer (Kon'kov, 2015). However, roe deer emigrates long before the first manifested signs of feed exhaustion or shortage appear. Most probably, the key role to initiate this process belongs to the same factors that underlie their intrapopulation mechanisms of number regulation.

MORPHOLOGICAL ABNORMALITIES OF *HEMIDACTYLUS PLATYURUS* (SCHNEIDER, 1797) (REPTILIA, SAURIA, GEKKONIDAE) URBAN POPULATION IN THE SOUTH-EAST ASIA

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There are many studies on morphological abnormalities of Amphibia and Reptiles, in which they look to find associations of the number of abnormalities with the anthropogenic load that affects urban populations most often. In addition to natural (congenital) causes of developmental disorders of a living organism, there are anomalies that arise under the influence of anthropogenic factors, such as pollution emissions of domestic or industrial origin. Therefore, the occurrence of anomalies reflects the quality of the environment and can serve as an indicator of its status (Borkin et al., 2012, Vershinin, 2015). There are two main groups of morphological abnormalities: a) related to the morphogenesis abnormality; and b) traumatic. Due to difficulties with separation of two categories of "atypical morphology", many authors use the word “abnormality (anomaly)”, meaning any deviation from the norm, regardless of the causes (Borkin et al., 2012).

This topic has high potential for research in the group of house geckos because of the lack of previous studies. This group is widespread, synanthropic, sympatric, so it can be used as model for ecological and microevolutionary studies in the rapidly changing urban environment (Konstantinov, 2013).

The studies were conducted on *Hemidactylus platyurus* (Schneider, 1797) on the territory of Bangkok, Vientiane and Phnom Penh in 2013–2014. 531 individuals examined.

We identified four groups of different anomalies (Nekrasova et al., 2007): limb malformations (abnormalities 57–84%), the head (2 cases – 3%), the spine (3 cases – 4%), and skin (6 cases – 9%). Of those, we also found: 1) limb malformations, including reduced number of pins and their parts: 1.1. ectrodactyly – an anomaly in the claws form, 1.2. oligodactyly – the lack of whole finger or fingers, 1.3. brachydactyly – reduced number of phalanges, 1.4. ectromelia – missing parts of limbs. 2) spine malformations, 3) the tail anomalies (bifurcation), 4) head malformations: jaw malformations (microagnathia – small jaw), 5) skin malformations (pattern abnormal and papilloma).

There were 68 abnormalities from 531 individuals examined, whereas limb malformations were the most prevalent (84%), and of those, brachydactyly (reduced number of phalanges) was the most common.

The analysis of pholidosis deviations in the outskirts and in the city center revealed heterogeneity, depending on the degree of urbanization (population). There were no differences between central and suburban populations in Vientiane (800 thousand people), whereas the number of pholidosis anomalies increased in the city center in Phnom Penh (2 million). On the contrary, the number of abnormal variations was greater in the suburbs in Bangkok (9 million).

The analysis of the stability of the coefficient of fluctuating asymmetry showed similar trend, where the indicators did not differ within Vientiane, breach of stability in the center of Phnom Penh, and in the outskirts of Bangkok.

Comparison of the community structure of house geckos using the Simpson index of species diversity showed the consistency of the indicator with the change in population characteristics (number of pholidosis anomalies, and stability evaluation). We did not find differences in the structure of communities in Vientiane between the outskirts and the center, as well as the decrease in geckos species diversity in the center of Phnom Penh and the outskirts of Bangkok.

GENETIC DIVERSITY OF DUCKS *ANAS ACUTA L.* AND *ANAS PENELOPE L.* IN THE SOUTH OF WEST SIBERIA

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In Eurasia, they select several populations of various anseriformes species based on nesting location, moulting and wintering, identified via band returns (Shevareva, 1968, 1974; Birds' migrations…, 1997; Linkov, 2002). Birds of one generation are known to have different wintering. Since different species of ducks in the Western Siberia may have up to 3 sites of wintering, whereas in general they may fly to five different sites of wintering, because this territory is situated in the center of Euroasia. Determination of certain territorial nesting groups would allow differential approach to the use and protection. Molecular and genetic assessment of birds' diversity using various gene loci could probably be one of the markers of such territorial groups. We selected two most prevalent species of duck in the Western Siberia, pintail and wigeon, whose nesing areals cover the entire Euroasia, and even North America in pintail for the purpose to test molecular and genetic methods in groups identification. We selected 5'-hypervariable locus of control site, a fragment of mtDNA as a molecular marker, frequently used in animal phylogeography, including anseriformes (Kulikova et al., 2005, Peters et al., 2014).

The analysis of control site fragment (659 pn) in 46 individuals of wigeon from Tomsk Province yielded only six variable sites and 8 haplotypes. One most prevalent was found in 33 individuals. The second haplotype was detected in four birds, the third in 3, fourth in 2 and four more haplotypes that were original. In general, haplotype and nucleotide diversity was quite poor: $H = 0{,}488 \pm 0{,}089$ and $\pi = 0{,}0011 \pm 0{,}0006$ respectfully. When we excluded samples from one locality (30), of possibly relative birds, haplotype and nucleotide diversity improved to have $H = 0{,}88 \pm 0{,}04$ and $\pi = 0{,}025 \pm 0{,}0017$. That H was higher compared to thee similar species in Primorye: $H = 0{,}59 \pm 0{,}08$ and $\pi = 0{,}0015 \pm 0{,}0012$ (Kulikova, Zhuravlev, 2010). Built with ML, phylogenetic tree of Tomsk sample showed no clear clustering with this marker. We saw similar picture in the net of haplotypes in which all individuals formed one clad with minor 1–4 mutations differences.

The analysis of control site fragment (655 pn) in 54 pintail individuals from Tomsk and Novosibirsk Provinces showed 26 polymorphic sites. In total, we identified 29 haplotypes, one of which was found in y 15 individuals. Six haplotypes were also found in few individuals with low frequency, from 2 to 5 inds., whereas 22 were original. Haplotype diversity (H) was greater compared to wigeon and equaled $0{,}9032 \pm 0{,}0424$. Nucleotide diversity (π) was also greater: $0{,}005 \pm 0{,}003$. Built using ML, phylogenetic tree elucidated 2 clads, not confirmed via bootstrap support though. With this, we failed to find any geographic connections or any association in grouping.

In summary, we could not find any isolated clusters of wigeon and pintail on the studied territory that was probably related with some individuals exchange between groups in nesting and wintering areas.

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THE MAGPIE (*PICA PICA* L.) INDUCTION IN THE CHEREPOVETS ECOSYSTEM

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The genetic fund of any species is formed in the process of adaptive evolution and is stabilized by all complex of abiotic and biotic environmental factors (Kolomiytsev, 1990). Ecological factors on the planet constantly change, and organisms inhabiting it change. Addressing insufficient biodiversity protection, "it is more pertinent to speak not about preservation of the genetic fund, and about maintaining natural rates of genetic fund progression, that is about the prevention of species and intraspecific structures involvement in the accelerated microevolutionary processes of anthropogenic transformation" (Kolomiytsev, 1990). Monitoring the rates of progression of ecological attributes of animals is one of the vital ecological and evolutionary problems.

The purpose of our study was to find out features of adaptation of the magpie (*Pica pica*) to urbanized environment in the Northwest of Russia. Observations were made in Cherepovets (59°07′00″ NL 37°54′00″ EL) and in adjacent territories. Magpie urbanization was studied earlier in Leningrad region (Malchevsky, Pukinsky, 1983), where this bird, usually tethered to places of birth, inhabited urban environment only in the mid-fifties, being rather common species in the cities of this region already in early eighties. In Cherepovets and in the western areas of Vologda region, magpie occupied traditional habitats, which were lowland forest on the banks of reservoirs near rural settlements, until recently. In the late 1990s, it widely inhabited undersized plantings along large thoroughfares, where forage is present throughout the year. In 2012, the first two pairs nested on the border of the city and the forest in the coastal part of the Sheksna Reach, penetrating into the city in the last three years. In 2015, magpie nests (less than ten) were found only in the suburbs of the city. The birds built two nests in a residential area (the park and grove) in 2016.

The magpie builds nests on the willow, aspen, and bird cherry. In all cases, two nests located at a distance of 2–3 meters from each other, one of which was residential, were found. Nests in a residential part of the city were located 3–5 meters higher above the ground than in its outskirts (5–8 m and 2–3 m respectively), that was due to typical vegetation here, such as trees and shrubs, and may provide comfort and safety only at such height.

Recent years were also noted for magpies' visitation to the city. Magpie's occurrence on survey routes with the length of 73,6 km covering the entire city was 0,13 individuals/km on average in 2014, which is 9 times less frequent than the rook (*Corvus frugilegus*), 14,5 times than the hooded crow (*Corvus cornix*) and 20 times than the jackdaw (*Corvus monedula*). Magpie's occurrence on the routes ranged from 0,04 individuals/km in summer to 0,26 individuals/km in autumn (Shmatova et al., 2012). Two urban districts, Severny and Zasheksninsky on border with forest were the most favorable for birds. This bird is less prevalent (0,07 individuals/km) in Zayagorbsky district with high building density. Considering Cherepovets as habitat for magpie, the bird will likely inhabit all suitable sites (around 10) with a total area of over 100 hectares by the end of the current decade,

Thus, the urbanization of magpie as a rural synanthropic in the west of Vologda Province lagged 60 years compared to other territories of the northwest Russia and currently runs fast. The species is obviously involved in the accelerated microevolutionary processes of anthropogenic transformation. Species reaction norm expands, and magpie ecological niche (as a function of species in an ecosystem) changes.

THE TULAREMIA FOCI IN KALUGA PROVINCE

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Tularemia is zoonotic infection; it is widespread in Russia and other regions of the moderate zone of the North hemisphere. It caused by the bacterium *Francisella tularensis* (McCoy, Chapin, 1912) (СП 3.1.7.2642-10).

First studies of tularemia in Kaluga Province were initiated in 1942, when an outbreak occurred in Borovsk district, followed by isolation from the common voles (*Microtus arvalis* Pallas, 1778 and *Microtus rossiaemeridionalis* Ognev, 1924). Tularemia foci were studied by sanitary zoologists in 1960-1970s, and results were published (Fomushkin, Scorukina, 1965; Olsufiev et al., 1971). This report is based on extracted tularemia cultures, obtained via biological method.

From 1942 to 2004, 621 bacterial cultures were extracted. Since 2004 until now, they did not find tularemia agents in the environment. The greatest number of cultures (51,17%) were isolated from the small mammals: *Sorex araneus* Linnaeus, 1758 (1,13%); *Sorex minutus* Linnaeus, 1766 (0,16%); *Crocidura suaveolens* Pallas, 1811 (0,32%); *Arvicola terrestris* Linnaeus, 1758 (0,32%); *Myodes glareolus* Shreber, 1780 (0,81%); *Microtus oeconomus* Pallas, 1776 (0,16%); *Microtus arvalis* и *Microtus rossiaemeridionalis* (43,64%); *Micromys minutus* Pallas, 1771 (0,16%); *Sylvaemus uralensis* Pallas, 1811 (0,64%); *Apodemus agrarius* Pallas, 1771 (8,05%); *Mus musculus* Linnaeus, 1758 (1,13%); *Rattus norvegicus* Berkenhout, 1769 (0,16%); *Rattus rattus* Linnaeus, 1758 (0,16%). Second most prevalent carrier was *Apodemus agrarius*, a species attributed to the second group of animal susceptibility to tularemia (Tularemia, 1960). Five tularemia cultures (24 samples) were extracted from the striped field mouse in 1990 near Dol village of Kozelsk district, whereas four cultures (19 samples) identified near Aleshino village of Meschovsk district in 1988. Solitary culture was extracted from a dead body of the striped field mouse in hibernal epizootic outbreak in Cosmatchi village of Babynino district in 1986.

Environment may be as important as small mammals as carriers for tularemia circulation and may account for 37,36% of cases. Stripping of grain, vegetables, sedge and other plant substrates accounted for 12,88% of cultures. Other environmental objects were less important: water (9,66%), rodents' turds (9,02%), rodents nest (3,87%), rodents skin pieces (0,97%). Solitary culture from blood on snow was also identified. 5,48% cultures from isolated from the mites (Parasitiformes), 4,03% from Ixodidae, and 1,45% from Gamasoidea.

The most common type of tularemia foci in the region were meadow fields in all three physiographic provinces (see Atlas of Kaluga Province, 2005) and in nearly all municipal districts of Kaluga Province. The most active tularemia foci of meadow-field type are confined to the most ploughed central districts: Babynino, Kozelsk, Meschovsk, Peremyshl, Sukhinichi districts (57,97% of cultures). Quite active tularemia foci were located in the east and northeast parts of the region (Ferzikovo and Tarusa districts), accounting for 20,45% of cultures. Floodplain-bog foci are less active. Floodplain-bog spots with cultures from ground voles (*Arvicola terrestris*) are located in Khvastovichi (flood plain of Resseta), Duminichi (flood plain of Bryn), and Dzerzhynsk (flood plain of Protva) districts.

SEASONAL CHANGE OF THE PINEAL GLAND SIZE IN THREE SPECIES OF FOREST VOLES (*MYODES*, CRICETIDAE, RODENTIA)

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We studied seasonal change of pineal gland size in the Northern red-backed (*Myodes rutilus*), Bank (*M. glareolus*), and Grey-sided (*M. rufocanus*) voles from southeast of Western Siberia. Pregnant females were captured in the vicinity of Tomsk (Tomsk Province) from May to August 2014–2015. Females were bred in vivarium with unlimited access to food, and water and temperature and illumination equivalent to natural environment. After birth, young animals were kept with females for 20 days. Then we divided young animals into two groups. Group 1 included individuals growing separately from their mothers. In Group 2, we modelled conditions of high-density population, and young animals stayed with their mothers. We decapitated animals and performed immediate pineal gland ectomy on the 60th day. In total, 286 animals were analyzed. All pineal glands were fixed in neutral buffered 10% formalin for 24 hours. Following fixation, digital snapshots were obtained and pineal gland size was measured, as a frontal projection surface of the gland using via AxioVision 4.9.1 software (Zeiss, Germany). Statistical analyses were performed with Statistica 7.0 (StatSoft, USA). We tested associations of pineal gland size with such variables as “species”, “sex”, “month of birth”, and “social conditions” using factorial analysis of variance (ANOVA) and Fisher’s least significant difference (LSD) test.

Significant interspecific differences in pineal gland size were found (ANOVA, $n = 286$, $F_{2,280} = 3{,}2$, $p < 0{,}04$). Since there were no significant intersexual differences (ANOVA, $n = 286$, $F_{2,280} = 0{,}3$, $p = 0{,}6$), we eliminated “sex” variable from the following tests. Sizes of pineal gland (mean ± SE) were similar in *M. rutilus* (0,41 ± 0,015 mm^2) and *M. glareolus* (0,44 ± 0,015 mm^2) (LSD test, p = 0,13), whereas *M. rufocanus* had the smallest gland (LSD test, $p < 0{,}01$) (0,39 ± 0,016 mm^2). We corrected “species” variable in other comparisons. Pineal gland size with significantly associated with the month of birth (ANOVA, $n = 286$, $F_{6,274} = 5{,}8$, $p < 0{,}001$). In *M. rutilus*, it was slightly lower in animals born in May–July. In individuals born in August, pineal gland size was significantly smaller than in those born in previous months (LSD test, $p < 0{,}001$). In *M. glareolus*, pineal gland was the largest in individuals born in May (LSD test, $P < 0{,}01$). Pineal glands of August-born individuals were twice as small as of those born in May. *M. rufocanus* elicited a different pattern of season-dependent association, and there was no consecutive season-dependent reduction in gland size. May- and June-born voles did not differ significantly in pineal gland size between each other. In individuals born in July, this size was significantly smaller (LSD test, $p < 0{,}01$) with no further reduction in August-born animals. Thus, *M. rufocanus* had smaller pineal glands in May- and July-born individuals and bigger ones in animals born in August compared to similar groups of *M. rutilus* and *M. glareolus* (LSD test, $p < 0{,}01$).

Social conditions did not affect seasonal changes of the pineal gland size in any studied species (ANOVA: *M. rutilus*, $n = 99$, $F_{1,91} = 0{,}9$, $p = 0{,}4$; *M. glareolus*, $n = 103$, $F_{1,101} = 0{,}2$, $p = 0{,}2$; *M. rufocanus*, $n = 84$, $F_{1,82} = 1{,}2$, $p = 0{,}3$).

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AGE-RELATED AND SEASONAL DYNAMICS OF FECAL CORTICOSTERONE IN VOLES (*MYODES*, CRICETIDAE, RODENTIA)

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Age-related dynamics (20, 40 and 60 days) of fecal corticosterone in voles born in May-August was studied. Young Northern red-backed (*Myodes rutilus*), Bank (*M. glareolus*), and Grey-sided (*M. rufocanus*) female voles captured in their natural habitat were bred in vivarium with unlimited access to food and water, and temperature and illumination equivalent to natural environment. 20-day old animals were divided into two groups of different social conditions. Group 1 included individuals with no contact with their mothers. In Group 2, we simulated conditions of a high-density population, and young animals stayed with their mothers. Corticosterone concentrations in 325 fecal samples of Northern red-backed (*Myodes rutilus*), 259 Bank (*M. glareolus*), and 279 Grey-sided (*M. rufocanus*) voles were determined by radioimmunoassay and enzyme immunoassay. In order to combine results, we used both methods in 17 samples and derived correlation coefficient. Statistical analysis was performed in ANOVA and LSD-test.

We found significant interspecific differences ($p < 0{,}001$). The Northern red-backed (*Myodes rutilus*) vole had the highest glucocorticoid level (779,5 ± 26,6 ng/g), the Bank (*M. glareolus*) vole had a moderate (596,2 ± 29,8 ng/g) concentration, whereas Grey-sided (*M. rufocanus*) vole had the least glucocorticoid readings (408,9 ± 28,7 ng/g). In order to normalize data, we compared logarithmic corticosterone concentrations and then stratified them into years. In multivariate ANOVA (sex, month of birth), we found intersexual variations in Northern red-backed (*Myodes rutilus*) ($F_{(1.317)} = 24{,}1$, $p < 0{,}001$), Bank (*M. glareolus*) ($F_{(1.251)} = 38{,}9$, $p < 0{,}0001$), and Grey-sided (*M. rufocanus*) ($F_{(1.271)} = 34{,}2$, $p < 0{,}0001$) voles. Northern red-backed (*Myodes rutilus*) vole showed intersexual differences only in the first half of the breeding season, when females had higher corticosterone level ($p < 0{,}01$). On the contrary, Bank (*M. glareolus*), and Grey-sided (*M. rufocanus*) females had lower corticosterone levels than males ($p < 0{,}03$; 0,001) during the entire season. Age-related hormone level was modified by the species and sex. Northern red-backed (*Myodes rutilus*), Bank (*M. glareolus*) voles males differed from females in age-related corticosterone concentrations. Males of those species aged 20–60 days showed significant increase in corticosterone concentrations, whereas the females had an opposite trend. In Northern red-backed (*Myodes rutilus*) vole, sexual differences were found in individuals born in May and June, whereas in Bank (*M. glareolus*) vole we found that trend in animals born in May and August. At any other time during the year we did not observe age-related differences. Grey-sided (*M. rufocanus*) vole didn’t have sexual differences in age-related corticosterone concentrations, albeit the latter depended on the season, which we demonstrated earlier in this species (Kravchenko at al., 2012). These species individuals showed age-dependent corticosterone concentrations decrease in the first half of the breeding season. In contrast, animals born in July and August had age–dependent corticosterone concentrations increase. Population density affected corticosterone concentrations only in Northern red-backed (*Myodes rutilus*) vole. Individuals of this species bred isolated differed from others in higher corticosterone level at the age of 40 days, whereas at the age of two months those differences were not observed. Taking into account transient character of those differences, we assume that increase in corticosterone concentrations in individuals aged 40 days, which were bred isolated, was caused by high demand for energetic and plastic resources at this period. Adrenal cortex activation eased access to resources. In two other species, typical differences in corticosterone concentrations in animals bred under contrasting social conditions were not observed.

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NON-STATIONARY NONLINEAR POPULATIONS DYNAMICS: DIAGNOSTICS, MODELING, PREDICTION

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The central problem of the theory of population dynamics in its applications is the art of “back-engineering” – the reconstruction of (possible) system design from its observed noisy dynamics, selection among existing (or their modification) or building a new (better in some sense) dynamic models. A stationarity assumption is an important prerequisite in routine time series analysis. The stationary process is the one for which parameters of distribution (e.g. the first Central moments) do not change over time. It is clear that real populations often exhibit very complex dynamics; therefore, its quantitative description and interpretation, decomposition in several regular components and their prediction are not a trivial task.

I studied long-term (1982–2015) population dynamics of small mammals (SM) in the dark coniferous forests (southern taiga) of the Middle Urals. We discovered unexpected feature of SM dynamics in its auto-covariation structure (“regime shift”): there were three-year and weak annual cycles just before 2005(6), but later we observed quasi-biennial and a more pronounced annual rhythm. Some possible indicators and omens (species composition, reproductive-age structure) of that regime shift were tested. Some appropriate diagnostics of stationarity assumptions (windowed version of: autocorrelation, autoregressive and Fourier analysis; wavelet analysis, etc.), some modeling and short-term forecasting tools (nonlinear autoregression, and difference equations, etc.) were suggested. We showed (possibly critical) inadequacy of the conventional log-linear auto-regression (AR) modeling (see Royama, 1981; 1992; Bjornstad et al., 1995; Tkadlec, Stenseth, 2001; Lima et al., 2006; Husek et al., 2013; Cornulier et al., 2013) to evaluate statistical effects of density dependence for its interpretation and prediction. However, the expansion/generalization of the AR modeling is quite suitable as diagnostic tool for non-stationarity detection in studied time series and as formal quantitative characteristics of its dynamic modes. The phenomenon, interpreted as a regime shift in population dynamics (attributed to, for example, is not always measured external interventions) can be the evidence of endogenous chaos, emerging from strong nonlinearity of interactions (e.g., threshold effects) in the system under study. Despite the “transparent” – fast (annual) and slow (long-period trend) components, the presence of this kind of “nonlinear element”, which is responsible for mesoscopic scale in the multicomponent oscillations, makes the mid-term forecast a real challenge for a researcher.

ACTIVITY OF THE NATURAL FOCUS OF HANTAVIRUS INFECTION: STATISTICAL AND SIMULATION MODELING

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Understanding mechanisms of Hantavirus (HV) activity fluctuations in natural foci and predictions of epidemic outbreaks in humans are pivotal in epidemiology and medical theriology. HV is widespread worldwide within population of its small mammal hosts – rodents and insectivores. Puumala virus (PUUV) is the agent that causes hemorrhagic fever with renal syndrome (HFRS) in humans and ranked first zoonotic disease in temperate/boreal zone of Europe in terms of incidence. It is highly endemic at cis-Urals (Udmurt republic and Bashkortostan) with an annual incidence up to 56 per 100,000 inhabitants. The main object of the present study was to evaluate a set of statistical and simulation mathematical models for interpretation and prediction of PUUV reservoir activity. We conducted epizootic monitoring of the bank vole (*Myodes glareolus*, the main host of PUUV) on the territory around Izhevsk (56°50′ N 53°11′ E) and tested PUUV antigen in lungs of voles with ELISA.

Harmonic model. The first part of time series (4 observations per year) of log-density of infected voles (1981–1995) looks like oscillation with about 3-years periodicity and can been described adequately (R = 0,89), with only harmonic – $lg(I+1) = 0,52 + 0,48*sin(0,36*t-0,79)$, where argument ‘t’ is the month number since the start of 1981.

Difference equation. One time per year (in August) data can be modeled successfully via nonlinear difference equation for density-dependent growth of infected (I_t) population with discrete (non-overlap) generations: $I_{t+1} = \varepsilon + \alpha * I_t/[1 + (I_t/\beta)^{\gamma}]$, in which r ε, α, β, γ have simple and clear biological interpretation. We obtained reasonable estimates $I_{t+1} = 1 + 2,8*I_t/[1 + (I_t/4,3)^{25}]$ with $R_{1981–1998} = 0,89$, and found strong overcompensation (further, we explored model sensitivity via slight variations of key parameters – not shown). However, the naïve forecast of I_{t+1} loses the phase of observed fluctuation (and thus its value) without taking into account a pulse of external force – mast events of *Tilia cordata* (in previous year). The drive to early start of voles breeding by extra food supply and, therefore, synchronized rise of PUUV activity via a large influx of susceptible individuals (newly matured and thus under high infection risk if they are not immune and alongside this involved in reproductive activity) assumes that it took at least two years after previous PUUV outbreak. Accounting of winter breeding – (WB: 0, 1) gave us the most accurate (with advance of about 0,5 years) predictions both for PUUV activity and HFRS outbreaks (HFRSO – dichotomized yearly sum of cases HFRS to ‘0’ or ‘1’) in humans (1973–2012: $\tau_{Kendall}$(HFRSO|WB) = 1,0, Z = 9,1). The harvest level of Linden nuts (points, 0...5) drown as the only predictor, provided earlier but less accurate forecast (1973–2012: $\tau_{Kendall} = 0,7$, Z = 6,3).

Differential equations. In the our “final crusade”, we built deterministic system “resource–consumer/host–parasite”, taking into account seasonality and specified it as two coupled subsystems, each of which is a system is nonlinear and/or linear differential equations and studied its dynamics. We showed qualitative similarity in the dynamics of introduced model and observations, and supposed the cascading effects, namely, the leading role of trophic interactions in dynamics of other systems of natural-foci infections similar to the one studied.

INDIVIDUALS QUALITY DYNAMICS AND POPULATION CYCLES IN BANK VOLE

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We studied the size and weight characteristics of individuals of the Bank vole (*Clethrionomys (Myodes) glareolus* Schreber, 1780), inhabiting dark coniferous forests (southern taiga) of Middle Urals, in 1995–2015 (n = 1834). The studied population dynamics was noted for a regular three-year "population cycles" up to 2006, which in first approximation can be represented as regular alternation of three annual phases: “trough”, “growth”, “peak”... With high density of overwintered individuals, the "peak" was characterized by retarded maturation of young of the year (Kalela-Koshkina effect). From 2006–2007 fluctuations profile changed, and severe three-year regularity (and weak seasonality) was replaced by another pattern, with more pronounced seasonality and quasi-biennial “slow” component, and total suppression of maturation of young of the year was not observed ever since. The main objective of our study was to quantify the “net” (purified from confounding age effect) deficit of the body mass and body length in individuals from trough (Chitty syndrome) in contrast with the other phases.

We report statistical modeling – selection for optimality (accuracy/complexity), a convenient parameterization and biological interpretability of the nonlinear and linear models (considering or ignoring the confounding effects and control for predictors collinearity) that explain observed variability of body mass (BM), body length (BL), and body condition index (BCI). The main factor of variability of size attributes, of course, was the age (growth and maturation). Thus, using nonlinear functions of age as the only predictor allowed to adequately describe two-phase growth of young (that did not attain maturity in the year they were born) to reproduce from one-half to 2/3 of full dispersion ($R^2|y{\sim}f[age] = 0{,}67$ – BM, 0,69 – BL, 0,52 – BCI), respectively. We then explored the residuals from proposed growth equations, using them as new explained variables. The proportions of variability explained by the cycle were: $R^2|Res{\sim}f[phase] = 0{,}09$ – BM, 0,13 – BL, 0,05– BCI; with $F_{3;925} = 29{,}2$; $F_{3;784} = 39{,}9$; $F_{3;782} = 12{,}6$. The estimates for deficiency were (contrasts/se, 95% CI): $\Delta BM = 6{,}6/0{,}84$ (5,0–8,3) g; $\Delta BL = 13{,}0/1{,}50$ (10,1–16,0) mm; $\Delta BCI = 0{,}07/0{,}01$ (0,04–0,09) g/mm. Scrutiny exploration of dependent variables categorized histograms showed that all voles captured in the trough phase belonged to their left tail (below median, subnormal) In other words, super-normal individuals in the Bank vole population were not observed at all! On the contrary, there were the same and super-normal individuals in other years.

A long list of effects from the proposed by Chitty (1958, 1960) – “swing” selection fast/slow growing genotypes to the assumptions of Krebs & Myers (1974) about living longer, growing faster, etc. can be all considered as candidates for interpreting observed individuals quality dynamics (not associated with age yet). The verifiable and most likely explanation is a real challenge for the researcher, and we herein “add a penny in the piggy Bank” of hypothetical mechanisms. In our case (Kshnyasev, Davydova, 2010) main culprits of falling Bank vole population in the trough phase are the lagged effects of numerical response and pressure of specialized predators (small mustelids). Therefore the voles that survived population crash can be yearling of latter cohorts, and are alive just because they have shorter “exposure time” or occupied low-quality habitats, suffer by indirect effects of predators (via frightening chemo-signals, shortening time to feeding or low quality of their food), be doomed to high energy costs while finding conspecifics for breeding in sparse populations, etc.

MONO- AND BIPHASIC GROWTH OF *MYODES (GLAREOLUS)*: PARAMETERS ESTIMATION

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Reproduction seasonality of is strong characteristic of many species of short-lived small mammals in moderate climate, as for our case of Bank vole (*Clethrionomys (Myodes) glareolus*), which reproduces only once (April–September) during its lifetime, when the females bear several litters (2-3-4). Yearlings born in spring or early summer have a chance to mature and breed in the birth year; others born later (or under high population density – i.e. Kalella-effect) usually attain maturity by the spring of next year. Thus, the quasi-semelparity is typical for Bank vole and two strategies (ways) of ontogenesis exist: M – maturing ("spring") young of the year which has monophasic growth, and IM, immature "wintering" generation, has another pubertal growth period prior to their maturation by next spring (biphasic growth).

Based on the multi-annual data (1995–2015) of Bank vole population in dark coniferous (southern taiga) forests of Middle Urals (Visimskiy state biosphere reserve) our objective was to parameterize the dependence of body length and weight on age and/or calendar dates for two ways of ontogenesis: M – "fast grow and maturate in the birth year … and die young"; IM – "grow and live slowly and breed next year … and if you are lucky meet senescence".

Mammalian growth traditionally qualifies as asymptotic, and the sexual maturity implies the strong growth inhibition. For comparison of two growth patterns of IM and M, the simplest two-parametric Michaelis-Menten equation was used: $y = a*x/(b + x)$ where a is an estimate of population average for the upper asymptote, b is the "Michaelis constant" that numerically is equal to the abscissa (age, weeks), at which the ordinate reaches the half of its maximum level. We obtained the following parameter estimates [95% CI]: body length (mm) – $Y(IM) = 96{,}1[94{,}8–97{,}5]*x/(0{,}7[0{,}5–0{,}8] + x)$ and $Y(M) = 100{,}7[98{,}1–104{,}1]*x/(0{,}2[0{,}01–0{,}5] + x)$; body weight (g) – $Y(IM) = 22{,}2[21{,}5–22{,}9]*x/(2{,}5[2{,}1–2{,}9] + x)$ and $Y(M) = 26{,}1[24{,}4–27{,}9]*x/(1{,}2[0{,}5–1{,}8] + x)$; body condition index (g/mm) – $Y(IM) = 0{,}23[0{,}22–0{,}23]*x/(1{,}56[1{,}27–1{,}84] + x)$ and $Y(M) = 0{,}27[0{,}24–0{,}27]*x/(0{,}88[0{,}29–1{,}40] + x)$. Since the confidence intervals do not overlap, we can conclude that the M are not only characterized by higher asymptotic values of the body length, weight and condition index, but also reach its half approximately 0,5–1 weeks before the IM.

To approximate timing of second growth spurt in IM, we used the S-shape equation: $Y = \max–\{(\max–\min)/[1 + (x/t_{50})^{p}]\}$, where t_{50} (day) is interpreted as the time of 50% growth. The obtained estimations allow us to conclude that the onset of body length growth precedes the body weight increase by about two weeks, and the average [95% CI] time of 50% increase of body length, mass and condition index, respectively, corresponded to: 09.03. [02.03.–17.03.], 25.03 [11.03.–08.04.], 20.03. [05.03.–05.04.]. That is in good agreement with the idea that photoperiod has a signaling role to synchronize small mammals growth and maturation in conditions of moderate climate.

SOME ASPECTS OF THE ROADS' USE BY BIRDS

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Roads are an essential component of man-made environment. Being linear communication structures, they bring mostly local changes to the biotope, the extent of which depends on the category of the road and ranges from 2 to 20 meters width or even more. The roads constructed within the city and in other settlements differ, and the first are man-made and transformed environment. Therefore, the road network acts as a segmented structure that contributes to one of the elements of mosaic sphere.

Due to the length of roads, animals and birds in particular, are forced to get in contact with them (Vladyshevsky 1972; Hell, 2005; Kukhta, 2013). The species use most of all their outdoor space for foraging (Lysenko, 2000), collecting invertebrates, alive or knocked down by trucks, from the roadway, curbs and ditches. Granivorous birds feed along the roads, collecting seeds on the sidelines in summer. Highways provide forage for birds, that is why certain types concentrate near them in search of food. The negative impact of roads is primarily confined to bird deaths from collisions with motor vehicles.

Causes of bird deaths on the roads are primarily determined by their behavior. Regular traffic contributes to adaptation and natural reduction of flight zone, that is why the bird often do not have time to react to the environmental changes, especially young birds such as crows and rock-pigeons. In other circumstances, tolerance contributes to the bird`s weakening of attention to regular hazard when doling something else, for example, when procuring forage. Because of such behavior, thrushes and small passerine birds (finch, yellowhammer, and tree sparrow) are killed primarily while crossing the road at low level when foraging.

The intensity of destruction depends on the environment biotope around the road. Most intense destruction is observed on the roads passing through populated areas (Kukhta, 2011) causing distraction and leading to an excessive attention dispersion. Rock pigeon can be hit by a car in the city moving at a speed of only 20–30 km/h or even by a bicycle. That is aggravated by small flight zone, which is common for rock-pigeons in general. These birds are so accustomed to motor transport and do not fly up, but only sheer out. On the contrary, sparrow also residing in settlements and using roads to collect food reacts differently leaving the risky zone in advance, probably resulting in their significantly lower mortality on the roads (1–3 birds for the entire summer).

Behavioral type can change during life. For example, snowbird and finch perish on country roads mainly in the beginning of summer, at that time collecting shot down insects along the roads and curbs to feed chicks, crossing the road at low level. Later on, there appear more young fieldfares at the end of breeding period with almost no finches. Interesting to note that common starling, like fieldfare, often feeds along the roads in the beginning of summer was not among observed dead birds on the road. That probably happens because of greater flight zone, and the birds did not allow vehicles approach closer.

It is obvious that on the one hand, birds` adaptation to motor transport allows them to advantage of roads for foraging, but on the other hand, that increases the risk of being killed on the road.

CYTOGENETIC STUDIES OF ECOLOGICAL HOST OF AMUR HANTAVIRUS IN FAR EAST OF RUSSIA

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Some members of the *Muridae*, *Cricetidae Sigmodontinae* families are ecological hosts of Hantaviruses, pathogenic to people, and strongly associated with them in the process of co-evolution. Parasitic system "hantavirus-rodent" is binomial and the rodents are direct members of the Hantavirus transmission and the sources of human infection (Bennett, 2014; Jonsson, 2010). 22 pathogenic Hantaviruses are known to cause hemorrhagic fever with renal syndrome (HFRS) in Eurasia and Hantavirus pulmonary syndrome (HPS) in the Americas. In Asian part of Russia, natural foci circulation of *Amur* virus (Primorye, Primorye1-China, Khabarovsk, Amursk genetic variants) in populations of Korean field mice (*Apodemus peninsulae*) natural host and of *Hantaan* virus (Far East genovariant) in populations of striped field mouse (*Ap. agrarius*) ecological host were identified in forest and forest-steppe HFRS (Slonova, 2008; Yashina, 2012). A number of publications exist on chromosomal damage under viral infections, in which the occurrence of chromatid breaks and exchanges were considered a specific feature of viral clastogenesis. *Ap. peninsulae* is a unique species, because high frequency of some specimens of B-(additional) chromosomes and variations of number and size-morphological types were found in those populations (Roslik, Kartavtseva, 2012). T.S. Bekasova and N.N. Vorontsov (1975) proposed a hypothesis on the role of viral infection agents in the emergence of B-chromosomes in the rodents' karyotype. So far, no karyological analysis of chromosome complement of Korean field mice as carriers of different genetic variants of *Amur* hantavirus in natural foci of HFRS was done.

We used material the from forest foci of hantavirus infection in Primorye territory. Hantavirus antigen and specific antibodies were detected in ELISA and IFA. We processed metaphase chromosome preparations in the laboratory using direct standard method from red bone marrow (Ford, 1956). 68,0% of all catches and 76,2% of all infected rodents in forest natural foci of hantavirus infection were *Ap. peninsulae*, dominating both during decline and rise of animal counts. We obtained preliminary results of karyological analysis of Korean field mice from the western and southern regions of Primorye, where phylogenetically different genetic variants of *Amur* virus circulate. Chromosome composition of the examined specimens did not go beyond *Ap. peninsulae*. Forty-eight decreasing acrocentrics were determined in the A-(basic) set. Individuals with Hantavirus antigen and specific antibodies also had two additional chromosomes. B-chromosomes of western region mice, unlike southern mice, were small-dotted $2n = 50$ (2B: mS) or even very small-dotted $2n = 48$ (+2B). According to the geographic distribution of *Amur* virus (Yashina, 2012) our *Ap. peninsulae* populations carried two different genetic variants of this virus. *Ap. peninsulae* populations from the western regions carried Primorye1-China genotype, which is prevalent on the border territory of China. *Ap. peninsulae* populations from southern region carried Primorye genotype, known in the eastern part of Primorye. Karyological analysis of Korean field mice from different locations showed differences in dimensions and morphology on the inter-population level in line with other studies (Kartavtseva, 2004; Roslik, 2012). Our results confirm and complement data on *Ap. peninsulae* polymorphism of this epidemically significant species for Russian Far East as transmission vector of different *Amur* Hantavirus genetic variants, pathogenic for people. There is a need for further comprehensive studies of *Apodemus* genus species to explore the involvement of Hantaviruses in the chromosomal rearrangements and B-chromosomes appearance in the karyotype of their ecological hosts in terms of time and space.

MULTI-YEAR DYNAMICS OF PIED FLYCATCHER REPRODUCTION IN THE IMPACT ZONE OF SIBERIAN CHEMICAL PLANT

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This study was conducted in the sanitary and protected (impact and experimental) zones of Siberian chemical plant (SCP) near the plants in Tomsk Province in 1994–2016. Control site was situated 25 km southwards from of Tomsk off the dominating winds. SCP is a group of plants specializing in weapon plutonium and uranium production until 2008. Because those plants stopped, radionuclides and inert radioactive gases emission also discontinued. At present, they still process used fuel and purify raw uranium.

We traced 453 pied flycatcher nests in the artificial locations, and measured 1523 eggs. This species is an obligatory insect eater and collects food in the tree crown and in the underbrush. In order to track the technogenic impact on reproduction, we used embryo mortality in preserved nests, partial chick mortality and reproduction success in the nests preserved until birds departure. We excluded those nests, where females bred chicks without males. We sampled soil to test radionuclides concentration using envelope method to a depth of 10 cm. “Gamma-plus“ spectrometer (Department on environmental protection and resources use of ZATO Seversk, 2004)was used to test radionuclide activity as well as “Progress” spectrometric set (Radiosurveillance lab NII BB of Tomsk University, 2016).

The mean Cs^{137} specific activity in soil at the experimental platform was 180,2 Bk/kg (n = 5) in 2004, while 17,6 Bk/kg (n = 3) in control. Similar indicator at the experimental platform was 102,8 Bk/kg in 2016. During 12 years, there was a 43% Cs^{137} specific activity reduction, which is very close to the calculated reading (40% with a period of half-life 30,2 years) and confirms no meaningful penetration of radionuclide in soil in the during the studied period.

From 1994 until 2008, nesting density, laying and eggs volume in the impact zone (6,88 ± 0,03 eggs and 1669 ± 7 mm^3) did not differ from the control (6,92 ± 0,06 eggs and 1672 ± 4 mm^3). This prompts no serious radioactive or toxic impact on the ovulation and laying in the experimental territory, and may be indicative of similar trophic conditions in SCP and control in pre-nesting period and during laying. Embryo mortality in the impacted zone (6,8%) was significantly greater compared to control (4,6%), which is indicative of embryotoxicity of SCP environment. Partial chick mortality (4,6% и 5,6%, respectfully), as well as reproduction success in safe nests before departure (88,9% и 88,3%, respectfully) did not differ between the territories.

From 2009 until 2016, the mean laying size in the impact zone was 6,81 ± 0,05 eggs (n = 340), embryo mortality 7,6%, partial offspring mortality 5,8%, reproduction success in safe nests before departure 88,2%. There was no significant change when compared to the previous period (1994–2008) with regard to these indices in the impact zone. Therefore, 40% reduction in soil contamination with Cs^{137} in the impact zone, coupled with full discontinuation of inert radioactive gases emission did not result in embryo mortality reduction in the experimental pied flycatcher population. This still testifies environmental conditions in the sanitary and protective zone of SCP as embryotoxic with regard to the studied species.

DIVERSITY, PREVALENCE, DISTRIBUTION AND NATURE CONSERVATION STATUS OF WESTERN SYBERIA AMPHIBIA

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This work was built on collections and field research of authors in spring and summer of 1975–2015 from various locations in Western Syberia. We used 40-years (1972–2012) electronic Amphibia records of V.A. Yakovlev from Northeastern Altay along with zoo data bank of the zoomonitoring lab of the Animal Ecology and Systematics Institute of RAS SD (Novosibirsk). Literature search was conducted, followed by revision of collections and catalogues of zoology museum in AESI RAS SD (Novosibirsk), Development Biology Institute named after N.K. Koltsov of RAS (Moscow), Zoology Institute (St. Petersburg), Saratov, Tomsk and Moscow state universities and their relevant departments. We also analyzed questionnaires of professional zoologists, biology teachers along with the hunting and forestry industry personnel (1987–1989, 2002–2003). Using data obtained, we created cadaster schematic maps in MapInfo Professional v.7.

We ended up with summary data on diversity, modern prevalence and distribution with nature conservation status of Amphibia species, inhabiting various zones of Western Siberia limited by Republic of Altay, Altay Province, left bank of Yenisei in Krasnoyarsk Province, as well as Novosibirsk, Kemerovo, Tomsk, Omsk, Tyumen, Kurgan, Sverdlovsk and Chelyabinsk Provinces and Khanty-Mansiisk and Yamal-Nenets autonomous districts.

Western Siberia batrachofauna is relatively poor and is only represented by 11 species: *Salamandrella keyserlingii*, *Lissotriton vulgaris*, *Triturus cristatus*, *Pelobates fuscus*, *Bufo bufo*, *Bufotes viridis*, *Bf. pewzowi*, *Rana temporaria*, *R. arvalis*, *R. amurensis* and *Pelophylax ridibundus*. The number of species westwards decreases: *T. cristatus*, *R. temporaria*, *P. fuscus and Bf. viridis* inhabit only Western part of the valley (*Bf. viridis* is also introduced in Novosibirsk, found around Novosibirsk water reserve). Considering taxonomy of *Bufo (Bufotes) viridis* group, species composition of Amphibia of this region was enriched with new the tetraploid species of Pevtsov toad *Bf. pewzowi* in Altay (Litvinchuk et al., 2010), which was earlier attributed to *Bf. viridis* (Malkov et Malkov, 2002). This is the only territory where this species exists in Russia. We recorded gradual reduction of batrachofauna species diversity northwards and southwards wooded steppe. As a result of our analysis (more than 1800 new records and findings, illustrated with 11 maps and their cadasters), we clarified the species areal borders' origin: Northern for *T. vulgaris, Bf. pewzowi*, Western – *R. amurensis*, Eastern – *R. temporaria, T. cristatus, P. fuscus, Bf. viridis.* Invasive species imported for fish-farming in this region (*P. ridibundus)* expanded more than 900 km Northwards along Ob valley during the last 50 years.

10 out of 11 species (excluding *R. arvalis*) were introduced in the Red Books and their appendices of various regions with nature conservation status "rare", "areal peripheral species with sporadic prevalence", "species with academic and esthetic content". Pevtsov toad, *Bf. pewzowi* was recommended for inclusion in the Russian Red Book.

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POPULATION DYNAMICS OF RODENTS-CARRIES OF HANTAVIRUSES AND EPIDEMIC RISK IN FOREST ECOSYSTEMS OF PRIMORSKII KRAI

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Epidemiological deterioration of hemorrhagic fever with renal syndrome (HFRS) in forest ecosystems of Far East Region of Russia is connected with distribution and population dynamics of *Apodemus peninsulae* Tomas (1907) – the natural host of *Amur* pathogenic for human Hantavirus. *Myodes rufocanus* Sandervall (1846-1847) is codominant of *Ap. peninsulae* and carries nonpathogenic Hokkaido Hantavirus. The objective was to define threshold number of all / number of infected *Ap. peninsulae* on different phases of population change in order to predict HFRS in forest ecosystems of Primorskii Krai. Materials obtained during the expeditions and stationary investigations (2001–2013). The overall trap-nights was 30812. Number of caught and surveyed rodents (abs.) / fraction in catch (%): 2474/59,1 ± 0,8% of *Ap. peninsulae*; 205/4,9 ± 0,3% of *Ap. agrarius*; 1505/36,0 ± 0,9% of *M. rufocanus*. ELISA, IFA, HAI, RT-PCR, PH methods were used to verify antigen, specific antibodies and their avidity, anti-hemagglutinins, RNA, and infectious virus. Variables: a) infected rodents – Hantavirus antigen/RNA in organs and/or specific antibodies in blood of rodents; b) relative population count / relative population infectious rate – number of all rodents/number of infected individuals (recalculated to 100 t.-n.); c) acute Hantavirus infection in animals – Hantavirus antigen/RNA in lungs and secretion/excretion organs and/or antibodies of low/transitive avidity; d) epizootic activity in population – number of infected rodents with acute infection per 100 t.-n.

Active *Amur*-hantaviral infection foci are located on the Eastern and Western slopes of Sikhote-Alin Ridge with mixed coniferous/broad-leaved forests, which are auspicious for *Ap. peninsulae* dwelling. The means of long-term counts for populations: *Ap. peninsulae – M. rufocanus – Ap. agrarius*. Number of rodents per 100 t.-n: 8,0 – 4,4 – 0,7. Infected individuals per 100 t.-n: 1,5 – 0,6 – < 0,1. Proportion of catching (%): 59,1 – 32,7 – 4,9. Proportion of infected part (%) – 66,6 – 28,1 – 2,7. All values were much higher in *Ap. peninsulae.* Dynamics of epizootic process in *Ap. peninsulae* populations was noted for marked cyclic recurrence including rise, high and low activity. Growing and high activity last for no more than a year – from autumn of current year till autumn of next year, followed by a drop in activity. Decrease/low epizootic activity lasts for a few years, defining duration of all epizootic cycle from one rise of process activity to the other. During the period epizootic activity increase, the number of rodents with acute infection increased from summer until late autumn by up to 2 individuals per 100 t.-n. During the year of high epizootic activity, rodents count with acute infection in spring and summer seasons was more than 5 and 7 individuals per 100 t.-n. on average, and dropped by more than 3-fold in autumn with quite large population count. During the period of low activity, we met individuals with acute infection during all seasons, but their count did not exceed 0,3 individuals per 100 t.-n.

HFRS occurrence in wood foci. 68% of HFRS cases from annual incidence were registered in spring and summer during the years of high number of mice and epizootic activity of *Ap. peninsulae* populations. We noted two peaks of HFRS incidence during the period of *Ap. peninsulae* count rise and peak: late fall-winter (≥ 37% of cases) and spring-first half of summer (≥ 55% of cases from annual incidence). Threshold indicators of relative number of *Ap. peninsulae*/number of infected mice were confirmed in different phases of its cycle: I* – rise; II* – high; III* – low. Basic parameters of rodents count per 100 t.-n: N – all population, n – all infected, n_{ai} – individuals with acute infection. Threshold indicators for *A. peninsulae* populations were: I* $N \geq 8{,}0$ – $n \geq 1{,}8$ – $n_{ai} \geq 1{,}5$; II* $N \geq 20{,}0$ – $n \geq 7{,}0$ – $n_{ai} \geq 5{,}0$; III* $N \leq 6{,}0$ – $n \leq 0{,}5$ – $n_{ai} \leq 0{,}3$.

The number and infectious rate of *A. peninsulae* populations results in the inter-annual and seasonal distinction of distribution and number of HFRS cases. The new approach to the epizootic activity assessment in populations of ecological host allows predicting periods of increased risk for people in acquiring Amur Hantavirus in forest ecosystems.

ON THE MECHANISM OF POPULATION CHANGE OF THE COMMON FROG (*RANA TEMPORARIA*) AND THE MOOR FROG (*R. ARVALIS*)

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Observations of changes in the number of brown frogs were carried out in the Nature Reserve “Kivach” (Russia, South Karelia, subzone of middle taiga, the mean coordinates 62°17' N, 33°55' E). Physical and geographical conditions of the region are favorable for two coexisting frog species, and inhabitation on the protected area excludes any anthropogenic impact. In 1982–2015, the size of reproductive frog population was assessed via the number of spawn clumps laid in the control breeding ponds in several locations of the territory.

Time series analysis showed that the size of *R. temporaria* breeding population in “Kivach” did not follow any trend. Periodic component and an exponential trend were found in only one gradually increasing breeding group (length of series 32, model describes the variation of 74% of its value). Spatial groups of various levels showed not completely synchronous, but interrelated population count. *R. arvalis* count fluctuates randomly also, and the rhythm of isolated populations change was independent. We failed to trace consistency in the count of two species. Moreover, in case of syntopy of two large breeding groups, a process which I would call “progressive desynchronization” occurred concurrent to observation period increase.

The use of multiple regression analysis (Kutenkov, Mosiyash, 2000; Kutenkov, 2009) allowed quantifying the impact of factors generating variation in the abundance of *R. temporaria* on the main stages of ontogeny. The abundance of newly metamorphosed juveniles, their abundance in the beginning of autumn, fluctuations on the stage of “yearlings”, as well as the number of mature frogs determined by count on the preceding developmental stage in 12–37%, and by fluctuation in weather conditions in 16–63% determined (R^2 coefficients of determination of regression models were 0,52–0,89). Such important variable as the size of juveniles before their first hibernation was determined by weather condition in 63% (Kutenkov, Mosiyash, 2013). Number of spawn clumps (used in this paper, “number of frogs” variable) was almost completely (92,3%) determined by an abundance of mature frogs a year before. Differences in the nature of the trajectories of *R. temporaria* and *R. arvalis* population change were determined by the spatial structure of these species. *R. temporaria* reproductive and feeding habitats range was wide, and frogs hibernated in numerous permanent water bodies. On the contrary, *R. arvalis* were confined to certain mire habitats only throughout the annual cycle, and the nature of separated populations change was determined by the local meteorological situation.

Most investigators adhere to the concept of density-dependent population regulation in amphibians (Wilbur, 1980; Berven, 1990; Meyer et al, 1998; Lyapkov et al, 2006; Pellet et al, 2006; Salvidio, 2009). This concept, however, does not explain the observed amplitude excursion and instability rhythm of fluctuations of the studied populations. Weather conditions as possible “generator” or “driver” of number fluctuations are not significant. However, there is no doubt, that the main reason of number change is the variation of weather conditions impact on the survival of specimens at the early stages of ontogeny. In natural environment, the process of brown frog species’ number change is variation of the number and the “quality” of new generations, caused by weather conditions.

COVARIATION PHENOMENON OF PHYSIOLOGICAL STATE IN TWO SPECIES OF FOREST VOLES IN THE COURSE OF THE LONG-TERM POPULATION DYNAMICS

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We analyzed physiological state variability of two populations of forest voles (*Cl. rutilus and Cl. rufocanus*), inhabitants of mountain taiga of the North-Eastern Siberia in the course of the long-term study in three ecosystems. Those were typical for the region floodplain river valleys of the Northern Priokhotie (1980–2000), continental Kolyma (2001–2009) and sparse larch forest of the Northern Priokhotje (2010–2015) (Cherniavsky, Lazutkin, 2004; Lazutkin, 2016; Lazutkin 2016, etc.).

The study of population dynamics of both species while being similar showed distinct species' specificity in terms of both population density and different phases of the cycle. Geographic variability also appeared to be peculiar for each species. One of the aims of the work was the study of physiological aspect in rodents' number regulation. A number of metabolic and immune parameters was used as an estimate of animals' physiological status (lipids and glycogen in the liver, glucose and leukocytes in blood, bone marrow cellularity, weight index of spleen and thymus). We found significant associations of these parameters with population density – population rise was preceded by good physiological status, while population peak resulted in its breakdown afterwards. Physiological status was also shown to be species-specific, i.e. almost all studied variables, including population density, were significantly higher in the northern red-backed vole compared to large-toothed red-backed vole.

Despite these species-specific population characteristics, both seasonal and annual variability of the studied physiological parameters in both vole species was synchronic in all study sites throughout the study. In other words, two species of forest voles functioned in the same physiological rhythm.

Environmental analysis showed high degree of compatibility of both spatial and trophic niches in both species. Survival rate of *Cl. rutilus* and *Cl. rufocanus* equally depended on the winter climatic factor. Finally, both closely related species co-existed under the impact of their common density.

Thus, the mentioned phenomenon of similar lability of physiological status in two species of forest voles appears to be under common environment control, and it well illustrates known theoretical principle of I.A. Shilov (2002), who considered homeostasis to be "a state of dynamic equilibrium with the environment".

LONG-TERM DYNAMICS OF *TESTUDO GRAECA NIKOLSKII* POPULATION ON THE ABRAU PENINSULA

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The areal of *Testudo graeca nikolskii* (Chkhikvadze, Tuniev, 1986) extends in a narrow strip (3–15 km) from the northwestern part of the Abrau peninsula down to the southeastern part of the Pitsunda peninsula (Leontyeva, 2004; Pestov et al., 2009). Human settlements and roads dissect the areal of the tortoise. The largest and most stable group of subspecies remained on the Abrau peninsula (northwestern part of the area), where the State Nature Reserve “Utrish” was created in 2010.

Study of *T. g. nikolskii* population dynamic are held on the Abrau peninsula since 1991 (in spring and autumn) via standardized square and route counts methods (Novikov, 1953). Two sample squares were created for this purpose, one of which was on the hillside southern exposure, covered with juniper-pistachio light forest and with *Palliurus spina-christi* along the edges, while the second was in the mid-part of Lobanova valley with hornbeam-oak forest. The routes ran in different directions of the peninsula and crossed different types of landscape and vegetation. During 15 years of studies, about 1000 km of routes were explored and about 900 tortoises of different age groups (40 to 80 individuals per year) were found. Caught tortoises were measured, tagged and released into locations, where they were captured.

Route counts allowed estimating tortoise biotope distribution on the Abrau peninsula (Kostenko, Leontyeva, 2007). Animals preferred gentle slopes of the southwest – southeast exposures at an altitude less than 100 meters above sea level (more than 40 ind./km^2), covered with woodlands mainly of juniper, pistachio and hold-wood with well developed grass stand.

The size-sex structure analysis of this populations showed that 17,5–22,5 cm (62% females and 72% males) individuals, which corresponded to age 25–30 were more prevalent. Tortoises of such size had 15–22 “growth rings” on the scutes of the carapace, while males and females had different size with similar growth rings. Young males grew faster than females, but their growth slowed down with age. Therefore, the distribution of size peaks of males and females was not similar, and an interval of 17,5–20 cm (42% of the total count) in males and average rate of 20–22 cm in females. There were three times more females than males in the greatest size category (250–300 mm). This agrees with the assumption that adult females grow faster than adult males. Such changes in tortoise population structure (with small deviations) were typical for all years, which demonstrated relative stability of age and sex structure of the group.

Small number of young individuals in the samples throughout the observation (up to 100 mm – about 10% of the total number, 100–150 mm – 9%) is explained by the ecology of this species and errors of the observation methods. Tortoise count reduction in descending order corresponding to their size found via any methods leads to a distorted understanding of tortoises’ distribution in size categories.

In 1985, A.A. Inozemtsev and S.L. Pereshkolnik (1985) showed similar age and sex distribution for a sample of 96 individuals. They concluded that the population of Mediterranean tortoises on the Abrau peninsula was very vulnerable and predicted almost complete disappearance of the tortoises in the next 10–15 years. However, no change occurred since then. Thus, *T. g. nikilskii* populations in the Abrau peninsula should be considered relatively stable throughout the observation.

POPULATIONS OF ROCK VOLES IN THE RODENT COMMUNITIES OF OPEN LANDSCAPES OF SIBERIA, KAZAKHSTAN AND MONGOLIA (ENVIRONMENTAL STRATEGIES AND PHYLOGENETIC RELATIONSHIPS)

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Rock voles inhabit rocky habitats in steppe, mountain steppe, alpine and sub-alpine landscapes of Central and North Asia. Because this group of animals is strongly confined to specific elements of landscape (the upper belt of mountains, rocky outcrops and deposits of stones), we assume that the rodents habitats are relict elements of the landscape in which animals survived so far. This is confirmed also by our long-term observation, which shows that the habitats of many species of rock voles become more fragmented and reduced in size.

The study was carried out on the territory of Kazakh Upland (North Kazakhstan); mountain ridge Saylyugem, Chikhacheva, North Chui ridge, Ukok plateau (Altai Republic); in Western and Eastern Tuva; on the ridges of the Eastern Sayan, Khamar-Daban; in Tazheranskaya steppe (Baikal region), Khakassia, and in the vicinity of lake Hovsgol (Nothern Mongolia).

The studies elucidated distribution of the following vole species: *Alticola macrotis* Radde, 1861; *Alticola strelzowi* Kastschenko, 1899; *Alticola semicanus* G.Allen, 1924 *Alticola barakshin* Bannikov, 1947; *Alticola tuvinicus* Ognev, 1950; *Alticola olchonensis* Litvinov, 1960. We studied rodents' communities occurring in the mountains alongside with rock voles.

We demonstrated that the rock vole sustained its dominant position in the landscape of rodents communities up to date. However, we found reduction and fragmentation of certain species habitats.

Cytochrome B sequences variation of five Alticola species were analyzed. We hypothesized their phylogenetic relationships as a result of this study. Monophyly of Alticola genus was confirmed. We generated gene tree that reflected relationship of nine species of the genus Alticola. One of the clade on the tree is represented by one species – *A. barakschin*. Other species' grouping within the clades corresponded to the species identified on the morphological basis. The analysis also showed *A. olchonensis* to be a valid species, which is associated with Mongolian silver vole *A. semicanus* and *A. tuvinicus*, closely related species to *A. strelzowi* vole. Our data confirm the findings of Coley et al. (2014), supplementing and expanding them to include *A. tuvinicus* and *A. olchonensis* in the analysis. Supported by a grant RFFI (14-04-00121; 15-29-02479).

LIMITS OF TEMPERATURE ENDURANCE OF REPTILES AND THEIR THERMOADAPTATIONAL BEHAVIOUR

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The critical thermal minimum and maximum of the body temperature are the absolute temperature limits, in which reptiles exists (Brattstrom, 1965; Prosser, 1977; Shilov, 1985; Slonim, 1986; Witz, 2001; Huang et al, 2008; Xu et al, 2006). These temperature parameters may be indicative of species plasticity temperature (Witz, 2001).

In natural environment, we measured the temperature in the esophagus of four species of Kama Urals reptiles (taking it for the body temperature, as the rectal temperature and the temperature of the skin are lower in most cases). Fast temperature measurement in the esophagus was performed with a thermistor MT-54, calibrated with the electrical thermometer Checktemp, connected to micromultimeter. Body temperature was recorded in animals in an active state, that is, outside the shelter. For long-term snake temperature recording in a cage, we placed a “tablet” type iBDL recorder under the skin on the back with working surface facing the body. To determine the sub-lethal and lethal temperatures, we used a portable computer “Valens” EKGK-02 cardiograph. We heated and cooled animals in ShN M climate chamber. Both heating and cooling lasted for 90 min., starting from 23,0 °C. The appearance of arrhythmia recorded with ECG was indicative of sub-lethal temperature, whereas isoline for at least 3 minutes indicated lethal temperature. Typically, when we reached sub-lethally high level, fast water cooling could reduce the animal's body temperature.

In natural environment, reptiles are almost never exposed to extreme temperature, which is achieved only in the experimental conditions. From the minimum or maximum body temperature, which animals can tolerate, to a critical level in the experiment there is always a “safety margin” equal to difference between the extremes of “natural” and “experimental” temperature. The average body temperature of Sand Lizard *Lacerta agilis* (Linne, 1758) (n = 220) for the entire period of activity was 30,7 ± 0,28 °C (lim 15,7–38,5 °C) with a range of 22,8 °C. In the experiment (n = 14), the mean sub-lethal body temperatures were -0,9 °C and 42,9 °C (range 43,8 °C), lethal were -5,0 °C and 54,6 °C (range 59,6 °C). For viviparous lizard *Zootoca vivipara* (Jacquin, 1787) (n = 120), the mean long-term body temperature was 27,9 ± 0,40 °C (lim 12,8–35,3 °C; range 22,5 °C). In the experiment (n = 3) sub-lethal temperatures were –4,0 °C and 42,0 °C (range 44,0 °C), and lethal are –5,0 °C and 44,1 °C with a range of 49,1 °C. For grass snake *Natrix natrix* (Linne, 1758) (n = 435), the mean body temperature is 25,4 ± 0,17 °C (lim 13,6–36,6 °C; range 23,0 °C). In the experiment sub-lethal temperatures are -0,8 °C and 44,0 °C (range 44,8 °C), and lethal were -2,1 °C and 47,6 °C (range 49,7 °C). For viper *Vipera berus* (Linne, 1768) (light morph (n = 211), body temperature was 27,0 ± 0,35 °C (lim 6,2–35,9 °C; range 29,7 °C). In the experiment (with only one light morph individual), sub-lethal temperatures were -5,0 °C and 38,1 °C (range 43,1 °C), the lower lethal was clearly low -7,0 °C, the high lethal was 48,9 °C with a range of no less than 55,9 °C.

Permanent registration of body temperature is probably the most informative method to assess thermo-adaptive behavior of reptiles. For the grass snake and viper, it was possible to determine predominantly two-peak summer daytime activity with such forms as morning heating, daily activity, gradual cooling in the evening and stay in a shelter at night. On a hot day, the snake does not allow overheating, actively regulating body temperature moving into the shade. Maximum temperature under the back skin of vipers is 37–38 °C. Daily activity time for this species lasts for 12–13 h. on a warm day, being 3–4 hours shorter on a cold, but sunny day.

MECHANISMS OF DIFFERENT POPULATION DENSITY THAT INFLUENCE MAMMALS REPRODUCTION

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In many mammals' species, reproductive rate depends on the density of population. Population increase results in reduced size of broods, proportion of breeding females, and increased embryonic mortality. The effect of different population density on reproduction may be both direct and indirect. Stress caused by dense habitation, blocks reproduction in low-ranking individuals, alters parental behavior leading to death of the brood (Christian, 1950; Chitty, 1960). Frequent contacts also block manifestation of reproductive heterosis in heterozygous offspring. At high population density, spotted gopher reproductive heterosis is not present even in the descendants of clearly unrelated parents. Reproduction due to heterosis will not occur (Lobkov, 2011).

At high density, due to free territory limitation and resulting territorial behavior, dispersal of young is hampered, and they are more likely to remain near the maternal burrows. As a result of their reproduction with time, number of related individuals that live nearby increases as does their homozygote rate. After few generations, population differentiation based on genetic characteristics in different parts of spatial groups and formation of genetic lines occur. Reproduction lessens not only because of stressful situations, but also due to inbred depression.

At the same time high population density being a factor in the temporary differentiation of gene pool for genetic lines in different parts of the spatial groups, sets conditions necessary to obtain the effect of reproductive heterosis in the offspring of parents belonging to different lines. At low population density, migration activity and the mating probability of unrelated individuals, living far away from each other before, increases. Their offspring is usually heterozygous and carries reproductive heterosis, which manifests only in certain conditions (Ivanova, Kravchenko, 1967). The latter include not only low population density, but also unformed spatial-ethological structure. This is confirmed by the fact that the count decrease with the adjacent population density decrease, but its spatial structure and kinship parents in reproductive groups remain, fertility of those born in such conditions does not increase, causing the inertia of reduced reproduction in few generations (Davis, Christian, 1976; Mihok, Boonstra, 1992).

Varying population density regulates its reproduction not through just physiological mechanisms based on stress effects, but also via genetic mechanisms based on the effects of different types of mating (between related or unrelated parents), which interchangeably dominate in conditions of high or low population density. They are non-specific as all species periodically end up in a condition, when because of natural or anthropic influence, spatial-ethological structure is destroyed, and the population is so small that does not allow quick recovery, or in a state of population high density and structuring. In the first case, the number of particularly fertile individuals increases, whereas decreases in the second.

ON THE REASONS OF CYCLIC CHANGES IN THE MAMMALS COUNT

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Number cycle are changes when its temporary increase ends with a return to the original values (Bashenina, 1977). The reasons of population rises and drops are genetic changes, due to a change in the prevailing mating types, both related and unrelated, such as inbreeding depression and heterosis (Abashkin 1974, 1976). It is known that heterosis is manifested with the body size as well as of the females' reproductive potential and other changes (Ivanova, Kravchenko, 1967). Big size and better survival of individuals of different mammals species born in the beginning of number increase (Lobkov, 2016), may indicate that heterosis was its cause. Temporary increase in the birth rate on the rise in the number can also be attributed to this phenomenon.

In conditions of poor spatial-ethological structure formation and low population density, which typically occur in the beginning of the rise in number, there are mass regrouping of individuals and unrelated parents mating, who previously lived in different parts of spatial groups, their offspring develops reproductive heterosis,. The level of reproductive potential of females (high or low) remains for the entire life (Lobkov, 2016); therefore, high growth rates remain until the extinction of old age of the most fertile generations. Heterosis is manifested in the first generation individuals only, fading in subsequent generations. Therefore decline in growth in the late phase of number rise occurs automatically with the change of generations.

Number cycle begins with the increase in annual growth as a result of not only increasing fertility, but also of lower mortality. The highest survival rate of the juveniles marked in the phase of population increase in spotted gopher (*Spermophilus suslicus*), fox (*Vulpes vulpes*), and mountain hare (*Lepus timidus*) (Lobkov, 1999; Korytin, 2002; Meslow, Keith, 1968). There occurs rejuvenation of the population as a result of intensive breeding and increased survival of offspring. Therefore, mortality due to aging temporarily drops. It increases later during the phase of count peak, when age structure changes. Individuals of the most numerous generations born at the beginning of the rise in number, die off with no replacement because of rate decrease. Therefore, the decline after its peak is inevitable and does not depend on the enemies, disease, and poor physiological state of the individuals, which only accelerate it. When growth rate returns to the previous values, and excessive population is dying of old age, its original number is restored with cycle completion.

The phenomenon of heterosis is common in all mammals, so it is involved in the formation of number cycles in different species. The indirect evidence of that is similar duration of cycles, expressed in life expectancies of individuals of these species. On average, one cycle lasts for 4–5 lifetimes of individuals of this species or corresponding to the replacement similar to the number of generations.

Changes in the indices of reproduction, body sizes, survival of individuals born at different phases of cycle, indicate natural transformation of qualitative composition of population during number cycle, which confirms the idea stated by I.A. Shilov (1998), that one should not speak about the population dynamics, but about population cycles.

BIODIVERSITY OF VIRUSES KINGDOM. FLAVIVIRUSES AND ZIKA VIRUS

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Flaviviruses are relatively simple positive RNA-containing spherical shell-like viruses 40–60 nm size. Flaviviruses are capable to infect different hosts, such as mammals, birds, reptiles and insects. In most cases, flaviviruses transmission occurs by vector: through mosquito or tick bites. The most relevant for humans flaviviral infections are associated with dengue, yellow fever, Japanese encephalitis, West Nile and tick-borne encephalitis viruses. For Russia, tick-borne encephalitis has a greatest importance from the medical perspective.

In the last decades, many new infectious diseases caused by various infectious agents were registered in different countries. Nowadays, the problem of emerging and re-emerging infections is considered very important for public health. Flaviviral infectious are not an exception, and new flaviviruses are discovered, their geographical distribution changes, and new genetic flaviviral variants emerge. Over 37 cases with new genetic flaviviral variants and the discovery of new flaviviruses marked the period from 1993 to 2016. This suggests that many species of flaviviruses develop high genetic variability and the ability to adapt to new climatic and geographic conditions.

Zika virus in recent years is a nice illustration of that. Zika virus was described in 1948 as new mosquito-borne flavivirus associated with monkey infection in Africa. In 1968, Zika virus was firstly isolated from human in Nigeria. In 2015, Zika fever became endemic for Brazil and other countries in South and Central America. Currently, many researchers confirmed practically global dissemination of Zika virus.

The emergence of new genetic variants of flaviviruses shows that the genetic variability and biodiversity of these RNA-containing viruses has not yet been fully studied. It is important to note that our knowledge about genetic variability of flaviviruses is essential for further development and improvement of prevention measures, as well as better diagnosis and treatment for flaviviral infections.

BASIC ADAPTATIONS OF BIRDS HABITATING IN THE URBANIZED LANDSCAPES OF THE CITY OF TYUMEN

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Emerging human settlements result in the natural biocenoses destruction with the following creation of free and peculiar ecological niches, quickly inhabited by animals. Anthropogenic factors produce huge impact in the city, forcing birds to develop adaptive reactions (Clausnitzer, 1990; Rakhimov, 2001). What are the main adaptations formed in birds dwelling in urbanized landscapes? We will review them using the example of the city of Tyumen.

Firstly, adaptive reactions in anthropogenic landscapes in birds are related with the way they look for food. For example, Hooded crow *Corvus cornix* L., 1758, Western jackdaw *Corvus monedula* L., 1758 and Rock dove *Columba livia* Gmelin, 1789 develop constant ways of flight to places of feeding. The majority of birds fly from the downtown to flour-grinding plants, poultry farms, and city dumps. Others disperse in the places of additional feeding by people in a city.

When the ways of procuring food of the same bird species in suburban environment and urbanized Tyumen locations are compared, the new ways of getting food emerge as part of conventional range of those ways. For example, hoodies in Tyumen acquired the skills of getting food from plastic packages (of mayonnaise or sour cream). When opening the package, a bird uses its beak along the package to squeeze food out from the cut in the corner. Food adaptations of Corvidae are very broad. Birds visit trashcans and city dumps the same time daily.

Secondly, nested ecology of elementary populations of birds changes in the urbanized landscapes. Fertility increase due to increase in number of reproductive cycles and amount of eggs in laying is typical for those individuals attracted to urban environment. Literature data and our own observations confirm earlier and more extended terms of birds' reproduction in municipal landscapes. (Ksenc et al., 1991; Dinkevich, 2001; Skilskii, 2001; Matveeva, 2005; Fedotova, 2005; Kuranov, 2009; Fleisher at al., 2003, Lupinos, 2013). Nest behavior of birds changes in the city also. Mean height of nests location of magpie in residential area to Tyumen was greater (7,65 ± 0,39; $t = 6{,}56$; $p < 0{,}001$) when compared to control territories around city (4,47 ± 0,29).

Birds use unusual places to place their nests: lamps, bridges and ferries, cable columns, planes, mailboxes, cranes shooters (Drozdov, 1967; Chernobaj, 1980; Prohorov, 2005; Berezovikov, 2007; Vanushkin, 2010; Londei, 2004; Heller, 2007). Common redstart *Phoenicurus phoenicurus* L., 1758, great tit (Parus major L., 1758) and Eurasian tree sparrow *Passer montanus* L., 1758 nest in metal pipes in the yards of multistoried buildings in Tyumen. Crows and jackdaw nest on power lines, which results in blackouts.

Thirdly, food of an anthropogenic origin and nesting in the municipal landscapes entails loss feeling of fear in birds. City birds fearlessly treat people, and do not react to street noise, people and vehicles passing by (Vladyshevskij, 1975; Rezanov, 2005; Vanushkin, 2010; Moller, 2008). Observation of birds in the suburb of Tyumen showed, that great tit and Eurasian tree sparrow do not allow human to approach closer than 10–12 m. In the residential area of the city with populous streets, the fly distance shortens to the minimum, being 0,2 and 1,5 m on average (Lupinos, 2013).

Thus, the birds' adaptation process to habitation in settlements is related to the series of various ecological and ethological adaptations to the anthropogenic conditions, as well as the spread of new stereotypes in their populations.

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SIMULATION MODELLING USED FOR THE ANALYSIS OF NATURE POPULATIONS

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The paradox of ecological science nowadays is rapid development of computers and math modelling, very poorly implemented in setting theoretical concept as well as practical applications. Moreover, abundant empirical data are usually utilized in low-yield statistical calculations. Because of over-complexity of biological systems, a researcher has to deal with fragments of their activity, but to conceptualize the whole system with some potential for extrapolation to other cases. Most unknown factors rest out of scope as "random", whereas statistical analysis is used for hypotheses "verification" of only known factors. That altogether does not improve comprehension of ecological processes.

As "practice is truth criterion" in application, possibility to artificially reconstitute system under study is an ontological criterion in science. Virtual experiments can resolve the problem. Since a researcher can build a simulation model at his/her own discretion and "play" different interaction options, the model's relevance is estimated by comparison of generated output data with field data collected. For relevant model, it becomes possible to find previously unknown values or to compare them with known values. Commonly a model development process itself suggests gaps in knowledge of important mechanisms in systems under study. Unlike easy realizable pure mathematical models (for example system dynamics; Nisbet et al., 2016), genuine simulation models simulate particular objects and allow to trace many indicators that cannot be calculated analytically (Maneerat, Daudé, 2016).

Models of small rodents and reindeer populations are considered examples of simulation modelling. We developed models in AnyLogic program package (University license; Karpov, 2006).

Simulation of spatial structure in territorial rodents allows testing probability of being trapped and velocity of home range displacement as well as the ratios in aggressiveness between animals of different intra-population groups. We elucidate these values by matching data of field counts with literature sources.

Simulation of seasonal migrations of wild reindeer population on Taimyr Peninsula, correlated with data of empirical observations, enables to select mechanism driving migration speed, which notably varies with time. In particular, we studied ambient temperature dependence.

Although the problem of over-complexity does not disappear in simulation modelling, it becomes accessible for operation and analysis. Decision on inclusion and exclusion some notions and evidences from consideration, i.e. determination of model simplification limits, rests arbitrary. Methodologically, determination of exact or conventional criteria should be the next step.

ADAPTATIONS OF PASSERINE BIRDS POPULATIONS TO METROPOLIS CONDITIONS: TRUSH NIGHTINGALE (*LUSCINIA LUSCINIA,* TURDIDAE) IN MOSCOW

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Moscow Trush Nightingale population appears to be unique because of its high density, endemic vocal dialect, and resistance to urban noise and anthropogenic stress. In 2009-2016, we studied the vocal behavior and ecology of Trush Nightingale in Moscow (Ivanitskii et al., 2012, 2013, 2014; Marova et al, 2013). The data collected allowed us to estimate the current state, the welfare of the nightingales in the city, and to identify trouble factors and threats.

Over 350 singing nightingale males were tape-recorded. We described habitats for most of them. We examined almost all city parks, protected areas and other large green areas of the city within the Moscow circle highway: Troparevo, Bitza, Izmailovo, Botanical gardens, Pokrovskoye-Streshnevo, Muzeon Park and others.

Currently, the Trush Nightingale is one of the most common urban birds in Moscow. About four thousand males sing each May in Moscow (Russian Bird Conservation Union, http://biodat.ru/db/birds/solo.htm). They are not shy and sing in the most crowded and noisy places. Moscow is often called the “Nightingale capital of the world”. Nevertheless, how constant is the Moscow population’s welfare? The main conclusions of the study are:

1) Nightingales adapted to high urban noise. Low-frequency noise of the city affects acoustic performance of their advertising vocalization. The value of minimal frequency of 12 studied vocal components of four song types in the city was on the average 260 Hz higher than outside the city (Ivanitskii et al., 2014). The data obtained confirm the hypothesis of bird songs frequency range shift as a response to the city noise (Slabbekoorn, Peet, 2003).

2) Nightingales tolerate presence of people and man-altered landscape elements - picnic places, footpaths, dog walking places and playgrounds.

3) Pruning of lower branches of shrubs, branches cleaning, grass mowing and other such activities in parks will inevitably lead to a dramatic decrease to complete disappearance of Nightingales, depriving them of their nesting habitat.

Our data confirm high pliability of Moscow urban population. Destruction of lower and middle vegetation tiers is the factor that has a most pronounced negative effect on the population. Specific ways to save Nightingales population are simple; do not require extra effort and investment. It is necessary to maintain differentiated approach to parks: leave (along with recreation and entertainment infrastructure) intact zones where grass mowing, bushes destruction, brushwood collecting, and tree cutting are not done.

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INTERACTION OF BIRDS AND RED WOOD ANTS FROM THE BEHAVIORAL ECOLOGY PERSPECTIVE

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In forest ecosystems, red wood ants *Formica rufa* are engineering species. They are known to transform a habitat for many species of animals and plants. With respect to vertebrates ants are studied mainly as their potential prey. Recently, it was found that interactions of red wood ants and rodents include elements of competition and commensalism (Vygonyaylova 2013; Panteleeva et al, 2016). Interaction of birds and ants in temperate forests was studied in details on the example of one of the mass species of birds - great tit. Red wood ants reduce tits' food base, decrease the foraging activity of these birds in the trees (Haemig, 1999). Trophic and spatial interactions of ants and pied flycatcher are almost not studied.

The aim of our research is to study in details the interaction of birds and red wood ants in mixed forests. We conducted our research on the territory of a large settlement of red wood ants near the Novosibirsk city. We also study some details in laboratory conditions.

In the four-year natural experiment we found that part of the forest inhabited by ants is more attractive for nesting of flycatchers in comparison with the control part of the forest with similar vegetation, but no ants. We found no influence of ants on the dynamics of the growth of chicks and breeding success of pied flycatchers. We study the effect of ants on the characteristics of flycatcher chicks with the method of analysis of stable isotopes of C and N. Chicks from nests located on the ants' territory, are characterized by lower values δ15N compared with chicks from the control area. This is due to a smaller contribution of *Diptera* insects and predatory invertebrates (with higher values δ15N) in the chicks' diet. This is also caused by ants (with less than a high value δ15N) in their diet. The reason why the birds prefer to nest in the ants' territories may be linked to food preferences of birds.

We simulated the situation of risky hunting in the great tits to examine whether these birds are able to make a choice between small and large quantities of live prey, both tasty and dangerous. We use red wood ants with whom passerine birds share territories in forest habitats. We placed tits one by one into specially designed cages in which they could choose between “food patches” containing ant groups of different quantities. Ants served both as food items and as a source of danger. We found that birds choose at random between 5 and 10, and they prefer more ants when choosing between 10 and 25. This means that tits value ants as food and quantities in this range do not bother them much. However, they always go for the smaller quantity when choosing between 10 and 50 ants, thus displaying the capacity for distinguishing between more and less in order to ensure comfortable hunting.

Thus, the interaction of red wood ants and small passerine birds is complex and includes elements of competition and predation.

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ABOUT THE HERPETOFAUNA OF THE CITY OF VLADIVOSTOK (PRIMORSKIY KRAI, RUSSIA)

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Biggest cities represent one of the most important and complex forms of natural environment transformation. Their zoning creates different kinds of species composition and groups of animals. The relatively high amphibian tolerance helps them survive where many other species of vertebrates do not exist (Vershinin, 1995). In addition, the distribution and abundance of amphibians and reptiles depend on the landscape and the accompanying microclimatic conditions (Adnagulov, 1998).

Vladivostok is situated on the Muravyov-Amursky Peninsula, surrounded by Sea of Japan and completely covered with cedar-broadleaf forests some time ago. Mountainous terrain, a small number of floodplains, naval and port specificity of the city altogether made it unique. All the urban streams are fully isolated from natural biotopes and heavily polluted (Avdeev, 2015).

Forested and suburban recreational zone is located in the northern part of peninsula and spread from the Bogataya River to the watershed of the Sedanka River and Vtoraya Rechka River. There are 12 species of the forest herpetofauna nowadays. *Salamandrella tridactyla*, *Bombina orientalis*, *Bufo gargarizans*, *Hyla japonica* and *Rana dybowskii* are Amphibians. *Takydromus amurensis*, *Elaphe dione*, *Elaphe schrenckii*, *Hebius vibakari*, *Rhabdophis tigrinus*, *Gloydius intermedius* and *Gloydius ussuriensis* are Reptiles.

Diverse zone lies in the center of the city up to the valley of Pervaya Rechka River. It encompasses high-rise buildings, industrial areas, private sector, isolated mountains (Kholodol’nik Mountain), wastelands and ravines. There are different groups of herpetofauna, which consist of one to five different species. *E. dione, E. schrenckii, H. vibakari, G. intermedius* and *G. ussuriensis* are the snake species observed in the upper reaches of Vtoraya Rechka River in the new neighborhood Snegovaya Pad, surrounded by forest and rocks. Despite strong anthropogenic pollution of the Firsova Cape in the mouth of Vtoraya Rechka River, four species of amphibians (*B. orientalis*, *B. gargarizans*, *H. japonica* and *R. dybowskii)* exist among warehouses and landfills. *E. schrenckii* was sporadically observed on Kholodol’nik Mountain and in the area of Tikhaya (Sukhoputnaya) Bay.

An interesting case of preservation of *R. dybowskii* isolated population with a total count of at least 500 individuals was reported in a residential neighborhood, in a ravine with a spring, which has a stream about 100 m in length. Frogs hibernate in the underground part of the spring, and then migrate to the ponds for breeding (area not exceeding 30 m^2), formed by the same stream.

Another case of fully isolated group of amphibians was reported in the zone of high-rise development (downtown), near the City Park Mingorodok, including such species as *S. tridactyla, R. dybowskii* and *H. japonica*. Small populations of H. japonica inhabit a vacant lot in the floodplain of Obyasneniya River (Fadeeva St.).

Periodically, invasive species appear in different parts of the city. Thus, on 21 April 2016 we observed an adult Slider Turtle *Trachemys scripta* in one of the ponds of Park Mingorodok. One of the local websites reported that it was observed there since 2011. In recent years, such invasive species were repeatedly recorded not only in the Russian South, but also in Moscow area (Semenov, 2009). The Chinese soft-shell turtle *Pelodiscus maackii* can often be found in city ponds brought by anglers into the city, returning from fishing. Therefore, since 1999 to 2005 several individuals of these species lived in the quarry pond on the Safonova St. on the Churkin Peninsula.

Considering that amphibians and reptiles are recognized as biological indicators of environmental quality, research must be continued aiming to study state of their populations in Vladivostok and to protect those few places where they still occur.

RELATIONSHIPS BETWEEN TOP PREDATORS AND THEIR IMPACT ON POPULATION DYNAMICS: A CASE STUDY OF BEARS AND STELLER'S SEA EAGLES ON SAKHALIN ISLAND

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Steller's sea eagle is the largest member of the genus *Haliaeetus.* Being the top predator of semiaquatic ecosystems, sea eagles are at the top of their food chains. However, this does not always guarantee no impact of other top predators, such as the brown bear, on their population. Sporadic cases of sea eagle nests destruction were recorded throughout the entire areal: in Kamchatka (Lobkov, Neufeldt, 1986), in Magadan Province (McGrady, Potapov, 1999), and in the Lower Amur region (Masterov, 1992). We observed mass destruction of sea eagle brood by brown bears on Sakhalin Island in the last decade.

Sea eagle population monitoring was performed in 2004–2014 on the northeastern coast of the island and involved 396 nesting sites. In 11-year study period, 785–878 chicks of the group fledged successfully, 163–277 chicks were killed by brown bears, and another 77–86 chicks died from other causes.

The predators prefer to ravage nests built on low trees (lower than 13 m on average and smaller than 50 cm in diameter). As the size of trees increases, their attractiveness to bears decreases. Trees more than 20 m in height and over 70 cm in diameter are safest for nesting. Stunted trees dominate on the seashore and lagoon bays in the north of Sakhalin Island. However, spatial distribution of major food resources force sea eagles to nest on such “suboptimal” substrate.

The pressure of brown bear predation was estimated by formula $P_b = N_b/(N_f + N_b)*100\%$, where P_b is predation, N_b is the number of eaten chicks, and N_f is the number of successfully raised chicks. The peak of predation was observed in 2005–2006, when bears destroyed 46–49% of all chicks (the mean value for all 11-year study period was 21%). The mortality of chicks from other causes was on average 9% a year. The decrease in population productivity due to bear predation is described by equation $y = –0{,}9648x + 0{,}8136$ ($R^2 = 0{,}41$, $p < 0{,}0$). The ratio of destroyed nests to the total number of nests with chicks is the “risk of predation”. During the study period, the risk of predation remained at a level of 21–23%. Apparently, this index should be considered a “fee” paid by the population for the opportunity to breed in the most productive foraging grounds.

To assess the impact of bear predation on the population of sea eagles, we simulated population dynamics using the linear matrix model (Caswell, 2000). The estimates of survival of immature birds were obtained from the ratio of abundance of different age groups. The survival of mature birds in nature, calculated using allometric formulas (Ricklefs, 2000), is estimated at 95,2% a year. Survival rate of a closely related species, white-tailed eagle, in nature corresponds to our assessment (91,3–98,6%) (Green et al., 1996; Helander, 2003). Data on the Steller's sea eagle population productivity were obtained in the course of monitoring.

Simulation showed that, even with "good" adults survival (0,95), population growth rate is –1,6% per year. At this rate, population will decline by half in 44 years. In the absence of bear predation, this value would have been –0,9% per year, which corresponds to a reduction by half in 78 years.

Thus, the predation by bears largely determines low population growth rate. However, even if the pressure of predation is eliminated, population growth rate will remain negative because of high anthropogenic load in the habitats of sea eagles and unstable foraging conditions. Another important conclusion made based on simulation is the assumption of an extremely high level of bird mortality in the first year of life, which we estimate to be 83–85%.

SEASONAL DYNAMICS OF WOODPECKERS' SPECIES DIVERSITY DISTRIBUTION IN SARATOV

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In the studies of large cities avifauna, it is crucial to assess species diversity in areas with different degrees of anthropogenic transformation. In addition to the typical urban species, birds from natural habitats, including woodpeckers (Piciformes) have adapted to existence in urban landscape. Previous studies noted that woodpeckers not only move to urban environment in winter, but use it during settling into new territories (Friedman et al, 2007; Melnikov, 2014). The aim of this work was to identify peculiarities of woodpeckers' species diversity spatial distribution in Saratov during breeding and winter periods.

The material was collected in 2003–2012. Territory of Saratov is limited with squares 38UNC4 and 38UNB3 with UTM projection and an area of 50×50 km (Hagemeijer, Blair, 1997). These large squares provide universal mapping to the terrain and were repeatedly used in regional research (Red book..., 2006). Due to small area of woodpeckers' habitats squares 38UNC4 and 38UNB3 were divided into small model areas 1×1 km. In each model square, we made censuses of woodpeckers using standardized methods to identify species density (species/km^2). We used full or partial data extrapolation in poorly accessible plots. We used MapInfo 8.5 and Vertical Mapper 3.0 applications to make isolines of woodpeckers' species density distribution in breeding and winter steady states on the basis of censuses.

The urbanised environment of Saratov includes three components: natural (suburban forest park "Kumysnaya Polyana"), natural-anthropogenic (parks, forest belts) and residential (buildings). In our study, we found eight species of woodpeckers in Saratov: *Jynx torquilla*, *Picus canus*, *Dryocopus martius*, *Dendrocopos major*, *D. syriacus*, *D. medius*, *D. leucotos*, *D. minor*. In nesting period, the areas of highest species density (7–8 species/km^2) were located in the forest park "Kumysnaya Polyana", a large forest, adjoining to the city. We observed only spotted and Syrian woodpeckers in parks, forest belts and built-up areas. Woodpeckers' species density in disturbed habitats was 1–2 species/km^2.

In winter, we observed woodpeckers' migration to natural-anthropogenic and residential components of urban environment. The area of residential plots unused by birds significantly reduced from 153,5 km^2 in breeding time to 9,3 km^2 in the winter. In parks and forest belts the density of great spotted, middle spotted and lesser-spotted woodpeckers increases. Building areas are used as wintering habitat by Syrian woodpecker. Usually birds are tied to permanent feeding spots. Great spotted woodpecker chooses pine belts and squares with spruces, whereas Syrian woodpeckers prefer areas with summerhouses and places with bird feeders. In forest park "Kumysnaya Polyana", species density reduces to 5–6 species/km^2, because of *Dendrocopos* species migration and increase of the area of black and grey-headed woodpeckers' fodder plots. However, they find white-backed woodpecker in suburban woodland park in snowy months. This species arrive there in winter only.

DYNAMICS OF NUMBER AND POPULATION HOMEOSTASIS OF SHOREBIRDS IN THE CONDITIONS OF A MOUNTAIN-INUNDATED WATER REGIME

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Dynamics of number and population homeostasis are the interconnected parametres of populations (Novoseltsev, 1978; Shilov, 1982; Sharov, 1986; Pavlov, 1989). However, there are very few studies on birds testing their teamwork. As a rule, those are settled species having more accurate and defined ecosystem communications. In migrating birds, especially shorebirds and waterfowls, animals count strongly varies even in consequent years of observation from brisk domination to almost total absence of specific species in a certain ecosystem. Quite often, it is not related to the rate of their reproduction during the previous season. Therefore, it is impossible in most cases to receive material correctly reflecting dynamics of their number, related to reproductive success even if death rate of birds on wintering grounds is known.

Classical example is the change of abundance of birds in the conditions of a mountain-inundated water regime in a 11-year-old climatic cycle (a variation 7 to 14 years). Its basic characteristics are short, but very strong vernal high water and some large flood flows during summer (from 2 to 7), sometimes catastrophic inundations. For ecosystems of this type, increases death rate of nests of all species of birds is typical, especially nesting on low bottomland. The needed level of reproduction in such conditions is provided with specific adaptations: completion of nests according to water level rise, defense reactions against feathery and ground predators, repetitive nesting after the death of clutches and dynamical spatial structure. We understand population homeostasis in this case as an ability of population to sustain specific structurally functional dynamic stability reflected in one reproductive parameter – overall success of reproduction.

Currently selection in populations is divided into “selection to survive” and “selection to reproduce” (Huxley, 1963). Reproductive selection is the direction of evolution providing production and perfection of adaptations to reproduce (Georgievsky, 1989). As we cannot restore true changes of population level on a certain plot of an areal (considerable part of birds leaves places of previous season of reproduction), it is necessary to find more suitable parameter for these purposes. Undoubtedly, that is the overall success of reproduction of birds during nested season. Each adaptation is limited to possible borders of compensation, and their joint work expands adaptive region of population. Within this region annual level of birds reproduction success changes. It is close to an average for population for the entire climatic cycle, i.e. reflecting population homeostasis. When limiting factors are strong, adaptations cannot compensate them, and reproduction success of a species sharply decreases. On the contrary, under very favorable conditions when limiting factors impact is the least, reproduction success of a species increases. Frequency of alternation of such years define the number and attributes of its dynamics of all species of shorebirds.

Thus, sustaining the number and possibility of its subsequent growth in shorebirds are related to substantial increase of success of their reproduction in selected years. In such events, complex age structure allows to keep number at high level at the expense of the numerous generation, which appeared in a very favorable year. During other seasons, reproduction only partly compensates the death of adult individuals, and number of a species gradually decreases until next successful year. Certainly, year with very low success of reproduction, not compensated during the subsequent seasons, can lead to essential decrease in the general abundance of a species (Mel’nikov, 2010). Hence, for terrains with a mountain-inundated water regime in populations of shorebirds opportunistic type of dynamics of number is typical.

EFFECT OF INTERACTIONS WITH PARENTS ON THE PERSONALITY TRAITS FORMATION IN BLACK-HEADED GULL CHICKS (*LARUS RIDIBUNDUS*)

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“Personalities” are sets of consistent individual traits of an animal, that determine its behavior in different situations. Personalities, including aggressiveness, exploratory behavior, boldness and coping with stress are genetically controlled (Oers, Sinn, 2011). However, non-genetic factors may also play significant role in their development (Stamps, Groothuis, 2010).

In particular, behavior associated with feeding of offspring by parents, can significantly influence the formation of its personal traits (rats: the Stern, 1997; Liu et al, 1997; Francis et al, 1999; Caldji et al, 1998; tits: Carere et al, 2005; Oers et al, 2015). There are many different variants of parent-chicks interactions among birds, whereas the effect of these interactions on formation of personalities remains poorly understood.

Our goal was to study how interactions with parents influence the development of personalities in chicks of black-headed gull. We identified personalities of gull chicks, using the “open field” test, specially modified for behavioral characteristics of gulls, and we studied parents-chicks interactions by monitoring behavior of gulls in natural environment. At the age of 13–21 days, gull chicks showed consistent individual variations in coping with stress.

Chicks with “active” coping style could be characterized by high exploratory activity, boldness, territorial aggressiveness and more frequent running to the parent before feeding during the first 3 weeks of life. “Passive” chicks attempted kleptoparasitism more often. One brood chicks usually had similar coping styles. Parents of “passive” gull chicks broods spent more time with them at the age of 7–9 days, and fed them less often at the age of 3 weeks.

We assume that prolonged contact with parents often provokes begging in chicks. When it is not positively reinforced by a portion of food, those chicks stop begging, and other active reactions decrease, forming ‘passive’ way of behavior. We also believe that the ability for self-foraging (kleptoparasitism) in “passive” chicks can compensate lack of food that they receive from their parents during the second half of living in the colony.

KAWAU POPULATION ON JULUKUL LAKE AND FACTORS AFFECTED IT’S QUANTITY

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Colony of kawau on Julukyl lake is unique nesting venue of this species in Altai Republic and Altay Krai (Mitrofanov, 1995; 2006; 2015; Kuchin, 2004). According to A.M. Sudilovskaya’s (1951) map of cormorant family (Phalacrocoracidae), South Siberia Mountains are related to high-mountain boreal subzone of III mountain zone, where subspecies *Phalacrocorax carbo sinensis* resides. Kawau is included in Red Book of Altai Republic from the first edition (1996; 2008). In Altai State Reserve, monitoring of kawau colony is conducted regularly, including author’s observations in 1991–2012. Julukul lake is situated in Julukul basin at an elevation 2200 meters near the border with Altay Reserve and Tuva Republic. It is the largest high-altitude water body in Altai Republic. It is a running water lake, not too deep (max depth is 9 m) and fishy. The first reports on kawau near Julukul lake were published by E.A. Irisov (1963) and the first description of nesting colony made by V.A. Stakheev (1981). Cormorants arrive to the nesting sites in late April – early May. The earliest date of arrival was April 27, 1998. Brooding starts in the first half of May. The main colony is situated in the highest stony part of the biggest island of two in the middle of the lake. In certain years few couples nested on the next smaller island on the brink of the herring gull (*Larus argentatus*) colony. The dynamic of colonies nesting in 1977 – 2013 is as follows (inhabited nests only): 1977 – 13, 1986 – 86, 1987 – 81, 1991 – 117. Starting in 1992 , few couples built nests on the second island: 1992 – 128 on main island and 3 on the next one, 1994 – 94 and 1, 1996 – 102 and 1, 1999 – 120 and 5, 2001 – 125 and 3, 2002 – 115 and 3, 2010 – 53, 2011 – 15, 2012 – 8. Nesting density index ($K = L/R$) was 0,32 ($n = 30$) where L was the mean diameter of nesting hollow = 255 mm (Lim = 220–320); R – mean distance between nests in the colony = 808 mm (*Lim = 570–870*); mean distance between nests ($M \pm m$) was 1000 ± 32б31 (*Lim = 570–2800; C = 3,23; n = 77*). In 1987, cormorants occupied two plots with 46 and 35 nests (Maleshin, 1987); two plots again with 67 and 31 nests with 5 single nests in 1991. In 1992, the number increased to four plots with 45, 52, 23 and 10 nests; in 1994 – two: 55 and 29; in 1996 – three: 32, 43 and 15; in 2001 – four: 43, 27, 23 and 32; in 2002 – four: 33, 27, 12 and 43. From 2010, the colony consisted of only one plot. The highest nests were situated in the middle of plots; the lowest ones were on the periphery and in few detached nest buildings. Full *Ph. Carbo* egg layings consisted of 3–4 eggs, which made 60% of all examined egg layings ($n = 100$). Average size of egg laying (*M ± м)* was *3,12 ± 0,11* eggs (*Lim = 1–6*). The egg sizes ($n = 40$) were: *L* (*M ± m*) = *63,56 ± 0,5* (*C = 0,79*), *Lim = 56,1*68,2* (*56,1*39,1*) and (*68,2*39,6*); *B* (*M ± m*) = *39,14 ± 0,81* (*C = 2,07*), *Lim = 56,1*68,2* (*56,1*39,1*) and (*68,2*39,6*). Variability of egg’s length depended on the environment, while the egg’s width depended on bird’s size (Gromadzki, 1966). The mean egg’s weight (*M ± м*) in grams was *54,29 ± 0,81* (*Lim = 46,0–67,0; C = 1,49; n = 34*). Period of brooding was extended because of abiotic factors. Eclosion starts in the last decade of June. The mean size of brood is *2,36 ± 0,29* nestlings (*Lim = 1–4; n = 11*). Long-term monitoring showed quick growth of kawau colony in the beginning with the consequent stabilization phase. In our opinion, gradual recession that commenced in 2002 was related to weather conditions in the area, especially in the first half of brooding, as well as to ice hummock when ice starts to move on the lake (Mitrofanov, 2000). Human factor is minimal because when anglers fish on the rivers flowing into the lake, while the lake itself is under ice cover. Moreover, the islands are surrounded by vast space of open water blocking easy access to the colony.

POPULATION CHARACTERISTICS OF THE COMMON SHREW IN CONDITIONS OF URBANIZATION

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The work was carried out in the Middle Ob Region in the city of Surgut in 2010–1012. We surveyed more than 70 habitats in undeveloped areas with different technogenic and anthropogenic load. During the entire study period, we accomplished over 74000 24-hour trap periods, accounted 1221 common shrew. Control study was conducted the vicinity of village Yugan, the overall material comprised 145 individuals. We used plastic cylinders 35–40 cm high without directing systems to catch small mammals. Correction factor of 3.4 was used to compare abundance data (Starikov, Shmakova, 1985). Quality was ascertained using standard indicator of relative abundance, recalculated for 100 24-hour trap periods. To assess the abundance, we used scale, developed by A.P. Kusjakin (1962).

We used conventional methods (Novikov, 1949; Dehnel, 1949; Dunaeva, 1955; Ivanter, 1975) to study common shrew population.

Common shrew dominated the community of small mammals in the urbanized area, accounting for more than 57% of all recorded animals, which is typical for natural biotopes of the Middle Ob Region, to a lesser extent affected by man-made transformation. Being eurytopic and most abundant species in the city, common shrew was found in 70% of all studied habitats.

We recorded the following abundance in the city in descending order: shrub in mixed woods, waterlogging areas of forest; in the ecotone: birch-pine forest wet dwarf shrub – sedge-sphagnum bog, shrub small-leaved forests. The least common shrew abundance was recorded in riparian willow and floodplain meadows. Its abundance varied depending on the zone: thus, it was average (2,0–4,8 animals per 100 24-hour trap periods) in the central zone, the zone of industrial enterprises, and the floodplain of the Ob river, whereas it was numerous or regular (8,3–10,9 animals per 100 24-hour trap periods) in the peripheral zone. Over the study period, there was a slight increase in the abundance of this species in urban environments.

Demographic structure was different from that of this group of animals. In overwintered animals, there was a significant shift towards females in both urban population and controls. In urbanized areas, a youthful population compared to control characterizes demographic structure. However, such changes in demographic structure are observed by scientists in the depression of population, or may evolve because of urbanization (Ivanter, 1975; Bolshakov and others, 2001).

Breeding common shrew in the city of Surgut began in mid-May and ended in late September, with the overall duration of about four months. The intensity of reproduction is low, confirmed by low percentage of participation form females (no more than 2%). Normally, overwintered females brought two litters during reproduction period in the city, and no more than 5% of females had a third litter.

The average brood size of females from untransformed areas was slightly higher and equaled 7,53 ± 0,49 in the overwintered females, whereas only one animal had seven embryos. The fecundity of the overwintered females of the urbanized and undisturbed territories did not differ significantly ($t_{(63)} = 1,28$, $p = 0,22$) and equaled 6,88 ± 0,13 in overwintered females and 6,44 ± 0,38 in new females. We did not find significant annual and age-related fecundity differences in females in the city of Surgut. Zonation of urban area had no significant effect on average fertility. Common shrew fertility indicators were not lower compared to the one from natural habitats.

We found low embryo mortality (resorption embryos was less than 2%) rate in the city shrews with no embryonic loss in controls.

BRAIN AS TARGET FOR NANOSIZED AEROSOLS

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Inhalation of air-dispersed submicron and nano-sized inorganic and biogenic (virus) particles presents a risk factor for animal health. Here we show that nasal aerodynamics plays a pivotal role in the protection of subterranean mole vole *Ellobius talpinus* from an increased exposure to nanoaerosols (Moshkin et al., 2014). Quantitative simulation of particles flow has shown that their deposition on the total surface of nasal cavity is higher in the mole vole than in terrestrial rodent *Mus musculus* (mouse), but lower on the olfactory epithelium. Using MRI detection, we found a reduced accumulation of magnetic contrast nanomaterials in olfactory bulbs of mole voles in comparison with mice after the inhalation of nano-sized Mn aerosols. Aerodynamic model also predicts higher impact of nanoparticles on the dorsal area of olfactory epithelium than ventral, which also showed different ability to nanoparticle uptake by olfactory nervous. Together, we conclude that nasal geometry and functional heterogeneity of the olfactory epithelium contributes significantly to the protection of brain from accumulation of air-dispersed particles and virus especially in chisel tooth diggers, such as mole vole.

TERRITORIAL SPECIES AND POPULATION CONSERVATISM OF SPARROWS IN THE OB HIGH-WATER BED

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In biodiversity studies, assessing functional traits of genotypes, which determine group differences in birds in the population and species structure, should be a priority. That directs differences inside the species and population in the way those species are linked with the birth and nesting territory. Distinguishing birds on the basis of such qualitative features (phylopathric and nomad) is important not only methodologically, but also to understand population stability and resolution of critical situations.

One of the ways to determine those may be birds' affinity to the territory. Banding and marking allows for quite valid material, which describes birds' affinity to particular sites of their areal, first of all with regard to nesting and natal, and nomadic conservatism to a lesser extent. All that is phylopathry. With this, we mean the reference spots in the areas of species and populations, which are constantly used by individuals, and then groups. Separating and studying structural types with regard to the territory helps resolve the issues of profit, which birds benefit from such approach. Theoretical advantages of phylopathry over nomadism so much typical for birds, may be related with stress suppression, energy saving, impact on the psychoemotional comfort, foraging, better reproductive environment, and probably higher offspring quality, better survival, etc.

We used data on sparrow birds banding, caught with nets and from the nests in "Manatka" stationary in the Ob high-water bed during 15 years to study phylopathry. In total, 22622 birds of 84 species were banded. Of those, we used data of 20 species returning to the stationary territories after one year or more, for the current presentation. We calculated phylopathry index for them, calculated as proportion of those returning in one year or more. Files sparrow nesting group showed the highest phylopathry (6,3 ± 1,5%; n = 1005), followed by lentil (4,0 ± 0,9%; n = 498), common swallow (3,4 ± 0,8%; n = 704), germander (2,6 ± 0,6%; n = 1558), yellow wagtail (2,1 ± 0,6%; n = 1942), garden millerbird (2,0 ± 0,8%; n = 1457), singing cricket (1,9 ± 1,3%; n = 688), Luscinia svercica (1,7 ± 2,5%; n = 1942), starling (1,6 ± 0,5%; n = 1194), long-tailed rosefinch (1,3 ± 1,0%; n = 312), sedge warbler (1,2 ± 1,0%; n = 1490), booted warbler (1,0 ± 2,3%; n = 96), sand-martin (0,4 ± 0,2%; n = 3483). The all are most typical for the Ob high-water beds in the nesting period.

Thus, these species are the best models to study biological advantages, which they may have from the affinity to the nesting site and birthplace. Additionally, these affinity data not only allow studying their biological advantages, but can also be selected to assess qualities using gene, physiological and behavioral analyses.

THE MODERN NUMBER AND PREVALENCE OF HAMSTER (*CRICETUS CRICETUS* L.) IN THE VALLEYS AND MOUNTAINS OF WESTERN SIBERIA

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Having vast Eurasian areal (Gromov, Yerbaeva, 1995), European hamster (hereinafter hamster) population reduced on a significant part of its European habitat, which entailed its inclusion in the protected list in a number of countries (Poplavakaya et al., 2015; Surov et al., 2016; Ziomek, Banaszek, 2007; Rusin et al., 2013). Asian part of its areal was studied in detail only in Omsk Province in recent years (Sidorov et al., 2011). That is why the analysis of prevalence and distribution change in the Western Siberia is of great interest related to years after publication of monographs on mammals of the valleys and mountainous regions of this territory (Laptev, 1958; Yudin et al., 1979).

The present report is based on the materials, prevalence, and distribution of hamster from the Databank of the zoological monitoring lab in the ASEI of RAS SD from 1957 until 2015. We used reports of 4501 habitation options from catching using grooves, fences and mashers. Our predecessors used data from meeting this animal in real situation and reported its prevalence not only based on catching, but feedback from the local population and fell stocking-up. The scale of this stocking-up is prompted by archives and published data (Neronov, 1965; Sidorov et al., 2001; Mashkin, 2007). In 1929, 5741174 fells in total were stocked up with almost 1000-fold reduction compared to 1925, based on the data of All-Union Cooperative Hunting Union, in charge of stocking-up at that time. 3389514 hamster fells were stocked in the USSR in 1951. Number of fells dropped by five times already in the 50s in Altay region, noted for the greatest number of fells to stock-up (Savinov, 1953). Due to virgin soil reclamation in Omsk Province, they also reported almost 5-fold reduction of fells stocking-up (Sidorov et al., 2011). Before, hamster fells stocking-up was considered as backup of agriculture from losses, incurred by “unlimited hamster reproduction” (Kaverznev, 1931).

Fells were not stocked at a time of our studies, and the absence of such information may reduce the number of locations where it exists. Nevertheless, within the last 40–60 years the hamster prevalence notably changed and, most probably, nowadays is not recorded in Southern taiga of Irtysh and Ob rivers nearby locations, as well as earlier reported expansion into mid-taiga and southwards along Biya River down to Teletsk Lake. Hamster prevalence during the last 60 years dropped by almost third; however, there are no grounds to claim catastrophic reduction of its population, as well as its areal, which lessened only because of expansion into river valleys in taiga zone and Altay lowlands earlier.

FIELD MOUSE POPULATIONS (*APODEMUS AGRARIUS* PALL., 1771) IN THE URBAN ENVIRONMENT

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Field mouse (FM) is a species inhabiting all Eurasian cities within its areal (Ivanter, 1975; Andzejewski et al., 1978; Lisin, 1982; Tikhonova et al., 1994).

In Tomsk, FM was identified since the commencement of detailed research of Siberian fauna (Laptev, 1958). This report is based on small mammals (SM) catches (1984–1990; 2001–2016) in Tomsk parks and peripheral green zones, where this species has 3,70–100% prevalence. Such attributes as habitats fragmentation and FM spatial dissociation may imply those are independent populations. We studied the interrelation of the species in SM communities, population count dynamics, reproductive activity, demographic and phenetic (10 items, including number of openings for nerves and vessels on the skull bilaterally) structures, morphological traits (body mass and length, nutritional state index) and mandible shape variability.

One of the populations, named ‘grove’, inhabits relatively isolated park, called University Park where it dominates (91% on average). The second population, named ‘southern’ is part of so-dominants (3,70% to 51,72% in different years). ‘Gove’ population has high and stable count (4,2 to 24,0 individuals per 100 trap-days) with 3-year cycle. “Southern” population count ranges from 0 to 4,9, reaching the level of 10 individuals per 100 trap-days only once). The first population females bring one to three pups, and underyearlings bring mostly one pup. Embryo count ranges from 4 to 10 (mean count 7,68 ± 0,28). The proportion of females with 8–10 embryos is 68%. In the end of 80s (Moskvitina, 1999), this population was found to have a number of forms with different fertility. Thus, overwintered females had most diverged counts from the mean, which reproduced in early spring or winter, and having 1,8–3,7 embryos less compared to those females reproducing in late spring; that resemble reproductive behavior of synantropic house mouse. In ‘Southern’ population, underyearling females brought 1–2 pups, while overwintered females had three pups. Embryo count varied from 5 to 10, being 8,24 ± 0,31 on average. 81% females had eight and more embryos. The populations had similar age and sex structure sad (approx. 68,5 %) age group of underyearlings prevailed, whereas there were twice more males in both populations. Therefore, with regard to ecological indicators, the populations firstly differed in the count and its span, which were determined largely by saturation of communities with species. Almost similar environmental “volume” allows for stable and high count of one species in one case, whereas in the other – distribution of resources among all 11 species of the community. Morphological traits analysis showed sex dimorphism in the ‘grove’ population ($p < 0,05$), i.e. males are bigger than females, and their nutrition state index is higher. There were no morphological differences between populations.

In terms of phenetic structure, the populations differed in the extent of phenological fund implementation (“grove” – 94,9%; “Southern” – 74,4%) as well as its structure. Thus, the first population notable stands out because of the rare and unique variations of craniological phenes – 61,5% vs. 30,8% in the “Southern”. “Grove” population mandible geometry was noted for large mandible curvature, smaller angle of tooth row, and a different arthrodial appendix condyle.

We suppose that the attributes of urban population field mouse are on the one hand largely determined by the quantity and composition of accompanying species, whereas on the other by spatial isolation, entailing genetic originality of each of them.

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STUDY OF THE RELATIONSHIP BETWEEN THE HYDROMINERAL REGULATION AND THE REPRODUCTION CYCLE IN *TYPHLONECTES COMPRESSICAUDA* DUMERIL AND BIBRON, 1841 (AMPHIBIA, GYMNOPHIONA)

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Typhlonectes compressicauda is a viviparous gymnophiona amphibian living in tropical areas of South America. This lengthened amphibian is submitted to seasonal variation characterized by a rainy season (January till June) and a dry season (July till December). In this species there is a superimposing of both the seasonal and breeding cycles, allowing the birth at an ecologically favorable period for new-born survival. When animals were maintained in aquarium, the absence of dry season mainly disrupted the female reproductive cycle. The aim of this study was to understand the links that could exist between the reproduction of this animal and its hydromineral regulation. For that, we chose to work on the arginine-vasotocine (AVT) / mesotocine (MST) system, two neurohormones implied in hydromineral regulation and sexual behavior. The study included males, pregnant and non-pregnant females captured during the dry or the rainy season. After the localization of both neurohormones at the hypothalamic level, we worked on the kidney in order to perform a morphometric study of Bowman's capsule and blood capillaries, and also to localize the neurohormones' receptors. We also localized aquaporin-2, the vasopressin-regulated water-channel protein. AVT, the antidiuretic hormone, its receptor and the aquaporin-2 were more expressed during the dry season. However, no difference was observed between males and females. It has been shown that there were interactions between neurohormones, pituitary hormones and steroid hormones, which remain to study in *Typhlonectes compressicauda*.

LONG-TERM DYNAMICS OF BANK VOLE REPRODUCTION DURING REDUCTION OF INDUSTRIAL EMISSIONS

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Currently, industrial pollution poses a real threat to the biosphere. It has a significant impact on all components of natural ecosystem, as both direct (toxic effect of pollutants) and indirect (through the transformation of habitats, increased interspecific competition, reduced resistance of the organism) impact. In recent decades, there has been a downward trend in emissions as a result of improvement in technology and/or shutdown of enterprises. Reducing the anthropogenic impact initiates ecosystem restorations of impact areas, which makes it possible to analyze the processes in “real time”, which were previously assessed only based on modeling. Long-term studies of the dynamics of separate components of the biota in the impacted areas are either absent or scarce and are based on a comparison of 2–3 time slices for a short period of observation, which does not elicit true causes of recorded changes. Reproductive characteristics of small mammals (SM) are sensitive to the toxic impact and their deterioration is indicative of poor condition of local populations (Bezel, 2006; Lukyanova, Lukyanov, 1992, 1998; Moskvitina et al., 2000; Mukhacheva 2001, 2007; Mukhacheva, Bezel, 2015; Kozlov et al., 2005; Kataev et al., 1994, etc.).

The main aim of our work was to analyze long-term (1990–2015) dynamics of SM reproductive parameters resulting from significant (98%) reduction of industrial emissions of a large copper-smelter (Revda, Middle Urals).

We used bank vole (*Myodes glareolus*) as model object, as one of the dominating SM communities in the forest habitats in the impacted zone (1–2 km from the plant, I), the buffer (4–6 km, B) and the background (20–30 km, F) areas. Animals were caught by trap-lines each year (May–September) at the same time in all areas. We accumulated 83000 trap-nights, captured 2354 *M. glareolus*. We assessed the following indicators in vole’s females (F – 284, I + B – 238): number of litters (NL), potential fertility (the number of corpora lutea in the ovaries, PF) and litter’s size (the number of viable embryos, LS). We tested the interrelation of reproductive parameters with the level of contamination, the period of the study (1990–1997 – high emissions, 1998–2009 – reducing emissions, 2010–2015 – low emissions), age and local abundance of animals in multivariate ANOVA.

Females reproductive parameters of *M. glareolus* from background sites were superior to polluted areas, while the fecundity of voles from impact and buffer areas differed a little (NL: F – 1,64 ± 0,06; B – 1,59 ± 0,04; I – 1,49 ± 0,07; PF: F – 6,48 ± 0,11; B – 6,32 ± 0,16; I – 6,18 ± 0,39; LS: F – 6,02 ± 0,11; B – 5,80 ± 0,14; I – 5,82 ± 0,25). Reproductive parameters coefficient of variation (Cv) didn’t exceed 25% and was similar at all sites. The level of toxic load did not affect main parameters of *M. glareolus* reproduction ($p > 0.05$), indicating high resistance of the species reproductive characteristics to anthropogenic factors. At the same time, the age of females (overwintered animals were more fecund) and the abundance of animals (its decline has led to a consistent increase in PF and LS, but NL/per 1 female has decreased) significantly affected the vole’s reproduction. All studied parameters significantly differed during various periods of observations; however, a distinct temporal trend wasn’t detected. The observed changes were due to the effect of naturally occurring factors (first of all, population density and peculiarities of demography). Annual (after 2010) captures of pregnant/lactating females and young animals which left nests in the affected areas showed some improvement in habitat quality for SM during the period of stable low emissions.

Thus, time-series analysis of basic bank vole reproductive parameters showed no effect of reduction of emissions during 25 years of observations.

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SMALL MAMMAL COMMUNUTUES IN THE IMPACTED AREAS: THE IMPORTANCE OF LANDSCAPE-ECOLOGICAL DIVERSITY CONSIDERATION

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Anthropogenic impact, including industrial pollution, leads to the transformation of natural habitats, their fragmentation and/or degradation. Small mammal' (SM) communities respond to these changes differently. The abundance and species diversity may decrease (Andren, 1994; Didham et al., 1998; Fahrig, 2003; Silva et al., 2005), increase (Kirkland, 1990; Fisher et al., 2011), remain unchanged (Burel et al., 1998; Jacob, 2003; Pocock, Jennings, 2008; Bates, Harris, 2009; Men et al., 2015), or change non-monotonically (Connell, 1978; Grime, 1979; Conde, Rocha, 2006). Despite these unfavorable conditions, several SM species are adapted to life in the transformed environment. One of them form isolated settlements, while others set up meta-populations, where individuals move between separate fragments (Adler et al., 1985; Quental et al., 2001; Pires et al., 2002). The generalist and invading species use advantage of such conditions (Shore et al., 1997; Burel et al., 1998; Gentili et al., 2014).

The impacted areas (sites around of sources of industrial emissions) are characterized by strong fragmentation and high mosaic structure of habitats, but importance of environmental heterogeneity in formation of SM communities under the conditions of industrial pollution is poorly studied so far. The reaction of SM communities to the industrial impact are traditionally studied by comparing population within the limits of 1–2 options of habitats, presented in the entire load gradient. It shows that an increase in pollution level resulted in dramatic decrease of the species diversity and the abundance of SM community (Luk'janova, Luk'janov, 1998; Davydova, 2007; Mukhacheva et al., 2010; Kataev et al., 1994; Kozlov et al., 2005). Few attempts to consider landscape-ecological diversity of the areas led to essentially other conclusions about the reactions of SM populations to the industrial pollution compared to the traditional approach (Mukhacheva et al., 2012). This work is a continuation of previously initiated studies.

We carried out our investigations near the Karabash Copper Smelter in two areas: the impacted zone (IZ, 1,5–5 km from the factory) and the background zone (BZ, 20–25 km south of the factory). Catches were made in seven pairwise variants of habitats (VH), typical for studied region: pine, floodplain, birch and birch light forests, reed marshes, meadows and dumps of household waste. We caught animals in July 2012–2014 in all VH simultaneously within the zone limits. Three lines of traps were installed in each variant of habitats (10 snap-traps, 5 live-traps). We assessed the abundance and species composition of SM communities. 5500 trap-nights were checked, and 443 individuals were caught.

Fragments of the same habitats in the IZ occupied smaller area and were characterized by more severe conditions. This is reflected in the abundance of animals, which in the IZ was twice lower than the BZ (5,8 и 10,6 ind./100 trap-night). Species richness of the compared areas differed slightly: 12 species noted in BZ, and 11 in IZ. Because separate habitats are fragments of a single landscape mosaic, the presence of species in these sites depended not only on quality, size and degree of fragment isolation, but also on the adjacent habitats. The wood mouse (typical generalist species) actively inhabited all studied VHs: in IZ it occupied the entire sites (36 % of total abundance), whereas in BZ – 5 of 7 versions MO (17 %). Animals occupied even unsuitable habitats, where they survived due to their high mobility and ecological plasticity by using adjacent habitats resources. In the BZ, other 11 SM species were distributed evenly, except water shrew and bank voles in one VH. In IZ, on the contrary, other 10 SM species were inhabited very unevenly. As a rule, animals were observed in 1–3 VHs, where they reached high abundance (close to BZ). For example, common shrew, bank and tundra voles inhabited mainly floodplain forests, while common vole settled down solely in meadows.

Thus, the study of SM communities' response to the industrial pollution is important to consider the landscape-ecological diversity of areas.

ACTIVITY OF THE WATER VOLE DURING THE PRE-WINTERING PERIOD WITH HIGH NATURAL POPULATION COUNT

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Seasonal change of habitats is a phenomenon characteristic of water vole *Arvicola amphibius* (Linnaeus, 1758), in Western Siberia (Maksimov, 1959; Panteleev et al., 1980). For the breeding season, it mainly inhabits riverside areas with hydrophilic vegetation. In autumn breeding stops, and the animals move into drier habitats with meadow vegetation. During this period, they intensely dig burrows with feeding tunnels and make stores for the winter. In the autumn-winter season, both males and females live alone, occupying separate burrows, and rarely come to the surface, leaving secret life (Panteleev, 2001). Obviously, because of this reason many important aspects of species ecology, which are characterized by pronounced population dynamics, have not been sufficiently studied so far. In particular, the question of which factors and to what extent are able to affect population reduction, especially at its high density, when competition for vital resources becomes extremely acute, still needs clarification.

The work was carried out near Lisii Norki village, Novosibirsk Province, in September and October. In 1994, during the phase of a high number of water voles, we used methods of full capture with marking (6♂♂ and 11♀♀) and recapture combined with radio-tracking (Rogov et al., 1992) to study the activity of individuals during their transition to winter lifestyle in a fenced area of uncut meadow (1350 m^2). 24-h position and activity of each animal scanning with radio transmitter was conducted with the intervals of ½ hours (4♂♂ and 5♀♀, 289 entries).

In 1986–2001, 139 burrows were excavated; their structure and weight of feed stores were studied. In 1999 and 2001, 25 young-of-the-year and 3 wintered voles were placed in individual cages in a vivarium with free access to water for a period of 2 to 7 days. Room temperature was kept at +10 ± 3 °C. Each cage was equipped with two plastic tubes. One of them served as a shelter where nesting material was placed, and the other served as a pantry equipped with a feed (100–150 g). Both bedding and food were taken from the burrow of the corresponding experimental animal. To control natural drying of feed, we left one similarly equipped cage without animal. Every day all the experimental voles, their nests and feed residues in the cages were weighed, and the cages were rebooted with fresh nesting material and food. Daily feed intake was corrected for natural drying (Potapov et al., 2004, 2012).

It turned out that at high numbers, voles were active underground in burrows mostly nearby the nest for the periods from 18^{00} to 19^{00} and 21^{00}–24^{00}, rarely came to the surface or moved within 5 m from the exit hole, and did not contact with each other directly. The mean radius of the area occupied by the burrow during the study period was no more than 10 m. We found that feed stores set by females were significantly smaller than those of males. Weighing stocks adjusted for individual daily feed intake showed that only a small proportion of voles were provided with enough food for wintering in a period of high population numbers. We found that in such years animals were unable to create feedstocks sufficient for safe wintering. Food deficit during the winter also lead to increased female mortality (Potapov et al., 2004, 2012).

Thus, our findings of relatively small areal ranges and low activity of water voles in pre-wintering period at high numbers, as well as an insufficient food supply they entail, especially females, confirm that winter food deficiency can cause decline of population size during the subsequent period.

CORRELATION OF PHYSIOLOGICAL STATUS OF MOTHER AND OFFSPRING IN FELIDS

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Individual differences of animals is a unique material for the realization of natural selection in evolution. Diversity of life-strategies related with the inherited traits of physiology and behaviour may be set on the early stages of ontogenesis. They are depend directly on “maternal factor” which is related in mammals not only with the heredity by offspring of mother’s traits but also with of prolonged period of pregnancy and lactation. In felids, almost nothing is known about the effect of females’ condition during the pregnancy and lactation on physiological status of offspring. Some studies were dealing with the effect of maternal status and behavior on offspring growth rate but nothing is known about the effect of hormonal and immune status of females on offspring status. The aim of our study was to describe the dynamic of some physiological parameters of offspring and their correlation with the maternal physiological status. This study was conducted at the biological station “Tchernogolovka”. Husbandry conditions for the lynxes were often described earlier (Sokolov et al., 1994; Naidenko, 2005). Domestic cats lived in small outdoor enclosures (2 m^2 each) and were fed six days per week. We collected blood samples of lynx and domestic cat’ kittens after birth once per two weeks for the hormonal analysis. Serum was stored at -18 °C. We used commercial kits to detect testosterone (T) level (Immunotek, Moscow, Russia). Moreover, blood sampling was conducted for 6 Eurasian lynx females at the 15 days of pregnancy. In domestic cats blood samples were collected under physical immobilization at the 15th day of pregnancy and at the day of birth and once every two weeks during lactation. The estimation of “immune status” was conducted with the immunocomb kits (Israel) for the detection of antibodies titer to panleukopenia virus, herpes virus and calicivirus. We described the dynamic of T level in domestic cats during lactation. T concentration changed significantly during this period (Friedman ANOVA: N = 20, df = 6, T = 17,25, p = 0,01). T level increased gradually more than two times from the birth until the 10th week of kittens’ life (from 0,69 ± 0,25 to 1,47 ± 0,35 ng/ml). T concentration in lynx kittens was at the maximum soon after birth (3 days of age).Factor “age” had significant effect on T level in lynx kittens (GLM: F = 6,61; df = 6; p < 0,001), but not the factor “sex”. T level in lynx kittens was at the minimum at 6th week of age and then increased significantly to the age of three months. Factor “litter ID” also affected significantly T level in kittens (F = 9,72; df = 15; p = 0,000). Common effect of this factor and factor “age” was also significant (F = 7,70; df = 90; p = 0,000). It allowed us to suggest that T level of kittens may correlate with the mother’s T level. Average T concentration in felids’ females increase significantly during the pregnancy in comparison with the other life periods. Probably it may result in T increase in newborn kittens, but we did not find correlation of T levels in newborn kittens and their mothers during the pregnancy. The titer of antibodies to herpes virus, calicivirus and panleukopeninia virus in newborn kittens and their pregnant mothers correlated significantly and positively for herpes and calicivirus (N = 11, R = 0,78–0,84, p = 0,00), and with the titer of mothers’ antibodies after the parturition – for all three pathogens (N = 11, R = 0,76–0,97, p = 0–0,01). The changes of androgens level in carnivores ontogenesis were described just in a few cases (Frank et al., 1991; Naidenko, 2005). High level of testosterone in newborn kittens may be related with the intrauteral exposure to high T level in pregnant mothers. During the pregnancy T level in felids’ females was much higher than in all other periods. In other carnivores (spotted hyaena) androgens level was also high in newborn cubs. Females of mammals transfer antibodies to the offspring through placenta or milk after the birth defending them at the pre- and postnatal ontogenesis. Comparing antibodies titer in kittens and their mothers we found their strong correlation after birth that support the transfer of maternal antibodies to kittens and probably determine different quality of offspring. Such way, an effect of physiological status of mothers on offspring is reflected in their immune status and testosterone level in kittens and, possibly, result in significant differences in their individual life-strategies. This study was supported by RFBR grants 16-04-00757 and 16-34-00844.

SEX AND AGE STRUCTURE OF THE POPULATION OF STRAY DOGS OF SURGUT AREA AND SURGUT REGION

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Currently, the solution to the problem of stray animals is important in the life of any large municipality. Neglected pets worsen sanitary-epidemiological situation, because they are the source of 27 infectious diseases transmissible to humans, including 3 virozov, 12 bacterial, rickettsial 3, 9 fungal infections and the reservoir 22 agents of dangerous diseases common to humans and animals. They can be combined in large flocks, are very aggressive, attacking people (Blokhin, 2002; Snegirev, 2010). One aspect of human impact on the nature of the relationship are domesticated animals and human wildlife species. While seemingly isolated from wild animals carnivores come home with them in a variety of interactions (Rakhimov, Shamsuvaleeva, 2006).

The purpose of the study – the definition of sex and age structure of the population of stray dogs, the laws of its distribution in chorologic territorial administrative boundaries of the Surgut city and towns of Surgut region.

Study of stray dogs was carried out in October 2014 for the June 2015 study of the area in the Surgut city was 126 km^2 (the area of the municipality of about 213 km^2), covered 625 km route. The settlements of the Surgut district - town Solnechny (7,3 km^2 area), town Barsovo (2 km^2), town Bely Yar (7,1 km^2) (located in the vicinity of the city), town Fyodorovsky (60,1 km^2) and Lyantor (63 km^2) covered 210 km route. Taking into account the architectural and town-planning zone territory of settlements divided into low-rise, multi-storey, forest park, industrial and horticultural area (Master Plan ..., 2008). Registered homeless and neglected dogs: 1267 individuals in Surgut and 419 individuals in the localities of the Surgut district.

Paul and approximate age adjusted visually (Poyarkov, 1989). Distinguish the following age categories: 1 – puppies; 2 – young; 3 – probably young; 4 – probably old and 5 – older individuals.

The population of stray dogs in the city of Surgut is represented by males more often than females. Males – the most moving part of the dog population. In the winter and spring periods of research in all areas have seen their dominance. The low-rise, horticultural and industrial zones in the winter, their share was between 13% and 25%, and in the spring of 10% to 16%. In the town Bely Yar, Barsovo Solnechny and high dominance of males in the low-rise and multi-areas in winter and spring. In the town Fyodorovsky and Lyantor in the area of low-rise buildings of a high proportion of males (31% and 38% – in winter, 33% and 34% – in spring) and females (25% and 34% –in winter, 13% and 22% – in spring).

The settlements account all age categories of dogs. Dominated adult dogs from the third and fourth category. The only exception was the age distribution of dogs in Lyantor in the winter and spring of studies have observed the dominance of puppies (males 15% – in winter, 22% – in spring; female 17% and 28%) and young individuals (males 13% – in winter).

Dogs life in zones of the city is determined by the strategies of social and feeding behavior, the attitude of people to their gender at neglected maintenance. Identical trends discussed the problem in the Surgut city and the town Solnechny, Bely Yar and Barsovo due to the close proximity of each other, which ensures the safety of the population of stray dogs under unfavorable conditions of existence. In recent years, the city of Surgut consistently favorable conditions for the life of dogs (Nakonechny, Ibragimova, 2016). In the town Fyodorovsky and Lyantor revealed the instability of the population by sex and age indicators, as small area of these settlements are provided with adequate housing and domestic control.

SOME ASPECTS OF THE CONDUCT OF POPULATION STRAY DOGS OF SURGUT CITY AND SURGUT REGION IN WINTER AND SPRING PERIODS

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Study of stray dogs as a component of urban areas - a necessary condition for resolving many important tasks related to the environment of the city. The severity of the situation is due to constant and increasingly strengthen the contact with these animals that reach in urban areas rather high number. The sharp rise in the number of stray dogs in Russia observed from the 90s (Rybalko, 2006), so the problem is particularly acute at the moment. To date remain insufficiently studied such important issues as the population dynamics, spatial, social structure of the population of dogs, there is no uniform classification of environmental types, evaluation of their role in the lives of urban ecosystems and urban society (Sedov, 2007).

Study of stray dogs was carried out in October 2014 for the June 2015 study of the area in the city of Surgut 126 km^2 (the area of the municipality of about 213 km^2), covered 625 km route. The settlements of the Surgut district - town Solnechny (7,3 km^2 area), town Barsovo (2 km^2), town Bely Yar (7,1 km^2) (located in the vicinity of the city), town Fyodorovsky (60,1 km^2) and Lyantor (63 km^2) covered 210 km route. Taking into account the architectural and town-planning zone territory of settlements divided into low-rise, multi-storey, forest park, industrial and horticultural areas (Master Plan ..., 2008). Registered homeless and neglected dogs: 1267 individuals in Surgut area and 419 individuals in the localities of the Surgut district.

Eating strategy stray dogs studied settlements ranged from a variety of factors, but the “Search” – that's the basic strategy of any dog food. Often dogs registered with the type of power “search” and “boarderition” rarely “begging” sporadically “predation”. Fatness stray dogs had seasonal stability: the type of fatness “1” was recorded in the majority of individuals, “0” - prevailed in puppies. Types of fatness “2” and “3” are met in pregnancy, giving birth and old individuals. Favorable factors for such dynamics are stable food supply, the presence of places for shelter, as well as high social adaptation of the population of stray dogs and dogs growing up on “puppies” and "young" in the category “most likely the young”.

All localities dominated mongrel dogs. Among thoroughbred often met husky-like and sheep-dog-like (German Shep-dog). The prevailing schooling behavior of dogs in city and in towns. In horticultural and low-rise and dog woodland area can form a flock for a short period of time to search for food and “hunt” of small vertebrates. Belonging to a man changed by seasons. In the snow season, taking into account population growth from the surrounding forest areas have increased in number of homeless (75%); in the snow-free period, the population consisted of 65% of the homeless. Any type of behavior takes place in the relationship between man and dog, are often recorded indifferent, the beggars and the cowardly, rarely met aggressive dogs (lactating females and neglected in an industrial zone).

One of the reasons why in the snow period there was an increase of stray dogs is associated with the completion of the population cowardly individuals, including breed characteristics. These dogs come from the surrounding forests, where food supply becomes inaccessible (Sedov, 2007).

FEATURES OF GENETIC STRUCTURE OF STEPPE MARMOT'S AREA IN RIGHTBANK REGIONS OF MIDDLE VOLGA REGION

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Studying genetic structure of steppe marmot's area (*Marmota bobak* Müll) is a challenging research issue, related to large-scale introduction of marmot in 70s in Russia. Introduction of large number of individuals from significantly remote maternal colonies resulted in greatly distorted gene pool of most colonies. Although gene pool estimation was almost impossible, there appeared some hope to recover lost information with wide use of molecular genetic methods. Genetic statistics helped identify genetic structure attributes of steppe marmot's actual living area.

For genetic structure and genetic variability analysis of spatially fragmented marmot's populations and their individual colonies, markers of mitochondrial (D-loop, 1063 bp, $n = 23$ and Cyt b, 1013 bp, $n = 17$) and microsatellite (IGS-bp, $n = 77$) DNA were used. Sequences of mtDNA fragments were analyzed using MEGA 6.06, DnaSP 4.10 and Network 4.6.1.3. Based on the frequency distributions of microsatellite alleles, the analyses of populations' and individual colonies' genetic structure were conducted using multilevel F-statistics (indices of inbreeding, fixation, heterozygosity and standard indices of diversity and variability) (Arleqin 3.11)

Results:

1) D-loop sequences analysis (ML-method) allowed clustering of colonies from geographically isolated sites into several groups: GR1 и GR3 were relict colonies of steppe marmot with genetically identical daughter colonies and GR2 were daughter colonies formed after reacclimatization. We identified 15 haplotypes. D-test (Tajima) points to possible colonies number and population increase after bottleneck effect. This conclusion is in line with reacclimatization history of steppe marmot area recovery in Volga Region. Median network created included two haplotypical groups of marmot's colonies uniting maternal and daughter colonies formed after reacclimatization.

2) Cyt b sequences analysis (ML-method) allowed to unite colonies from geographically isolated sites in two groups only (GR1 and GR2), relict colonies of steppe marmot with genetically similar daughter colonies.

3) Microsatellite DNA sequences analysis showed that most marmot's colonies were stable ($G\text{-}W_{mod} = 0{,}588$) and isolated, and gene flow between them was low ($F_{ST} = 0{,}55$).

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THE ROLE OF MORFOFIZIOLOGICAL HETEROGENITY OF BREEDING FEMALES IN THE REGULATION OF OPTIMAL POPULATION NUMBERS

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One of the most important factors that determine the relationship of reproductive function and the population size is the use of external environment resources and accumulated body reserves for reproduction (Pianka, 1976; Weiner, 1987). There is a great interspecies diversity in the role of endogenous reserves or external environment resources in the reproductive process initiation, success of pregnancy and lactation. Females of some species come into reproduction only once they reach a certain threshold of internal fat reserves. During lactation, they use predominantly accumulated body reserves (capital breeders). For others, the availability of food resources in the external environment (income breeders) is essential. Third (and most of them) need both of those (Jönsson, 1997; Boyd, 2000). Availability of deposited body reserves is very important to supply increasing energy needs at the peak of lactation, and to reduce physiological and ecological cost of reproduction (Reznick, 1992; Speakman, 2008). The role of the relative level of body reserves that maternal organism can spend on reproduction in the plastic regulation of life history and the numbers of individuals of parental and progeny generations is not well understood. It is believed that rodent overwintered females do not significantly differ in their reproductive fitness, since they usually all have placental scars or embryos in the uterus. Individual differences in the level of fetal or early postnatal losses that mostly contribute to the realization of actual fertility and assessing of which is difficult in the wild, are usually left out of scope. Based on the studies of water vole from cyclic populations and captive-bred animals, they obtained the following results: 1) presence of genetic differences between females in the ability to accumulate body reserves in the first half of pregnancy for the needs of lactation; 2) accumulation of body reserves was accompanied by morphological and physiological adaptations – enlarging the liver and spleen during pregnancy; 3) fat stores accumulated during pregnancy serve to increase the reproductive contribution of females; survival of offspring, because the growth rate of progeny was positively associated with the maternal fat reserve; 4) relative contribution of maternal effect to the variability of newborns body mass is 15%; 5) maternal effect has a significant modulating impact on the viability and reproductive potential of water vole from natural populations, thus, optimizing their numbers at the level, appropriate for the environment.

HUNTING BIRDS OF RIVER KET' BASIN (TOMSK REGION)

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The studies were conducted in 2009–2015 in the Ket' river basin of Tomsk region (oblast). We used the method developed by Y.S. Ravkin (1967) for the surveys. We conducted this study on the categories of the habitats elements, corresponding to the hunting resources: forests, young forests and shrubs, mires, meadow-steppe complexes, agricultural lands, inland water bodies, and floodplain systems. The overall territory coverage was 450 km.

The aim of our study to assess the state of game birds' resources in the middle course of Ket' river basin.

We found thirty-eight species of game birds in the study area. Species listed in the Red Book of Tomsk Province (*Rufibrenta ruficollis, Anser anser, Cygnus cygus, Grus grus, Haematopus ostralegus, Numenius arquatus, Numenius phaecopus, Limosa limosa*) were not included in this list.

Galliformes and Anseriformes were the most valuable as hunting resources. Different species of shorebirds and pigeons were less important. Chickens and geese had the greatest value as hunting and trading resources. Various kinds of waders and pigeons were less popular.

Number of upland fowl in the area increased in recent years. Population density of *Tetrao urogallus, Lyrurus tetrix, Tetrastes bonasia and Lagopus lagopus* averaged 2, 8, 12, and 3 birds/km^2, respectively. However, the number of grouse in its favorite locations (dark coniferous taiga and mixed forests of river valleys) reached 150 birds/km^2 by the end of summer. Number of *Scolopax rusticolla* reached one bird/km^2. An hour observations resulted in the identification of 5–15 individuals in the peak evening hours. Number of waterfowl was quite high and remained stable. We found 11 species of ducks during the study period in the area: *Anas platyrhinchos, Anas acuta, Anas penelope, Anas clupeata, Anas crecca, Anas querquedula, Aythya ferina, Aythya fuligula, Bucephala clangula, Mergus merganser, and Mergus albellus.* The most productive in terms of ducks nesting density were lake floodplain complexes, where the average density was 14,2 (up to 50 birds/km^2). Second most important habitat of waterfowl were taiga rivers with the ducks' abundance up to 5,23 birds/km^2. In the marshes and swamp forests nesting density did not exceed the level of 0,5 and 0,1 birds/km^2, respectively. Dabbling ducks were the most numerous, including mallard, widgeon and teal, whereas goldeneye lead the diving group.

Field game (including *Streptopelia orientalis*) has always belonged to the hunting resources, not as popular, however, in that region. The number of turtledoves in summer reached 8 birds/km^2. There were very few individuals of *Coturnix coturnix* (0.1 birds/km^2 it is favorite locations). Bog-meadow fowl groups includes the genus Gallinago, *Tringa*, *Limosa* and species – *Lymnocryptes minimus, Philomachus pugnax, Vanellus vanellus, Pluvialis squatarola, Xenus cinereus, Crex crex, Porzana porzana*, which are not popular as well. The most numerous were *Gallinago megala* and *Gallinago gallinago* – up to 3 birds per km^2. The abundance of other species did not exceed 1 birds/km^2. The total abundance of bog-meadow fowl reached a maximum of about 30 birds/km^2.

Thus, the stocks of hunting birds are sufficient for hunting. However, proper organization of hunting is necessary to count not only upland fowl, but also other groups of fowl, firstly waterfowl. It is necessary promote hunting of waders, pigeons and other game birds.

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TAXONOMICALLY MEANINGFUL ATTRIBUTES OF MOOSE’S LOOK IN THE WESTERN SIBERIA ASSOCIATED WITH ITS MTDNA

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Western Siberia moose population manifests high genetic diversity and specific mitotic composition (Nemoikina et al., 2016). Both unique Western Siberian haplotypes (Western Siberian haplogroup, HWS) and those prevalent in other areal types from Europe (European-Ural haplogroup, HEU) to East Asia (American haplogroup, HA) are present here. Therefore, combination of genetic traits of Western Siberian moose population with the borderline areal of the European and Yakutian subspecies may yield animals with external taxonomic traits typical for both *A. a. alces* and *A. a. pfizenmayeri*. To test this hypothesis, we used data on spine coloring (presence of absence of black line on the spine), coloring of lower abdomen, lower parts of extremities, muzzle (light and dark-colored) as exterior features along with horn shape (elk or deer type or intermediate). Black line on the spine, dark abdomen, lower extremities, and muzzle coloring together with elk-type or intermediate horns are attributes of Yakutian subspecies, which inhabits Siberia eastwards from Yenisei (Danilkin, 1999). We used exterior descriptive data of 50 animals in this study. They all were genotyped on the mtDNA control region (D-loop) (Mikko, Andersson, 1995). HEU included 30 specimens divided into five haplotypes, HWS had 18 specimens with five haplotypes also, whereas HA was only represented with two specimens with only one haplotype.

Animal coloring of various haplotypes varied from the one typical for European moose (12 animals) to Yakutia (7 animals), however combined type was more prevalent (31 animal). One animal with nucleotide sequences of HA looked like Yakutian moose, another one as European. Animals grouped with HEU and HWS differed in coloring also. 50% of HEU animals had black line on the spine; 23% and 53% animals had black lower abdomen and lower parts of extremities, 57% animals had dark-colored or black muzzle; and 50% had shovel-shaped of intermediate horns. These features was less typical for HWS look. Thus, 22% animals had black line on the spine; 17% and 44% had dark lower abdomen and darn lower parts of extremities; 44% animals had dark-colored or black muzzle; and 39% had elk-type of intermediate horns. Therefore, HEU moose demonstrated greater exterior variability compared to HWS. We explain that with a hypothesis that HWS passed through more severe bottleneck than HEU, preserved in only one Pleistocene refigium. Today, this yielded smaller area of HWS prevalence compared to HEU, as well as poorer genetic (Nemoikina et al., 2016) and exterior diversity of Siberian haplogroup compared to European-Urals.

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DATA OF LONG-TERM OBSERVATION OF KAMCHATKA BROWN BEARS FAMILIES

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The most effective and reliable method of counting the number of brown bears in Kamchatka is by the use of helicopters (usually Mi-2). The best time for that is from late May to early June. Bears count based on these results needs correction (Chestin, 2006). Correction is also needed for females with 1-year cubs (Gordienko, 2006), because most of them are still in dens at that time. Those who have already left their dens, usually occupy small individual territories. Therefore, their counting is quite challenging. It is important to calculate cub index of females. However, this index (even based on many-years observations) for the most territories of the region is either insufficient or, which is not rare, doubtful (Revenko, 1993). Data on Kronotsky Federal Nature Preserve and Yuzhno-Kamchatsky Federal Reserve, on opposite, are precise and sufficient, which is an exceptional case in Russia.

The author has almost finished processing many-years data on bear’s families on these territories. We previously published similar reports; however, they were attributed to selected seasons (Nikanorov, 2000, 2001, 2010, 2012, 2014).

In Kronotsky Preserve, data on 46 field seasons were processed. We started basic data logs in 1977. Many co-workers of the Kronotsky Preserve participated in this study together with the author. Specific environmental attributes on this territory allow cubs’ age determination only visually.

We processed data on 1780 bear families (778 of them with cubs). The mean index of bear family with 1-year cub was 1,89 with the amplitude of 1,68–2,10. While estimating the indexes variability, we only considered samples with the minimum index of 25.

We processed data on 13 field seasons in Yuzhno-Kamchatsky Federal Reserve. The overall count of families with cubs was 1050, and 320 were with 1-year cubs. The mean cub index was 2,16 cubs per one female. We reported the difference of bear fertility in the Preserve and in the Reserve earlier (Nikanorov, 2001), and the current material in this presentation confirms those findings.

In addition, we also processed data on the air counts made by our colleagues of KamchatSIFO in 2001–2002 on the entire territory of Kamchatka. In total, 787 bear families with cubs of different age were identified, 471 of them had with 1-year cubs. In the year 2000, the cub index was 1,88; falling to 1,62 in 2001, being unusually low. Besides, we also found bear families with four cubs in the river basin of each main river system.

We hope that this data, previously unpublished, will allow to conduct more accurate calculation based on data of bear number in the region and in the protected areas in particular.

SUMMER DYNAMICS OF THE TIT SPECIES (PARIDAE, AEGITHALIDAE) IN BIRD POPULATIONS OF THE STATE NATURE RESERVE KERZHENSKY AFTER CATASTROPHIC FIRES IN SUMMER OF 2010 (NIZHEGORODSKAYA PROVINCE)

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Forest fires hit more than 45% of the State Nature Reserve «Kerzhensky» territory during abnormally hot summer of 2010. In summer of 2011–2015, we used a line transect counting method here (Ravkin, 1967). We counted bird populations on the routes of total length of about 1620 km, including 420 km of routes for the rare species census. The main types of habitats were surveyed, including different-aged birch-pine forests with skirts of bogs and storm gaps – habitats with high level of damage caused by the crown fire, low level of damage caused by the ground fire and undamaged; as well as bogs with forests on elevations – damaged and undamaged by fire. Birch-pine forests along the border of artificially inducted preventive ground fire zone and mosaic meadows (the vicinities of cordons) were surveyed only in 2011 and 2012, and the territory of the Rustay settlement and flood-land mixed undamaged forests surrounding the settlement were examined only in 2014 and 2015 (Noskova et al., 2014; Noskova et al., 2015). All data were loaded into the database of the Zoomonitoring Laboratory of the Institute of Animal Systematic and Ecology SB RAS.

During five years of bird monitoring in the Kerzhensky Reserve we encountered all 6 species of tits, which occur in the region. Only the Blue Tit *Parus caeruleus* was observed mainly in the Rustay settlement and in the flood-land forests – no more than 4 ind./km^2 during the breeding season (from 16 May to 15 July), and 21 ind. were found in the post-breeding season (from 16 July to 31 August). The Coal Tit *Parus ater* was observed everywhere during summer, but it wasn't numerous (7 ind./km^2), except in flood-land forests (23 ind./km^2). The Crested tit *Parus cristatus* wasn't found on the territories damaged by crown fire in the first year after fire, and generally it was the most numerous on the bogs and in the undamaged birch-pine forests (41 ind./km^2) during summer. The Long-tailed tit *Aegithalos caudatus* was encountered generally on the bogs mainly undamaged (27 ind./km^2) during the first three breeding seasons. On the contrary, its abundance increased in the forests slightly damaged by ground fire and undamaged (55 ind./km^2) in 2015. In the last habitat its movements were noted during the post-nesting season as well. The Great tit *Parus major* wasn't numerous everywhere (11 ind./km^2) during the first year after the fire. Next year its abundance significantly increased during the breeding season mainly in the undamaged habitats (74 ind./km^2), but this abundance level remained only in the Rustay settlement and the flood-land forests. It emerged to be predominating even in the habitats damaged by fire (30% of the abundance) during the first two post-breeding seasons. Generally it prevailed in the undamaged and slightly damaged habitats (38%), its participation didn't exceed 12% of the abundance only in 2015.

The Willow tit *Parus montanus* is the most numerous species among tits in the Reserve. In the first summer, its maximum abundance was in bird populations of the territory damaged by crown fire (69 ind./km^2) as well as of undamaged bogs during the post-breeding movements (84 ind./km^2, 24% of the abundance). Later on its abundance increased in all habitats, mostly in slightly damaged and undamaged by fire – up to 120 ind./km^2 during the breeding and 174 ind./km^2 in the post-breeding seasons. The Willow tit was a dominant species in bird populations only in the undamaged habitats (12%) during the breeding seasons of some years, whilst in the post-breeding season it predominated practically everywhere (34%), except the Rustay settlement and the damaged bogs. In the last habitat it began to prevail only in 2015, when its abundance in the majority of habitats, including the damaged territory, exceeded 100 ind./km^2. During the first breeding season the total abundance of tits did not exceed 35 ind./km^2 (only 7% of total abundance of bird populations). The next several years they prevailed in the undamaged habitats (up to 25% on the bogs in 2012), and until 2015, their abundance increased gradually in the forests damaged by the ground fire (172 ind./km^2, 21%). During the post-breeding season the abundance and participation of tits in bird populations everywhere, excluding the territory damaged by crown fire, were much higher (57%), especially in the flood-land forests.

VARIABILITY OF METABOLIC RATES IN MURID RODENTS

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Apart from well-known allometric regularities (Suarez et al., 2004), variability of metabolic rates is affected by ecological factors: availability and caloric content of food (McNab, 1986; Mueller, Diamond, 2001), climatic conditions (Lovegrove, 2003), and oxygen pressure (Bredley et al., 1974; McNab, 1979). Among rodents, herbivorous species have generally lower metabolic rates compared to granivorous ones (Weiner, 1989), mountain and subterranean species have similarly lower metabolic rates than terrestrial ones (Novikov, 2007; Hayes, 1989). Rodents inhabiting thermostable environment have lower metabolic rates than those who live in habitats with high instability of climatic parameters (Moshkin et al., 2002). Environmental factors could obviously affect both basal and metabolic rates, although these two parameters correlate with one another weakly (Koteja, 1987). Since the data collected by different research teams often appear to be non–comparable, analysis of the inter-species comparison based on the standard instrumental approaches and protocols are of special importance to understand general evolutionary regularities of the metabolic rates variability.

In this study, we analyzed variability of basal and maximal metabolic rates in murid rodents of different ecological specialization, inhabiting forest and steppe landscapes of Eurasia, such as stripped (*Apodemus agrarius*) and pigmy (*A. uralensis*) field mice, dwarf hamsters (*Phodopus sungorus*), red-back voles (*Myodes rutilus* и *M. rufocanus*), mountain voles (*Alticola strelzovi* и *A. tuvinicus*), narrow-skilled voles (*Lasiopodomys gregalis*), steppe lemmings (*Lagurus lagurus*), northern (*Ellobius talpinus*) and zaisan (*E. tancrei*) mole voles. All individuals that were laboratory-born descendants of wild-trapped animals were studied under the same protocol, in which we measured basal metabolic rate and cold-induced oxygen consumption. Maximum value of oxygen consumption measured under acute cooling was assumed as maximum metabolic rate. The drop of body temperature after acute cooling was considered the index of individual's thermoregulatory ability.

The lowest values of basal and maximal metabolic rates were identified in high-altitude species: grey-sided and mountain voles, and also in subterranean mole voles. High-active granivorous and omnivorous species, mice and dwarf hamsters had the highest levels of metabolic rates. Herbivorous narrow-skilled voles and steppe lemmings that inhabited arid landscapes also had relatively high metabolic rates. We found significant correlation between basal and maximal metabolic on the inter-species level. Correlation between maximum metabolic rate and thermoregulatory ability was not so high.

Among ecological factors, that potentially may affect species-specific values of metabolic and thermoregulatory indexes, caloric content of food, stability of climatic parameters and oxygen pressure seem to be essential. Effect of spatial-ethological structure of population is not so pronounced.

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ECOLOGO-GEOGRAPHICAL MODELLING AS A METHOD TO STUDY AREA AND ECOLOGICAL NICHES

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Statistical comparison of geographical data with the animal species number or with other population indicators allows detecting and assessing the significance of environmental factors in organism distribution, the range structure and its well-being. We carried out this work using the example of red vole *Myodes rutilus* (Pall.) in the West Siberian part of its range: inter Ob – Irtysh – Yenisei Rivers from north to south (in Kazakhstan) of range boundaries. Using published data we determined the abundance of red voles during the seasonal population peak (in ind./100 trap-nights), the species percentage in the communities and other population indicators for each of the red vole localities. In addition, these materials allowed to estimate index favorability of territory for voles (IF) (from 1 (pessimum) to 5 (superoptimum) for each locality. When describing the location of voles capture, we used basic meteorological indicators, such as the mean annual air temperature and annual precipitation, and the duration of snow season, the dates of its formation and termination, maximum snow thickness for a season, taken from the climate database BIOCLIM and Digital Agricultural Ecological Atlas of Russia and neighboring countries (2009). We determined geographical coordinates of localities and their altitude as well. In this study, we used 51 localities for West Siberia and 285 localities for all red vole range. We found that West Siberia is characterized by the highest voles abundance: 13,12 ind./100 trap-nights in the West Siberia and 8,42 ind./100 trap-nights throughout all red vole range and has the greatest IF (2,98 and 2,65 accordingly). Western Siberia part of red vole range has warmer (-1,45 °C) and more dry (472,53 mm) climate compared with all range (-2,45 °C and 489,7 mm). The least altitude of Western Siberia part of red vole range is 96,84 m, and snow thickness is 72,27 mm. For comparison, relevant estimates for the whole vole range are 414,59 m and 105,35 mm. The duration of snow season and the dates of its formation and termination do not differ from the means. The correlation coefficient among red vole abundance and IF is great and equals 0,85 ($p \leq 0,05$). The distribution patterns in climatic field (in the coordinate system of the mean year air temperature and annual precipitation) differ insignificantly. Colder and moister territories were optimal. The dependence of IF from altitude in West Siberia differed significantly from the all range mean. The lowland territories are favorable for red vole in this region, whereas the associations are different in other regions. In West Siberia IF for red vole has a negative correlations with altitude, the mean air temperature, the start and end dates of snow. The statistical model describing the IF (y) associations with geographical indices, was ($y = 19{,}79296 - 6.649518*T + 0{,}00120*T*P + 0{,}01632*H + 0{,}09116*L - 0{,}00098*Db*De - 0{,}00005*Al$), where T is the mean air temperature in °C, P – year precipitation sum in *mm*, H – the snow thickness in *cm*, L – the snow period in days, Db – the data of snow start (in days numbers from 1 January) and De – the data of snow end (the same calculation), Al – altitude in *m*.

The method helped describe polynomial quantitative associations of ecological niche and compare both different species and the spatiotemporal parts of range of the same species.

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RED-TOOTHED SHREW WINTERING SUCCESS AS OF RESULTS OF INDIVIDUAL MARKING

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Success of wintering of the red-toothed shrews depends on the number of factors of which several seem to play a major role, such as density of population going for wintering, sufficient food supply, and weather conditions. However, density of population going for wintering is the only factor that could be quantitatively estimated. Population census data cannot be directly used to estimate the numbers of shrews from autumn to spring since home size range increases and females' mobility, yet more of males, rises drastically. These factors affect and change their catchability. The ratio between true numbers of shrews in different seasons was explored by A.A. Kalinin (2008) who used data collected during many-year research conducted in the southern part of Tver Province. Calculations based on approximation of home ranges with normal distribution adjusted for seasonal change yielded mortality rates of the common shrew, masked shrew, pygmy shrew *(Sorex araneus, S. caecutiens, S. minutus)* in the autumn-winter period and demonstrated dependence of mortality rate on maximum summer population numbers. The average density values for few years reflect the mortality rate during winter months as the rate that does not exceed the one of the previous autumn. The hypothesized that winter-spring period population numbers might not depend on the ones of the autumn period, but are defined only by the carrying capacity of the habitat.

Besides, the values of winter mortality, autumn and spring population numbers vary significantly across various years as well as across different biotopes, while averaging data makes it more difficult to identify correlations between them. In order to research the relations between the success of wintering (the share of animals that survived winter) and the number of individuals in autumn, we analyzed survival of marked animals (marking method: Shchipanov *et al*, 2000) throughout wintering in the same populations in the Staritsky district of Tver Province as the ones studied in the abovementioned paper. Shrew population in winter is settled, migration is non-existent, and in equal conditions they hypothesize that extremely low density in the beginning of wintering as well as the extremely high one will exert some influence on the density values in spring. We have analyzed data for 13 winter seasons (October-November till April) from 1995 to 2016 collected at 66 lines of 50 live-traps each, and tracked the fate of 679 common shrews and 527 masked shrews.

We found that the number of individuals that go for wintering in autumn and the number of animals that died in winter demonstrate strong positive correlation for both *S. araneus* and *S. caecutiens* (Pearson $r = 0{,}92$ and $r = 0{,}89$ respectively, $p < 0{,}01$; Spearman $r_s = 0{,}95$ и $r_s = 0{,}89$, $p < 0{,}01$). Besides, the number of individuals in autumn does not correlate with the number of those that survived winter for *S. araneus* ($r = 0{,}15$, $p > 0{,}05$; $r_s = 0{,}06$, $p > 0{,}05$), while in *S. caecutiens*, the correlation was positive ($r = 0{,}62$, $p < 0{,}01$; $r_s = 0{,}54$; $p < 0{,}01$). Success of wintering for *S. araneus* was 0–75%, 22,8% on average; and 0–83% for *S. caecutiens*, 30,2% on average.

Hence, the direct data analysis confirms the hypothesis about independence of spring population numbers from the ones of autumn (Kalinin, 2008) only for the common shrew. These indicators correlate in the analysis of masked shrew. This might be explained by the bigger share of plant food in winter ration of *S. caecutiens*, i.e. in case of good harvest, plant food decreases competition for food. Winter mortality depends on the density in autumn for both species: the more individuals begin wintering, the fewer of them survive winter. If autumn population numbers exceed a certain threshold that is specific for each biotope, the success of wintering drops to zero. This effect is quite common for the local spots and it is compensated with increased activity of animals from the neighbor sites. Under normal, wintering works as a filter with a negative feedback that decreases density of population if it was excessively high in autumn, while it does not prevent animals from survival if population numbers were low in autumn. This is the ultimate link in the optimization of spring density, which is a starting point of the annual reproductive cycle in shrew populations.

THE ROLE OF ECOLOGICAL FACTORS IN EVOLUTION (STRATEGY OF ADAPTATION OF RODENTS' POPULATIONS IN EXTREME CONDITIONS)

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We analyzed adaptive strategies of cyclomorphic rodents' populations (Rodentia Order) in extreme conditions of a drought (1975 year) based on functional-ontogeny approach. Similar drought in terms of duration and intensity was not marked for more than a century of meteorological observations. That was a real gift for a researcher. Field data were collected on the stationary plots of Southern Urals (Chelyabinsk Province). Mass individual marking of animals (the capture-mark-recapture – CMR method) was used throughout 30 years from the 40-year monitoring investigations. We present data on five species of cyclomorphic rodent' populations.

Ecological plasticity of species is pivotal for population preservation in extreme environmental conditions, firstly due to liability of complex intrapopulation structure, i.e. change of ratio of functional groupings (pathways of ontogeny development), which are typical for murine rodents. Observations of changes of demographic structure and numbers of rodents, belonging to different taxa, found an accessory existence of *different forms of reaction,* which were different strategies of populations' adaptation to the impact of similar environmental factors. All that results in dramatic changes of long-term oscillations of numbers of different species after drought.

The first type of reaction (voles of genus *Clethrionomys (Myodes*), two species) is the *increase of number only due to reproduction of overwintered animals and full growth maturing block with metabolism suppression.* This adaptive strategy in the conditions of drought turned out to be optimal and most expedient. From 1977 to the present time, the number (level of oscillations) of bank vole (*Clethrionomys glareolus)* remains stable. It is a dominant species in the community of small mammals during all years.

Another type of reaction (voles of genus *Microtus*, three species), was characterized *by traditional increase of population size in a droughty year due to reproduction of overwintered and young of the year, despite extreme adverse conditions.* This resulted in subsequent sharp drop in numbers and transition of grey voles' (*Microtus*) populations on lower level of oscillations (almost at an order) which persisted until now, i.e. throughout 40 years. Similar type of reaction was found in population of the pigmy wood mouse (genus *Sylvaemus*). However, entailed not only preservation of former level of number, but also its relative increase in *Sylvaemus uralensis*.

Under the impact of extreme factor, they founds specificity of intrapopulation processes as following adaptive strategies in different species' populations, such as metabolism suppression, blocking of maturing, age cross, and prolonged period of reproduction of overwintered animals. The *role of overwintered grouping* is important. Their structure is formed in the previous year that provides possibility of transgenerational transmission of hereditary information.

Besides reactions of murine rodents' populations to drought, consequences of this extreme influence can persist quite, rigidly being fixed in the next generations.

We showed real time possibilities of fast population reorganizations of evolutionary scale occurring in the absence of long-lasting trend of the extreme ecological factor's impact.

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INVESTIGATING OF HOST SPECIES VIA PARASITOLOGICAL RESEARCH: OPPORTUNITIES AND LIMITATIONS

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Parasitological studies can be used to clarify many aspects of the host species biology that is of particular importance hen studying protected species. In addition, the study of parasites is often a minimally invasive for the host that just becomes especially important in cases when the object of study belongs to a protected group of organisms.

Below, we summarize tasks, which can be resolved using data on parasite fauna of the studied species:

1. Investigation of features of host ecology, in particular, the identification of shelters sharing;
2. Separation of cryptic host species;
3. Identification of races and cryptic species in the hosts;
4. Monitoring of endangered species ranges;
5. Study of the evolutionary history of the hosts.

Understanding old and contemporary relationships between separate populations of vertebrate animals for a variety of reasons is essential for the conservationists. Unfortunately, low level of intra- and interpopulation genetic variation in many taxa of vertebrates hampers studying their phylogeny and contemporary demographic processes (such can be seen, for example, in cheetah *Acinonyx jubatus* Schreber, 1775, northern elephant seal *Mirounga angustirostris* Gill, 1866, and Hainanese sika deer *Cervus nippon* Temminck, 1838). Meanwhile, population genetics of parasites of vertebrates may offer an alternative way to study hosts, their evolutionary history and ongoing demographic processes, that becomes yet another argument in favor of maintaining such “parasite-host” systems.

Thus, the study of ecology and evolution of parasites is of particular importance to describe endangered animal populations and species, and widespread use of these methods may help discover new hosts and new (possibly cryptic) parasite species. Meanwhile, the issue of parasites protection as a source of valuable information for research is still unresolved. Only one of 5000 extant louse species (Phthiraptera) and no species of flea (Siphonaptera), parasitic helminth (Platyhelminthes), parasitic nematode (Nemata), mite, or tick (Acari) is listed as threatened by the IUCN, despite impassioned pleas for parasite conservation beginning more than a 20 years ago.

Even from a utilitarian point of view (rare parasites should be protected, primarily as species), this group of organisms has not yet attracted attention of scientists and environmental organizations, and parasites were not even included in the standard Red Books and other lists of rare and endangered animals. In this regard, some scientists offer case studies in protected species to collect samples of biological material (blood samples, feces, hair, etc.), and then refer them to expert evaluation of specific parasites. It also requires the creation of repositories of endangered parasites.

POPULATION GENETIC STRUCTURE OF HONEYBEES IN SIBERIA

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Honey bee as social insect living under human control, is an ideal model for biocenological and population studies (Eskov, 1990; Krivtsov, Grankin, 2004). Monitoring of population genetic structure of honeybee, analysis of gene pool and its stability and dynamics for a number of generations in view of changes of the habitat are needed to better understand functioning and evolution of ecosystems (agricultural systems).

Population genetic studies of honeybee on the territory of Siberia, carried out at Tomsk State University, demonstrated some features of structural and functional organization of honeybee populations. As a natural pollinator, which depends on the nectar plants, honeybees react to various changes of biocenoses (co-adaptive system “honeybee – nectar plant”), including those that occur due to human activity. However, genetic features underlie adaptation potential, which determines phenotypic plasticity of individuals and population as a whole. A striking example of adaptive changes in the “honeybee–plant” system is the difference in length of proboscis in honeybee from different areas of habitat (Alpatov, 1948). On the one hand, honeybee races are characterized by variation in proboscis length. That is, in races of southern origin (*Apis mellifera carpatica, A. m. caucasica*) the proboscis length is greater compared to the Middle Russian bee (*A. m. mellifera*), living in more northern regions. On the other hand, for the Middle Russian bees from Tomsk Province, the proboscis length is below the standard for this breed (Konusova et al., 2013). This is indicative of the fact that the morphometric parameter may be determined not only genetically, but by environmental factors, possibly reflecting the adaptation to particular environment (a variety of flowering plants).

Based on the analysis of morphometric and molecular genetics (the study of polymorphism of the locus COI-COII mtDNA and microsatellite loci) data, they found widespread hybridization of different races of honeybees, originally adapted to different environmental conditions in Siberia. Those are *A. m. mellifera* (the most adapted to local environmental conditions, as cultivated in Siberia for a long time) and “southern” races of bees (*A. m. carpatica, A. m. caucasica*), imported into the territory of Siberia in an uncontrolled way (Ostroverkhova et. al., 2015, 2016). At the moment, only a few local populations of Middle Russian race preserved in Tomsk Province and Krasnoyarsk Krai. Honeybees hybridization originally adapted to different climatic and ecological conditions, can entail destruction of co-adaptive gene complexes. This may negatively affect adaptation of honeybee populations. An example is the emergence of various infections that have already been registered in a number of apiaries in Tomsk Province, where the hybrid bees inhabit.

Interestingly, according to the values of genetic distances (on a set of microsatellite loci, including royal jelly gene *mrjp3*) between different races and hybrids (originating both from Middle Russian, and from the Carpathian races), honeybees of southern origin lose their genetic specificity quickly and become similar to the Middle Russian race on genetic diversity (Kireeva et al., 2015) in the process of hybridization.

Noteworthy, with regard to genetic diversity (the spectrum of alleles and allele frequencies of some microsatellite loci), Middle Russian bees of Siberian populations differ significantly from *A. m. mellifera* populations of other areas (in particular, the Urals, Europe), which is indicative of different ecotypes of the *A. m. mellifera*. Therefore, it is important to conduct gene-geographical research of honeybee of different origin and to identify factors (including environmental), influencing specificity of honeybees gene pools structure in different regions.

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USE OF STATE MONITORING DATA OF GAME RESOURCES TO STUDY THE ECOLOGY OF WILD BOAR (CASE STUDY OF YUGRA REGION)

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First records of wild boar (Sus scrofa) in the north of Western Siberia were made about 30 years ago, and since then it expands northwards and eastwards (Vorobjov, 2009, Antipov, 2009). According to the data of the Department of natural resources and non-feedstock sector of Yugra region, population of wild boar raised 7-fold and its abundance is estimated at a level of more than 2000 individuals in the last five years. Expansion and adaptation of wild boar in the areas where there is no agriculture (which, according to Rusakov, Timofeeva, 1984 and others, support survival of animals in harsh conditions) is of great theoretical and practical interest.

While studying the ecology of game animals in large territories, a researcher often has a notion of using game resources state monitoring data, which are based on winter track counts (further – ZMU). In our study we tried to estimate the applicability of ZMU held in the region of Yugra in 2010–2016 for the analysis of spatial distribution, abundance and habitat preferences of the wild boar.

The area of Yugra region is 534801 sq. km and consists of nine administrative districts. According to the literature as well as data of interrogation surveys combined with our field observations, wild boar sporadic occurrence was registered in all administrative districts. According to the results of ZMU, they found wild boar in 4 of 9 districts and this partly reflected the pattern of its winter distribution in the region of Yugra. According to the data of ZMU in 2016, counts were made in 65 hunting grounds managed by non-governmental organizations (private companies of hunting clubs). These hunting grounds are unevenly distributed all over the territory of Yugra (from 1 to 42 per one administrative district). Transects length for track counts in the administrative district depends not on the area of district that much, but on the number of hunting ground (since each ground must perform counts of transects with a total length 350 km). Transect density in various districts varies from 0,017 to 0,24 km of transect per sq. km, the probability of meeting wild boar footprints varies substantially. Hence, ZMU does not allow discovering all wintering groups of wild boars. The evidence for this is data on "not counted" wild boars that were identified in Beresovsky and Sovetsky districts in winter. Transects network was found to be most dense and uniform in the Khanty-Mansiysky district. We further focus on this most properly sampled district. According to interrogation surveys, first records of wild boar were made in 1980s. The first record of wild boar in ZMU was made in 2012 (one track found, the experts estimates were 20 individuals). In 2013, they failed to find wild board during ZMU, but in 2014 and 2015 wintering animals were reported from two hunting grounds and its abundance was estimated at a level of 14 (2014) and 28 (2015) individuals. In 2016, wild boar was registered in 7 of 42 hunting grounds (population density varied from 0,4 to 3,34 ind./1000 ha), and the total number of individuals was estimated to be 168. However, such high population density of wild boar in Yugra is doubtful and requires verification.

To analyze wild boar habitat preferences in winter, we matched animals' tracks with the map of vegetation created using Landsat satellite images. We found that all records of wild boars in Khanty-Mansyisky district in 2016 were made in the forests of Siberian pine (Pinus sibirica) in the bottomlands of small rivers. Wild boar population increase probably resulted from good yield of Siberian pine nut, which could prevent animals from migration to southern areas, typical in other years. Habitat in hunting grounds where wild boars tracks were found since 2012 annually is a combination of Siberian pine forest, bottomland of small river, mixed coniferous-deciduous forest and bog.

THE COMMUNITY OF SMALL MAMMALS OF GARDEN SITES

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The community of small mammals of garden sites obviously consists of animals that live in natural habitats surrounding these areas. Proper maintenance of garden territory (ploughing or digging garden beds, cutting the grass, gathering plant residues in the autumn, etc.) makes it almost impossible for rodents and insectivores to survive there for the whole the year. Nevertheless, there exist unattended areas, in which living conditions of animals are more favorable. However, only a few species have adapted to conditions of garden areas (e.g., East European vole). Other species appear here only for feeding or during migration. The number of small mammal species on the garden sites is quite poor in comparison with natural habitats, but the abundance of some species here is higher than in the surrounded natural habitats, at least in autumn (e.g., common shrew, field mouse, water vole). The abundance and species composition of rodents and insectivores depend largely on the location of site and surrounding areas. Rodents are harmful, eating vegetables and gnawing fruit trees and shrubs, as well as arranging holes. The latter is especially typical for the mole. To reduce damage from small mammals it may be useful to undertake appropriate agro-technical measures: cutting grass, regular gathering of plant residues, isolation of compost heaps, etc.

RATION OF CHICK IN POPULATIONS OF *APUS APUS* L. AND *A. PACIFICUS* LATHAM MARTINS IN TOMSK

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Flying birds foraging has been described to a lesser extent compared to other ecological birds' groups, which is largely related to poor availability of matins nesting sites. This report presents materials we collected in the central (Pacific swift – PS) and suburb (Black swift – BS) locations of the city of Tomsk in the nesting period. PS nests in the garrets of the buildings, whereas BS does that in the starling-houses of suburbs in Timiryazevo village) located 3 km away from Tomsk in coniferous forest. We collected food samples by the end of breeding period when catching adult birds and chicks' banding. Birds were caught in the nests or blocking the way out of the starling-house, or of the roof. We extracted food clod from the chick's esophagus, or rarely from the adult bird. Alternatively, the one dropped near the nest was picked up. Fourteen samples in total were collected and analyzed.

In PS food clods (n = 10) we found 11 taxons of Arthropoda, and 9 taxons in BS (n = 4). Top (more than 10% of food clod) forage items in PS (n objects = 1751) were: dayflies (31,8%), dipterous (20,3%), caddis flies (18,2%) and Zygoptera (15,9%); in BS (n objects = 810): Zygoptera (44,1%), dipterous (15,6%), Lepidoptera (11,4%), and caddis flies (10,1%). All classes differed significantly when comparing these two species ($p < 0,01$). The overall proportion of dominating insect classes ranged from 81,2% (*A. apus*) to 86,2% (*A. pacificus*) of the entire forage.

Almost all groups of "air plankton" can be found in the rations of both species; however, few differences were noted. Thus, dayflies are the most numerous (31,8%) food objects for PS, which is completely absent in the ration of the alternative species. Zygoptera (44,1%) made almost half of BS ration, being three times more frequent than in PS (15,9%). BS eat twice more Lepidoptera (11,4%), than PS (5,1%). Coleopterans are much more prevalent in BS's ration (7,7%), being just sporadic in PS (1,48%). We also noted different prevalence of other insects: Hymenoptera (BS – 8,8%; PS – 5,7%); hemipterans (BS – 1,7%; PS – 1,0%); earwigs (BS – 0,12%), orthopterans (PS – 0,2%), as well as Arachnida (0,2 and 0,5% respectfully).

We hypothesize that feeding location influences martins' food preferences, which may not be similar in these two species: BS apparently prefers foraging in the woods and above them, whereas PS feeds above streets of the city and Tom River.

Comparing PS foraging spectrum of two years (2013 and 2015) found significant difference in the prevalence of three invertebrates' species. Thus, there were 8,4 more caddis flies in the samples in 2013 compared to 2015. Besides, there was 8,5 times rise in Zygoptera and Lepidoptera in 2015. Other six groups differed in 0,6–3,5 times. These data illustrate martin's forage variability as well as their potential to shift to other seasonally available rations.

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THE COMPARATIVE ANALYSES OF SOUND FREQUENCIES OF MOSQUITOES FORMS *CULEX PIPIENS PIPIENS* AND *C. P. MOLESTUS* (DIPTERA, CULICIDAE)

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Two biological forms were identified within the species *Culex pipiens*: *C. p. pipiens* and *C. p. molestus* (Vinogradova, 1997). *C. p. pipiens* is confined to natural ecological communities, including urban areas; females go to diapause, and males die in winter. *C. p. molestus* is a synanthropic species, develops in the basements of houses, and adults remain active in winter. Despite remarkable ecological differences, species validity of these forms is debatable. Considering the importance of acoustic signals from mosquitoes when they choose a sexual partner (Bertram et al., 2004; Perevozkin, Bondarchuk, 2015), the study of sound communication in f *C. pipiens* is important to understand the mechanisms of reproductive isolation.

We caught both forms of *C. pipiens* for the experiment. They differed in habitat and possibly artificial breeding. We selected female adults of *C. p. molestus* in the basement of an apartment block of Shegarka settlement in Tomsk Province. Keeping these mosquitoes is not problematic; they are easy to breed in the laboratory. Imago *C. p. pipiens* bred in the laboratory either larvae or eggs from the clutches of females caught during summer period in Podgornoe settlement of Tomsk Province. Therefore, we could not obtain offspring from them due to the peculiarities of reproductive behavior.

The acoustic characteristics of the mosquitoes were recorded on the second day after reaching the adult stage. For this purpose, we glued their dorsal chest side to the tip of the dissecting needle with «BF-6» glue. We then digitally recorded the sounds in the foam coated box with the microphone, first with each individual separately, and then in pairs of two sexes of one form, then in male pairs and females of the alternative forms.

The mean value of basic sound frequency in *C. p. pipiens* female was 250 Hz (n = 28), in *C. p. molestus* female 332 Hz (n = 24); in males of *C. p. pipiens* 459 Hz (n = 25), in males of *C. p. molestus* 505 Hz (n = 25). Thus, the average frequency of beating wings in «urban» forms of *Culex* was higher than in the alternative form (including sex). Recording two sexes of one form showed the increase of pitch frequency ♀/♂: *C. p. pipiens* 256/495 Hz; *C. p. molestus* 344/517 Hz. On the contrary, recording two pairs of alternative forms confirmed reduction of basic frequency according to individual characteristics: ”♀ *molestus* – ♂ *pipiens*” 307/418 Hz; “♀ *pipiens* – ♂ *molestus*” 240/483 Hz.

Sound frequencies differences and their modifications in the interaction of individuals of two sexes of *C. p. pipiens* and *C. p. molestus* the existence of at least pre-coitus ethological isolation between them, which theoretically can ensure no gene exchange between these two forms.

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INFLUENCE OF VARIOUS FACTORS ON DYNAMICS OF SABLE NUMBER IN THE YUGAN NATURE RESERVE

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The “Yugansky” State Nature Reserve is situated on the territory of Surgut region of Khanty-Mansi Autonomous Okrug-Yugra and occupies 648636 hectares. Sable (*Martes zibellina* L., 1758) is the dominating species in the reserve' marten population. Population of sable in Yugan Nature Reserve was studied in 1988–2014. They calculated the number of sable by means of winter route accounts, which are usually carried out in February every year. Calculation of traces was done separately in the main habitats, and four types of habitats were ascertained. Those were dark-coniferous taiga (with prevalence of cedar, fir and fir-tree), light-coniferous taiga (with prevalence of pine), small-leaved taiga (with prevailing birch and aspen in the first tier and obligatory presence of dark-coniferous breeds in the second tier), and riding bogs (overhumidified treeless or covered with oppressed pine). The average long-term size of sable population in dark-coniferous taiga was 5,1 individuals /1000 hectares (from 2,5 to 8,1), 3,3 individuals /1000 hectares (from 1,6 to 6,4) in pine woods, 3,2 individuals /1000 hectares (from 1,6 to 5) in small-leaved taiga, and 0,7 individual /1000 hectares (from 0,1 to 1,5) in the bogs.

Sable counts within adjacent years can spike 3-fold in both directions. The status of the reserve assumes full withdrawal of the protected territory from economic activity. Therefore, the vast majority of causes of count fluctuations in the reserve have natural origin. Apart from intrapopulation regulation mechanisms, both climatic conditions, and food factor are powerful regulators of the population count. We used factorial analysis to process data file with a number of sable as a dependent variable, because of large pool of predictors. In total, we included 12 variables reflecting sable number fluctuations in various biotopes and the abundance of its main fodder objects (forest voles, squirrels, and pine nuts), as well as some climatic environment variables, such as annual amount of precipitation and average annual air temperature. We used on-year lagging to assess reaction of sable population to the parameters of external environment present in the previous year, along with food affordability. We ascertained four predictors explaining 75,4% of the overall variation. The size of sable count predictors’ load reflected the response of its population to the biotic parameters, which were present in previous year (Bobretsov, etc., 2000). The first predictor, which explained 23,2% of variation, was the variability of temporary ranks of squirrel and annual amount of precipitation. The greatest contribution of the variable characterizing dynamics of sable population count was made by the second factor, explaining 19,2% of the overall variation. This predictor was the variability of temporary ranks of sable number in dark-coniferous and light-coniferous taiga, and on bogs. Factorial loading on these variables exceeded 0,70. The amount of precipitation was negatively associated with the sable count in these biotopes. The main contribution to the third factor (18,8% of variation) was made by the abundance of forest voles and sable count, inversely correlating with each other. That confirmed that the food range of sable was very wide and its abundance did not depend on any single type of forage. The fourth predictor (14,2% of variation) was a combination of two variables which factorial loading exceeding 0,80. That was the sable count in small-leaved taiga and the average annual air temperature, positively correlating with each other.

THE STRUCTURE OF *MYOTIS DAUBENTONII* (CHIROPTERA) SUMMER SETTLEMENTS IN THE SOUTHEAST OF THE MIDDLE URALS

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We studied summer settlements of water bats *Myotis daubentonii* in the vicinity of Dvurechensk settlement (Sysert district, Sverdlovsk Province) with the total area of 16 km^2 in 2004–2006, in. In the active period of the year, water bat was a background species, at least in the southeast of the Middle Urals outside the caves. The occurrence is a single animal or groups of 2 to 15 individuals. In the catches, we found all main age-sex groups (adult males and females, cubs of first year). Males slightly predominated (55%), (χ^2 = 0,47; p > 0,05; df = 2) in the adult group. The studied settlement of specimens had an individual-group structure. The composition of groups changed depending on the phases of generative cycle. In the first half of summer, the group consisted of dominating females with cubs, single adult males, spinsters and groups of no more than 3 males, and spinster males and spinsters. Adult males and males and spinster can occur in brood colonies, but we did not find such cases. In the second half of summer after cubs departure, besides mentioned clusters we found single female with signs of ended lactation, and single young animals, mostly males in shelters. Banding showed that the composition of brood colonies inhabiting one refuge differed year by year. In a colony (up to 15 individuals, together with the cubs), which occupied one and the same shelter for 3 years of banding we noticed returns of two adult females, and a return of a female to its birthplace. During one summer in the study area, we re-captured 18,2% of bats (breeding females and adult males). This suggested that the remaining animals captured within the territory, might have regularly moved or had hunting areas outside the study area.

Bats distribution in feed stations, according to the catches, did not directly depend on shifts of particular phases of the generative cycle. The individual hunting areas of several animals of different sex and age often overlapped. Such clusters of bats were formed in optimal feeding habitats, such as above water in the coastal area of the river or lake and limited with woody vegetation. We noted that for a group of about 20 individuals, the longest joint hunting area was no more than 1,5 km away. Hunting plots of single animals, on the contrary, were usually located above forest roads, remote from the reservoir; most frequently, they belonged to adult males and spinsters. We explained that with a notion that forest roads were too narrow and did not allow bats to form clusters. In this case, a uniform distribution of individuals is probably determined by intraspecific competition.

We assume that the studied settlement was formed with water bats from different populations, including individuals from a settled population for which Smolinskaya cave the southeast of the Middle Urals may be a permanent winter shelter, mating ground, and a centre of wintering area (Strelkov, 1958). At the same time, we support the idea of V.P. Snitko (2007), that there is a seasonal separation of habitats for different sexes in the Urals in boreal bat species. In warm season, females settled at a considerable distance from caves in the breeding areas (field breed), and most of spinsters and males remained in the areas of the caves, i.e. in wintering area. It is obvious that the studied settlement of water bats is located in the region of overlapping grounds. This is confirmed by the fact that all the main sex and age groups inhabited the study area. That means that wintering area smoothly passes into the breeding area.

HOME RANGES AND ACTIVITY PATTERNS OF ISLAND ARCTIC FOXES

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The analysis of space use helps elucidate environmental and social factors, which guide animal behavior. Food distribution and predation pressure are usually considered the main factors. We examined range use and activity of Arctic fox (*Vulpes lagopus beringensis)*, an apex predator on the oceanic island with rich, clumped food patches. We conducted the study in July-August 2014 in the northern part of Bering Island (the Commander Islands, North Pacific). Study area partially included the northern fur seals rookery. Thereby in summertime these foxes had an extraordinary abundant source of food resources (seal placentas and carcasses). Four adult foxes (2 males and 2 females) from 3 adjacent reproductive family groups were equipped with GPS-collars. *Collars* were set to record GPS positions at regular *5-minute intervals*.

We evaluated home ranges using the Brownian bridge movement model, BBMM (Bullard, 1991; Horne, 2007). BBMM estimates the probability density of a path between every two successive relocations. Then these densities are summed over the area to yield utilization distribution (UD). We considered 99,9% isopleth line of that UD as home range boundaries.

Mean seasonal *home range size was* 40 hectares for male and lactating female from the same mated pair, and 90 and 100 hectares for male and lactating female from two other family groups. These were 5–10 times less than summer home ranges of mainland arctic foxes (Anthony, 1997; Eide, 2004.). For foxes from adjacent family groups, the overlap in home ranges was 2–18% by area and 0-17% by time. The overlap of male and female from the mated pair was 82–84% by area and 99% by time. Our results suggest that abundance of food resources has led to the shrinkage of home range, but has not significantly affected fox territoriality.

If GPS position did not change for three and more successive relocations, we considered the animal as “non-active”, otherwise “active”. The activity pattern was estimated daily, then median (M), the first and third quartiles (1Q and 3Q) were obtained for each fox. Activity characteristics were similar for all four foxes and stable throughout the observation period: “active” status (M: 33–40%, 1Q: 31–37%, 3Q: 38–45%); average daily speed (M: 1,1–1,4, 1Q: 1,0–1,3, 3Q: 1,5–1,7 km/h); daily movement distances (M: 8–13, 1Q: 7–11, 3Q: 14–18 km). Thus, due to richness and high predictability of food resources, the activity level of Bering foxes was lower compared with mainland foxes (Eberhardt, 1982) and day-to-day variability of the activity level was also low.

We built regression model with activity as a response variable and time of day as a predictor. The daily activity pattern had two distinct peaks. The evening peak of each fox occurred at twilight (20:00-21:00 local time). The morning peaks differed significantly and occurred from 4 to 9 AM. Male and female from the mated pair had very similar morning and evening activity maximums (3:30 and 4:30, 20:00 and 20:30). To study stability of daily activity pattern we estimated models with identical specification separately for each day and determined location of peak points for the first and second halves of the day. Females’ morning activity peak varied greatly from day to day (1Q–3Q: 5:30–9:30 and 3:30–9:00); it was not the case for males (4:30–5:30 and 4:30–5:00). Evening activity peaks evening showed similar variance for all foxes (1Q: 17:00–18:30, 3Q: 20:30–21:30). The tidal schedule significantly affected the pattern of all four foxes daily activity, however, did not shift the time of morning and evening peaks. Although day–night cycle had no effect on distribution and availability of main food resources (seal placentas and carcasses) and there was no predation risk either, daily activity of artic foxes showed bimodal pattern similar to many other carnivores (Merrill, 2003; Heurich, 2015).

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DISAPPEARANCE OF THE EUROPEAN MINK *MUSTELA LUTREOLA* IN VOLOGDA PROVINCE

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The European mink (*Mustela lutreola* L.) is listed by the IUCN as Critically Endangered (The IUCN Red List…, 2015) species. European mink population began to decline in the 19th century (Novikov, 1939). In 1980s in Russia, its main population persisted in the region, which was partially or completely confined by Pskov, Novgorod, Tver, Vologda, Kostroma, Yaroslavl, Kirov, Arkhangelsk Provinces, Perm Krai and the Komi Republic (Tumanov, Rozhnov, 1985; Rozhnov, 1992; Tumanov, 2009; Skumatov, 2005, Maran, 2007). Introduction of the American mink (*Neovison vison* Schreb.) was believed to be the main cause of the count drop and complete disappearance in some places of the European mink (Maran, 2007). The Vologda Province is one of the few regions where special release of the American mink was never done, and this species penetrated here from neighboring regions, apparently only in the early 1980s (Tumanov, 2009). Therefore, the one could expect preservation of its aboriginal twin in somewhat better condition and, therefore, assume more opportunities to study it.

We tried to find out the current status of minks using both traditional methods of zoological research (of skin and skulls of animals caught by hunters) in 2002–2012, as well as molecular genetic techniques for the analysis of feces (molecular scatology), popular in recent decades. The feces analysis allows identification of animal species. To improve the method accuracy of the Mustelidae species identification using mtDNA isolated from the samples of feces (Murakami, 2002; Rozhnov et al, 2008), we used new primers for the amplification and sequencing of a fragment of mtDNA (Kolobova et al., 2015), such as MitDF (5'GGTCTTGTAAACCAAAAATGGAGA) and MitDR (5'CTGAAGTAAGAACCAGATGCCA). To collect excrements of minks we surveyed tributaries of most rivers and lakes of Vologda Province in 2010–2013. At the same time, we interviewed hunters and inspected game trophies. Both methods yielded similar results.

In the beginning of the 2000s, the European mink inhabited the greater part of the study area, whereas in the 2010s, its distribution rapidly dropped, and in 2015 the species almost disappeared. The European mink was found only in the far northwest and east of Vologda Province. The American mink was found in former habitats of the European mink. Replacement of one species with another occurred probably after the removal of aboriginal species by hunters, and an alien predator occupied free territory.

ENERGETIC PROVISION OF METABOLIC PERFORMANCE IN TWO POPULATIONS OF NORTHERN RED-BACKED VOLES (*MYODES RUTILUS*)

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One of the main determinants that limit distribution range and animals density is food availability that directly affects energetic provision of the organism's vital functions (Weiner, 1989). Besides the decline of food supply, suboptimal ecological conditions are often associated with additional environmental challenges that compromise resource allocation towards homeostatic functions. However there are almost no data about the real physiological constrains of species propagation. In our study, we compared the deposition of main metabolic substrates in two populations of northern red-backed voles (*Myodes rutilus*) with different density.

In voles trapped in the recreation forest near Novosibirsk city with relatively low density, metabolic and thermoregulatory responses on acute cooling were significantly higher than in voles inhabiting mountain taiga of North-Eastern Altay (Polikarpov et al., 2016).

In order to define associations between population density and availability of metabolic resources we estimated between-population variability of such indexes as nutrition state, total fat content and liver glycogen. Comparison of these indexes in voles trapped in two studied populations by snap-traps in August 2011, May and August 2012 and 2016 did not disclose any between-population differences in nutrition state and total fat content. In Altay taiga but not in Novosibirsk recreation forest, these indexes both significantly decreased from spring to autumn. In spring and autumn, liver glycogen content was significantly higher in recreation forest than in taiga population.

Studied populations differed by the magnitude of seasonal fluctuations of density: more than tenfold fluctuation in Novosibirsk recreation forest and threefold fluctuation in Altay taiga.

In Novosibirsk, population density was affected mainly by abiotic factors, whereas in high-density taiga population density-depended mechanisms played an important role (Novikov et al., 2012). In Novosibirsk population, dramatic decrease of population density, presumably caused by unfavorable climatic factors, occurred in autumn-spring period (Panov, 2001). In breeding season, when the samples were taken, the ecological situation might have been relatively favorable for the red-backed voles.

Regardless the relatively low density, red backed voles from the Novosibirsk recreation forest did not experience shortage of metabolic substrates, at least in warm season of the year, and maintained high metabolic capacity and relatively constant body temperature under the severe cooling. Therefore, the environmental conditions deterioration, even that decreasing population density is not always associated with the exhaustion of energetic substrates that could restrict metabolic performance.

COMPARATIVE ANALYSIS OF SOME MITOCHONDRIAL GENES IN VOLES IN RELATION TO ADAPTATION

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Adaptation of organisms to changing environmental conditions related primarily to climatic factors requires significant modification of energy metabolism, measured by the change of speed of the basic metabolism and the processes of oxidative phosphorylation in mitochondria. Genes needed to implement energy metabolism are located in the mitochondrial genome. Full mammalian mitochondrial genome is a circular DNA molecule with a size of more than 16 thousand pairs of nucleotides and 37 genes, including 13 protein-coding genes, 7 genes such as subunits of NADH dehydrogenase, 3 subunits of cytochrome C oxidase, 2 subunits of ATP synthase and cytochrome b, necessary for the implementation of oxidative phosphorylation and electron transport in the mitochondria. Mitochondrial genes of the genera *Clethrionomys* (*Cl. glareolus, Cl. rutilus* and bank voles with introgression mitochondrial DNA of the northern red-backed voles), *Microtus* (*M. arvalis, M. obscurus, M. rossiaemeridionalis, M. agrestis, M. oeconomus*) were sequenced, and NJ-dendrogram to compare these species phylogenetic relationships was built according to the nucleotide sequences of these genes. Comparison of genes nucleotide sequences of voles mitochondrial genomes allowed to identify a number of nucleotide substitutions, phenotypically expressed in the amino acid composition of mitochondrial proteins, which could affect oxidative phosphorylation in relation to adaptation to different habitats. The greatest number of radical amino acid substitutions that alter the structure of these genes were noted in the composition of four NADH dehydrogenase (1, 2, 4 and 5) subunits. We analyzed the scale, geographical distribution and frequency of occurrence of the discovered earlier introgression of the northern red-backed voles *Clethrionomys rutilus* mitochondrial genome in the *Cl. glareolus* bank vole population in the North of European part of Russia. That allowed hypothesizing about the adaptive nature of this phenomenon, associated with the dispersal of this species northwards to the extreme conditions of hypothermia (Potapov et al., 2007). Comparison of the cytochrome b genes nucleotide sequences of bank voles and northern red-backed voles showed amino acid substitution near the catalytic center of the protein cytochrome b in position 17 (alanine in northern red-backed voles to serine in bank voles) that lead to functional changes in protein enzymatic activity and modulated the energy metabolism efficiency.

The work was conducted with the support of RFBR (projects № 14-04-00751 and 15-04-03801).

DYNAMICS OF ALLOSYME VARIABILITY PARAMETERS AT THE RED-BACKED VOLE *M. RUTILUS* PALLAS, 1779 FROM THE TAIGA OF THE KOLYMA REGION IN THE COURSE OF POPULATION CYCLE

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Red-backed vole is an important component of ecosystems of the North-East of Russia. It dominates numerically over other small mammals in most parts of biotopes, it is a mass consumer of plant forage, and it represents one of the main forage objects for valuable fur-bearing animals. As well as other species of red-backed voles, this one is characterized by periodic fluctuations in number. Population cycle of red-backed vole in the valley of the Kolyma River and in the Northern Pryokhotye is 3–5 years (Chernyavskii, 1981; Chernyavskii, Lazutkin, 2004). One of the explanations of these fluctuations is the genetic behavioral hypothesis of D. Chitty (Chitty, 1960; Chitty, 1964). It implies that in different phases individuals with different genetic constitution take advantage. Natural selection plays important role in the process; it periodically replaces one genotype group by another one.

We studied fluctuating population of *M.rutilus* in Kolyma taiga from 2001 to 2010 and confirmed population cycle of three phases, including depression, growth, and peak, each lasting for one year. Fluctuating amplitude of number reached 5,5 (Chernyavskii et al., 2007; Lazutkin et al., 2012). In 2001-2005, we used allosyme analysis to study samples from over 1000 specimens of red-backed voles. We obtained data on eight loci, including LDH-1, LDH-2, PGD, SOD, GOT, EST-D, EST-M3 and PGM (loci were marked by enzyme activity; their short names are given according to Manchenko, 2003). We found that studied markers were not linked, dependent or restricted by sex. In most cases, the observed number of genotypes in samples correlated with those expected as of Hardy-Weinberg distribution. First of all we found abnormalities in EST-D and EST-M3 loci. They were connected with the excess count of some, often rare, homozygous genotypes in the samples. In one case, bearers of rare genotypes were stated to belong to one litter (Primak et al., 2007). Fluctuations of allozyme variability in different loci had different direction. Maximal change of frequency of main allele was observed in PGD locus from 0,706 to 0,605. Heterozygosity has twice fluctuation value in some loci, such as from 0,159 to 0,306 with regard to LDH-2 and from 0,063 to 0,133 for EST-D. In most cases Silander coefficient was negative and only in 2004 (peak year) and in 2005 the number of heterozygotes exceeded the expected number in most gene markers. Average heterozygosity in the studied period was practically the same, i.e. about 0,25. In the Kolyma and Pryokhotye (Kuryshev, 1988; Kuryshev, Chernyavskii, 1988), fluctuating populations of red-backed vole changes in some loci during the cycle were similar, and opposite in several gene markers. Significant differences in allele frequencies of LDH-2 and PGD loci were observed between the Kolyma and Pryokhotye species populations. However, fluctuations range of variability was incomparable with the number fluctuations range. We did not observe change of dominating genotype, as well as the main allele in any studied loci.

We hypothesize that the changes in parameters of allozyme variability in studied populations depend on the number and biology of the species. During the low number years, young animals of the current year breed in their family group, and that leads to increase in number of homozygotous specimens in samples. When the number increases, breeding among specimens of different family groups rises, among which are bearers of different homozygotous gene types. Thus, an increase of heterozygosity can be observed in the population. Based on the data obtained we can assume, that the observed changes in the studied gene markers are the consequence of population number changes, but not their cause.

THE AMENDMENT TO ELTON'S LAW OR THE PODDUBNAYA-KOLOMIYTSEV'S RULE

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At the beginning of the 1930s, Russian scientists, biologists and game wardens, realized the idea of establish a network benchmark areas (reserves), withdrawn from economic use. The aim of studies in nature reserves was to study the dynamics of natural processes and their causes. Long-term stationary all-year studies established many associations already in those years (Formozov 1934, 1948; Semyonov-Tyan-Shansky, 1938). The nature of number peaks lags of different species of forest mustelids and the peaks of abundance of rodents remained unclear. The peaks of prey sometimes preceded the peaks predator, and sometimes did not, which was violation of Charles Elton's law (1927). In the beginning of 1990s, the Elton's law for the number of predator-prey was clarified. N.Y. Poddubnaya and N.P. Kolomiytsev (1992, 1995), who worked in the forest reserves in the Russian Far East for about 20 years found that some recurrent increases and declines in numbers of those species with a short-term latent pregnancy (weasel, Siberian weasel, American mink) corresponded to numbers fluctuations of rodents. Meanwhile, all the phases of fluctuations of predators having long-term latent pregnancy (sable, ermine) appear to have one-year lag.

This was made possible because the studies were complex, i.e. for insectivores, lagomorphs, rodents and trophic related predators; habitat parameters, such as yield of plants and changes in various weather conditions in all seasons in the forests of the eastern slopes of the South Sikhote-Alin.

To assess populations of mustelids and their prey in the western part of Vologda Province and in the north of the Kostroma region, were conducted a census of the mustelids and collected their excrements and digestive tracts (n = 1382) in 2004–2015. We also counted the number of rodents in 1999–2008, 2010–2012, and took into consideration the data on the number of mustelids from the so-called winter route accounting (Kuzyakin et al., 1990) in 1995–2014.

The forest rodents' populations reached their peak numbers in the sample plots in Cherepovets district in 2002, 2006, 2008, and 2010–2011. The American mink, the European mink and the forest polecat peaked in 1995, 1998, 2002, 2003, 2006, and 2010. The maximum count of the marten and the stoat populations reached in 1996, 1999, 2003, 2004, 2007, 2011, 2012, and 2014. We obtained similar results in other areas of Vologda and Kostroma Provinces. Although in some cases there was a prolixity of population peak of the marten and the ermine for two calendar years after the murine count peak, it was obvious that the Poddubnaya-Kolomiytsev's rule (Stepina, Kashina, 2009) was true for the forests in the European part of the Russian Federation.

The growth of the forest mustelids, noted in the beginning of 2000s along with natural fluctuations (Poddubnaya, Kozlova, 2007; Stepina, Kashina, 2009) continues at present time, and it is most clearly pronounced in the pine marten (Skumatov, 2016; our data). Populations of the forest polecat, marten and ermine are increasing apparently due to a drop in demand for their skins and subsequent significant reduction in hunting pressure during the period of socio-economic difficulties in Russian Federation.

Thus, following scientists AN Formozov, OI Semyonov-Tyan-Shansky, Charles Elton, IA Shilov and others, we update our knowledge of nature.

THE ROLE OF URINE PROTEIN IN THE REGULATION OF AGGRESSIVE BEHAVIOR IN EUROPEAN WATER VOLE MALES

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Chemical communication plays an important role in the shaping and maintaining of spatial and ethological structure of populations (Shilov 1977). In mice and rats, low molecular weight proteins of lipocalin family in urine are a cornerstone in the process of information exchange. These proteins have a relatively low molecular weight (19–25 kDa), exhibit considerable genetic variability and species specificity. Urine proteins and pheromones transported by them convey comprehensive information on the certain characteristics of individuals, which is important for the maintenance of intraspecies territorial relationships and reproduction regulation (Robertson et al., 2007). In other rodents, the role of urine proteins in the regulation of conspecific interactions is poorly explored. In water vole, using chip electrophoresis method, they found that season, sex and conspecific olfactory signals affected the concentration of proteins with a molecular weight of 15–25 kDa in male urine. It was found that urine concentration of low-molecular proteins depended on season, age and sex of animals. Average protein concentration in adult males' urine was 37,6 times higher than in females. What role does urine protein play: intersexual communication or regulation of between-male aggressive interactions in water vole? To address the latter issue, we conducted an experiment to simulate introduction of adult males to the territory of same sex individuals as well as reproductive condition by daily presentation of intruder's litter in the resident cage. W observed olfactory stimulation individual behavioral and physiological responses during four days in experimental males. The observed behavioral reactions included spreading and trampling of intruder's litter, leaving feces and urine on the litter by a resident male. The intensity of litter scattering correlated positively with the frequency of urination on litter ($r = 0{,}45$, $p < 0{,}05$). Intensity of behavioral response of a resident on the litter of a strange male depended on the concentration of low molecular weight protein in urine of males from which the litter was collected. The more protein intruder's urine contained, the more active was the resident male to throw the litter placed in its cage ($r = 0{,}52$, $p < 0{,}05$). Correlation of the relative volume of discarded litter with creatinine protein index was positive and statistically significant ($r = 0{,}59$, $p < 0{,}01$). Indirect aggression, expressed in spreading litter of a strange male (Kudryavtsev, 2012), increased with an increase in testosterone levels in resident's blood ($r = 0{,}56$; $p = 0{,}01$). Physiological response on the daily presentation of unfamiliar male's litter manifested in a significant increase in the concentration of low molecular weight protein in the urine ($t_{19} = 2{,}80$, $p < 0{,}05$) of the experimental males. The protein/creatinine ratio was also increased ($t_{19} = 3{,}21$, $p < 0{,}01$). In control group, there was no significant change in protein concentration in urine in this experiment. Thus, stimulation by the olfactory signals contained in unfamiliar male's urine leads to increased aggression of recipients and the level of urine low molecular weight protein required to mark the territory. These results highlight the importance of quantitative inter-individual variation of low molecular weight urinary proteins in the modulation of physiology and conspecifics behavior.

POPULATION STRUCTURE OF SOME COLONIAL BIRDS OF BAIKAL

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Isolation of natural populations of birds is very difficult because of their mobility. Very few publications so far have shown to make it possible. The emergence of new methods of genetic analysis expanded the horizons of research, but traditional approaches are still relevant. Of these, ringing is the most effective method. For decades, we performed large-scale banding of colonial birds on the lake, where about 140 thousand birds of different species in total were banded. With a certain degree of approximation, these returns allow to talk about the population structure of some species of colonial birds.

Herring (Mongolian) Gull. Of all the colonial birds of Baikal, the bird is most committed to the breeding sites. Even in swamps, major colonies persist for considerable time, and on the islands of the Maloye Sea the return rate to the previous breeding places exceeds 93%. The remaining 7% stayed ear or were forced to dispersion. In this case, young birds genetically connect different spatial groups, and only half of them return to their native settlement, another 45% disperse closely and the remaining 5% disperse remotely. These returns show the genetic connection of Baikal settlements of this species, as well as a number of settlements outside of Baikal, such as the colonies near the city of Angarsk (Sushinskiy kaltus) and colonies on the Angara River below the city of Ust-Ilimsk. Of note, the connection of the latter with Baikal gulls was identified with minimal catching / shooting (Pyzhianov, 1997).

A significant focus of the settlements of this species on the lake Hovsgol in Mongolia exists near Baikal. However, despite considerable scope of ringing no return of Hovsgol gulls from the lake occurred, and vice versa. This is even notwithstanding the distance from Hovsgol to the nearest, the southernmost settlement of gulls on Lake Baikal is comparable or less than the distance from the colony to the other settlements of Baikal. Therefore, we undoubtedly state that the two great Asian ponds are inhabited by different populations of Herring (Mongolian) gulls, despite the overlap of their wintering territories. This is confirmed by other data, in particular by the key difference morphometric parameters (Skryabin, 1977).

The second species, banding results of which allow considering the structure of its population on the lake, is a *Black-headed Gull*. The very first long returns from this species have confirmed our expectations, and the main wintering sites are located in the Southeast Asia (Southern China, Vietnam). Suddenly returns occurred from the Western Europe, from Germany (Pyzhianov, 1997). These data allowed stating inhomogeneous population structure of the population of this species in Baikal (Pyzhianov, 1998). At least two populations of this species, whose ancestors inhabited Baikal at different times, inhabit the lake nowadays. As a result, the first gulls that inhabited Baikal formed new winterings in the Southeast Asia, whereas the descendants of individuals from the second wave of remain committed to the Western, European wintering. The question of their reproductive isolation in Baikal remains open.

Similar pattern is observed in another colonial species, the *Grey Heron*. Return of wintering birds occurred from two directions - from the Southeast Asia (Vietnam and southern China) and from the Southwest, such as Caspian countries. However, there is no full confidence of the population differentiation of this species in Baikal in this case, and those birds may be single population with a very wide coverage.

REACTION OF FISH-EATING BIRDS POPULATIONS TO ENVIRONMENTAL CHANGES

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Water birds in general and colonial fish-eating birds in particular usually inhabit dynamic habitats, to the changes to which they have to adapt. Species-specific food is the most important component of the environment. Most often, their deficit determines many parameters of population structure. Let us examine this with an example of some colonial fish-eating birds in Baikal region. We build in on a notion of colonialism as a biological phenomenon was formed as reaction of species to the use of abundant, but unpredictably dispersed food resources (Kharitonov, 1983).

Herring (Mongolian) Gull. It nests on Lake Baikal in stable (rock) and unstable (swamp) habitats. In the second case, the instability of nesting habitat does not allow to reliably distinguish changes caused by the shortage of food resources from the changes caused by restructuring of the nesting sites. However, in case of nesting on the rocks (which is the western shore of Lake Baikal, the Maloye More and the Gulf of Chivyrkuisky) such an analysis is possible. Since the early 70s of the last century to its end, the bulk of the birds nesting in the Maloye Sea (over 90%) was concentrated in the large (over 100 pairs) settlements, the main of which provided the overall growth of this species population. However, in recent decades the situation with access to food dramatically changed on the Maloye Sea due to acute shortage of fish because of overfishing (now the issue of complete prohibition of fishing on Lake Baikal is being discussed). As a result, either the growth of large settlements stopped, or birds fell. At the same time, there appeared plenty of small and single settlements in areas that contribute to the development of new food resources, as well as new settlements outside Baikal.

The change of fish stock structure has led to a change in the structure of the population of other fish-eating species – *Common Tern*. Mass fishing of predatory fish species, like pike and big perch, on the Maloye More (a place of mass tourism fishing on Lake Baikal) resulted in an increase of sor juvenile fish, especially roach and dace. Because of increased availability of food resources, since the early 80s of the last century, terns nested in the Maloye Sea (terns did not nest here before, though stray birds were observed on a regular basis). However, settling of this species on the unusual nesting habitats is the most interesting (Pyzhianov, 1999). The increase of food resources in the area of Lake Baikal on the one hand and the lack of typical nesting habitats on the other hand, resulted in terns nesting on the cliffs, which is not typical for the species. In addition, large colonies of this species were not known on Lake Baikal and the Baikal region, which were common for the coast with their almost unlimited food resources.

Cormorant is the last species showing substantial changes in the spatial structure of population in response to changes in the environment. Disappeared from the lake in the 60s of the last century, cormorant for the first time after a long break was noticed nesting in 2006 (Pyzhianov, 2006; Pyzhianov et al, 2008). Since then, its count is rapidly growing (Pyzhianov, Pyzhianova, 2010; Pyzhianova et al., 2015) and to date it has occupied all the historically known nesting sites, reaching a huge number. The return of this species to Baikal and the Baikal region is directly linked to the prolonged drought in northeast China and the adjacent areas of Mongolia forcing cormorants move out.

Thus, environmental changes, especially the abundance and availability of food resources, entails substantial reorganization of the spatial population structure on both global and local level.

PREADAPTIVE OPPORTUNITIES OF SYNANTHROPIC BIRDS TO SETTLE IN THE TRANSFORMED ENVIRONMENT

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Synantropization of birds is associated with diverse and serious transformations in all aspects of birds' ecology under the influence of anthropogenic factors, especially in the urban environment. However, not the entire pool of species but only a small part of avifauna species became synanthropic. For the Russia most cities, these species are rock dove (*Columba livia*), black swift (*Apus apus*), jackdaw (*Corvus monedula*), urban swallow (*Delichon urbica*), house (*Passer domesticus*) and field (*Passer montanus*) sparrows, and three or four other species, whose populations inhabit urban ecosystems. Ecological features of these species are associated with transformed areas, and their presence largely depends on human beings. Nutritional and nesting conditions favor the existence of these populations in urban areas.

Adaptive abilities of birds in the urbanized environment are built on preadaptation (Voronov, 1999; Grabowski, 1984) and synanthropization, the example of new adaptations origin through the initial stage of preadaptation. Preadaptations are widely distributed in nature and are one of the most important ecological mechanisms of evolution (Schwartz, 1980). On the grounds of extensive material, living organisms were shown to develop qualitatively new features under the impact of natural selection. Features that exhibit adaptive value for unperformed forms of interaction between the organism and environment or unrealizable body functions are called preadaptive; whereas preadaptation is the process of preadaptive state development (Cuenot, 1911). Anthropogenic environment poses specific requirements to its bird inhabitant species and always depends on human activities. This environment is the habitat of only those species and populations, whose responses to changing conditions correspond with their biology potentials.

When comparing Western European with Eastern Europe avifauna, species composition emerges to be quite similar, however bird populations are at different stages of synanthropization. The Eurasian Jay (*Garrulus glandarius*), wood pigeon (*Columba palumbus*), partridge (*Pedrix pedrix*) and other representatives of the Western avifauna populations are noticeably different their Eastern European counterparts in their behavior in conditions of anthropogenically transformed territories. This is indicative of broad adaptation potential within the process of synanthropization. As noted by S.S. Schwartz (1980), certain type of adaptation occurs in conditions when it promotes prosperity of species, when it is useful, but not necessary. Improving this adaptation allows the species to penetrate into the environment in which this adaptation is a necessary condition of existence. For these reasons, synantropization of eurybiontics with the broader adaptive capacities of species is more likely to happen. Eurythrophic and eurytropic properties are highly important for birds. Before settling in an urbanized environment, birds were supposed to already have the minimal adaptive features to the urban conditions. Most typical synanthropic birds exhibit wide opportunities in nutrition and nature of nesting.

Penetration into the new environment occurs with existing habitats, with the set of conditions acceptable for the species. Thus, the reclamation of anthropogenic landscapes occurs in habitats similar to natural habit areas. According to some authors, reclamation occurs on the land, physiognomically similar to native niches (Boehme, etc.). Conservation of natural habitats in urban sites promotes introduction of many species into the anthropogenic landscape. They serve as a buffer, transition zones for the most synanthropes. Thus, currently observed mallards' synantropization is based on its preadaptive potential and no persecution from human beings.

ANALYSIS OF LONG-TERM DYNAMICS OF CHROMOSOMAL INSTABILITY IN THE BANK VOLE POPULATION

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Assessment of the mutation process dynamics in natural populations is a complex and multifactorial problem. In particular, it is unclear to what extent the frequency of mutations in germ and somatic cells are modified by population-demographic processes, that can also lead to significant changes in metabolism and reproductive system (Chernyavskii et al., 2003).

In this paper we analyze the results of the unique long-term observations (1999–2014 years) of the dynamics of chromosome mutation frequency in the model cyclic populations of bank vole (*Myodes glareolus*) from the territory of the Middle Urals (57°15' N, 58°44' E), reported to be exposed to a background level of anthropogenic pollution (Gileva et al., 2006). The rate of structural chromosomal aberrations (CA) in the bone marrow of voles was used as an indicator of mutation intensity. We used general linear model with different combination of predictors, including sex, year of capture, relative abundance, age and reproductive status. The analysis of association between the frequency of cells with CA and demographics parameters showed no gender differences between animals in terms of frequency of cells with structural chromosome mutations ($G = 6,55*E\text{-}08$, $df = 1$; $p = 0,99$), and pointed to a significant interannual differences in cytogenetic parameter ($G = 126,32$; $df = 15$; $p < 0,11*E\text{-}09$). Age effect was tested only on a group of reproductive voles because reproduction affects mutagenesis intensity (Gileva et al., 2006). The frequency of cells with CA did not significantly correlate with age ($G = 1,98$, $df = 1$, $p = 0,16$). The impact of vole reproductive status was assessed only on the young-of-the-year voles as several studies showed a significant effect of age on the level of chromosomal instability (Gileva et al., 2006). We found that the frequency of cells with CA was significantly higher in reproductive animals ($G = 4,97$, $df = 1$, $p = 0,026$) compared to non-reproductive young-of-the-year, and it peaked with the medium population density. The contribution of mature animals (both overwintered and young-of-the-year), the percentage of which is significantly reduced at the maximum density of rodents, to the variability of mutation rates at the chromosomal level, apparently was associated with the reproduction intensification in the population growth period and the influence of sex hormones. Clastogenic effect of the latter was repeatedly described in the experimental conditions (Liehr, 2000).

We also demonstrated significant association of CA cells with population density ($G = 21,88$, $df = 2$, $p = 0,00002$). Besides, several periods of chromosomal instability increase, which were not directly related to the population density (in 2001–2003, 2006–2007 and 2010–2013) were identified. During these periods genomic instability increased, and we observed the cells with numerous damages of chromatid type, which served as markers of persisting viral infections, whereas in the remaining research years such cells were not detected. In addition to the functional and physiological state of animals in different phases of population cycle, a significant contribution to the mutation process in *M. glareolus* cyclic population was due to the spread of pathogens, which (in the first place, viruses) were known to have a distinct mutagenic effect (Buzhievskaya, 1984).

Thus, in rodents there is a complex dynamic association of the level of genomic instability and population-demographic parameters, with the lowest frequencies of cells with CA observed at a maximum population density (more than 40 ind./100 trap–days).

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SEASONAL VARIATIONS OF PITUITARY HORMONES RECEPTORS IN THE FEMALE GENITAL TRACT OF *BOULENGERULA TAITANUS* LOVERIDGE, 1935 (AMPHIBIA, GYMNOPHIONA) DETECTED THROUGH IMMUNOHISTOCHEMISTRY

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Boulengerula taitanus, a caecilian amphibian, is a cryptic burrowing animal living in the Taïta Hills of southeast Kenya. The climate is monsoonal with two rainy and two dry seasons. Reproduction is characterized with direct development and maternal care. Folliculogenesis is continuous, except during the period of ovulation from November to February. The oviduct can be divided into three classical sections (*pars recta* , *pars convoluta* and *pars utera*). Unlike the ovaries, the oviduct shows some important morphological variation according to the seasons with a maximal development during the reproductive period (from November to February) and a minima from March until August (quiescence). In September and October the oviducts increase their diameter. The immunohistochemical detection of pituitary receptor hormones was performed throughout the annual cycle. Results showed the signal for receptors of FSH, LH and prolactin reduced during the resting period and increased in September and October, immediately prior to ovulation. The partition of each hormonal receptor was different according to the location and tissue. During the breeding period, the FSHRs antibodies gave a positive signal in connective tissue in all regions of the oviduct. LHRs were mainly detected in the secretory epithelium of the *pars convoluta* and PRRs in the *pars utera*. These studies suggest a direct control of pituitary upon the oviduct added to that of ovarian steroid hormones, and a synchronization of metabolism and external conditions. Secondly, our results tend to prove the presence of a fine regulation according to the oviductal region and tissues: FSH seems to be implicated in all three regions of the oviduct, LH in the *pars convolute*, and prolactin in the *pars utera*. This last observation suggests a role of prolactin linked to an adaptive and evolutive convergence with the amniotic vertebrates and even placental vertebrates.

MALE-MALE COMPETITION, FEMALE MATE CHOICE AND MALE SEXUAL TRAITS. EXPERIMENTAL STUDY OF SEXUAL SELECTION IN CAMPBELL DWARF HAMSTERS

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The evolution of sex related characters, which include not only gorgeous secondary sexual traits, but also sizes (see criticism by E.N. Panov, 2015), may be due to the interaction of two mechanisms of sexual selection and depend on their directions. Number of empirical studies of the effects of intra- and intersexual selection considered either one mechanism or the other. Much fewer studies examined the effects of both mechanisms, and most of them were not performed simultaneously (Hunt et al., 2008).

The Campbell dwarf hamster (*Phodopus campbelli*) is a polygamous rodent with pronounced sexual dimorphism. Males are bigger than females, have a highly expressed mid-ventral glands (MVG) that produce secretion, used to mark territory, rear pups etc. In our study, we compared possible directions of sexual selection in two experimental models: 1). Male-male competition (an encounter of males at a neutral arena with free access to the receptive female). 2) Female mate choice (sexually motivated female chooses between two tethered males). We tested pairs of sibling males originated from the multimale litters with different expression of external sexual traits (EST). The hypotheses we tested were: 1). Male with the greater expression of EST dominates in the direct male-male competition (aggressive and sexual dominance). 2). Female chooses the male with higher expression of sexual traits. We limited our study to the assessment of male success at a precopulatory stage of interaction with the receptive, sexually motivated female. Males' EST included body weight, MVG size, anogenital distance and the average max diameter of testes as of their external contours. These characteristics correlate linearly and can be converted into one generalized variable, functionally associated with the lineal size (the result of PC analysis). However, each attribute may have specific meaning, so as the size of the MVG (the typical secondary sexual attribute) may reflect intensity of secretion being a subject of interest for a female, and the size of testes may reflect male's sexual activity and its aggressiveness. An increase in body size may be supported by both mechanisms. The dependent variables used in a multifactorial statistical models were the time the receptive female spends in a compartment with a male, sexual success of a male (the number of series of mounts), aggressive dominance (sum of aggression patterns during encounter tests). We used EST, testosterone level, stress hormone (cortisol), characteristics of adaptive immunity (antibody titer in response to SRBC and the Delayed Type Hypersensitivity response to PHA mitogen) as predictors or independent variables.

Forty-four tests using pairs of sibling males with the contrast expression of EST and unrelated sexually motivated females (in transition of proestrus to estrus) were performed in two years. Females did not choose males based on the higher EST expression. Male dominance in aggression in the encounter experiment was not associated with higher body weight or greater EST expression. Male sexual dominance in tests of free access of two male siblings to the female was not related to aggressive dominance in an encounter experiment. EST expression, sexual activity of the male, and its aggressiveness were independent or weakly dependent on the level of blood testosterone and male's immunocompatibility.

The data obtained suggest that the reasons for evolution of sexual dimorphism in hamsters may in fact lie outside the scope of sexual selection mechanisms.

VARIATION IN ADULT BODY LENGTH AND SEXUAL SIZE DIMORPHISM IN THE EUROPEAN COMMON LIZARD, *ZOOTOCA VIVIPARA*: TESTING THE EFFECTS OF LINEAGE AND CLIMATE

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Intraspecific variation is important because it links macroevolutionary patterns to microevolutionary processes that lead to the phenotypic diversity we wish to understand. Wide-ranging species present promising models for simultaneously evaluation of various factors shaping phenotypic diversity, because the variation of target traits can be documented for numerous populations exhibiting diverse combinations of putative predictors. However, comprehensive range-wide studies of geographic variation in widespread species are rare, even for fundamentally important traits such as body size (Roitberg et al., 2013, 2015 and references therein).

A particularly promising candidate for such study is the European common lizard, *Zootoca vivipara*, the most widespread terrestrial reptile in the world. It occupies almost the entire Northern Eurasia and includes several viviparous and oviparous lineages. Using original and published data on the snout-vent length (SVL, a conventional measure of body size in lizards) for over ten thousand individuals from 72 geographically distinct study samples covering a major part of the species range from northern Spain to the Sakhalin island, we analysed how sex-specific adult body size and sexual size dimorphism (SSD) is associated with lineage identity and two climatic variables (continentality rate aridity rate f the warmer season).

Geographic differences in mean male size were weak and were poorly explained with our predictors. In contrast, mean female size and SSD showed a considerable intraspecific variation, a substantial proportion of which (up to 60%) could be predicted by lineage and two climatic variables, and/or by their interactions.

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POPULATION DYNAMICS OF RED-BACKED VOLES IN THE MIDDLE LENA RIVER BASIN

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Population density of the northern red-backed vole in the Middle Lena River basin reaches 110–140 voles/ha, while gray-sided vole stays at 35–40 voles/ha. Seasonal fluctuations of vole populations were caused by large annual winter mortality and a compensatory increase in reproductive potential. According to 1973–1985 surveys, annual fluctuations in the population number of northern red-backed vole correspond to 3–4-year cycles. The amplitude of spring changes in the number reached 7,3–8, whereas autumn count changed by 3,9 times. The rates of spring population number in different years (0,4–4,4%) were characterized by a distinct inverse correlation ($r = -0,8$, $p < 0,01$) with the summer growth. We observed the highest population growth rate (94,7–95,2%) during the low phase, whereas the lowest (78,4–79,3%) was noted in the peak and decline phases. Despite high level of population growth (average – 8,4-fold, maximum – 19-fold) for 12 years, it was higher than winter mortality in only 3 times in relation to the autumn population number , i.e. after winter periods of 1976/77, 1980/81 and 1983/84. During these periods, elimination of voles declined sharply. The peak phenomenon was caused not by intensive reproduction but a significant mortality reduction in the previous winter. Environmental prerequisites for this phenomenon appeared during low and increase phases. Reproduction intensified when spring population density was low (0,4–2,0%). Female fertility reached an average of 8,1 ± 0,3. 45,4% of females and 37,7% of males of first generations were in breeding condition. Growth rate reached 95%. The proportion of immature voles of previous summer and autumn generations with a higher “cold resistance” increased (69,2–79,7%), whereas winter mortality decreased (57,8–68,6%). Large number of overwintered population (3,2–4,4%) remained by spring and the peak phase was reached at relatively low growth. At the same time reproduction intensity decreased (fertility 6,1 ± 0,3, breeding young females 15,1%, males 3,3%), the proportion of last generations decreased (11,5%), winter mortality increased (88,3–97,0%), population size declined after the peak phase. Similar density-dependent population regulation mechanisms were observed in gray-sided voles. Thus, the survival rate of red-backed voles in winter depended on the temperature conditions and the snow depth. Previous state of the population and the numerical ratio of different seasonal generations were of some importance. In reproductive season, they were mainly affected by the endogenous factors as in the West range of population (Zhigalsky, 1989).

Winters warming and increase of snowing in the last decades resulted in better survival and overpopulation of voles adapted to harsh winters. In such conditions in spring of 2007, the abundance of the northern red-backed vole was 33,0%, gray-sided vole 14,8%. By August, population count of the northern red-backed vole decreased to 0,3%, gray-sided vole disappeared in catches. Only three northern red-backed voles with reduced fertility (with 4–5 placental scars) were registered in August 2008, and gray-sided voles were absent. Signs of the end of depression appeared in 2009. The abovementioned effects of climate warming in the populations of these species will result in their essential structural and functional changes with constantly changing conditions in future.

CORRELATION OF SPLENOMEGALY IN RODENTS WITH THE NATURAL ZOOGENOUS INFECTIONS

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The increase of spleens size, splenomegaly (SM), in natural rodents populations was described in numerous articles of domestic and foreign authors (Rensch, 1948; Schwarz, 1953; Yablokov, 1966; Ivanter, etc. 1985, etc.). This phenomenon has wide geographical spread and it was found in rodent populations of Karelia, the Volga region, the Urals, Central and East Siberia, North America, Eastern and Western Europe, Japan, and Great Britain. The analysis of considerable spleen size variability is of interest in hypotheses of correlation of SM with technogenic intoxication (Gagarsky, Chernova, 2013, etc.), radiative effects (Ekimov, Shishikin, 2010, etc.), infections and invasions (Fay and Rausch, 1969; Krampitz and Bäumler, 1978; Krivopalov, 2011, etc.).

The purpose of this paper is to report the first results of target research of possible association of SM with the natural zoogenous infections. The study was carried out in Ilmen National Park (South Ural) allowing exclusion of technogenic impact on rodent populations. We tested the hypothesis on the most prevalent natural infections in the Urals (Bolshakov, etc., 1965, Ponomarev, 1974; Korenberg, etc., 2013, etc.) including babesiosis, ixodic tick-borne borreliosis (Lyme borreliosis), human monocytic ehrlichiosis, human granulocytic anaplasmosis, hemorrhagic fever with renal syndrome (Hantaan fever), tularemia and leptospirosis (canicola fever). Functional and ontogenetic approach (Olenev, 2002, 2004) was the methodical basis for the study, which considers attributes of animals' growth and reproductive status and allowing separating homogeneous groups of animals, i.e. physiological functional groups. The rodent sample included 39 individuals of *Clethrionomys*, *Sylvaemus* and *Microtus* species. Examined animals had "normal" spleen (relative weight to 10‰) and splenomegaly (relative weight from 10‰ to 169‰). Laboratory analysis of contamination found 70% individuals had agents of ixodic tick-borne borreliosis (Lyme borreliosis) and hemorrhagic fever with renal syndrome (Hantaan fever). This fact argues the existence of natural enzootic area of Lyme borreliosis and Hantaan fever in the Ilmen National Park. Isolated cases of human monocytic ehrlichiosis were registered, whereas agents other agents were not identified. In our earlier article (Olenev, Pasichnik, 2003) the phenomenon's genus specificity was determined in the study region via its occurrence in three species of *Clethrionomys* voles and absence in *Microtus* voles and mice. The rate of animals with SM in *Clethrionomys* voles went up to 36%, 1,6% in *Sylvaemus*, and 3,6% in *Microtus*. We also found some association of infectiousness with SM. In red vole (*Cl. glareolus*), SM was associated with Lyme borreliosis agent in 75% of cases. We suppose that SM can be considered a diagnostic marker of this infection for the studied population. In less than 50% of SM cases we found Hantaan fever agent. In mice population (*S. uralensis*), SM was not associated with contamination. The infected animals were only among individuals with "normal" spleen.

We conclude that splenomegaly can be considered an indicator of damaging factor, when regional epidemiological situation is assessed.

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SPLENOMEGALY AND ITS ASSOCIATION WITH AGE AND FUNCTIONAL STATUS OF ANIMALS

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Nowadays transformation of landscapes and changes of animal environment determine deterioration of transmissible infections in Russia (Onishenko, 2002). The attention of teriologists during the last years is attracted to a phenomenon of splenomegaly (SM), which is frequently seen in small mammals. It was hypothesized (Olenev, Pasichnic, 2003; Olenev et al., 2014; Salichova, 2015; Yekimov et al., 2015) that this phenomenon may be a marker of damaging factors in populations and ecological indicator of adverse epidemic situation. SM has wide geographical distribution and is registered in different rodent’s species mainly in Cricetidae family. In some cases SM may be prevalent in up to 50% of natural populations, however many aspects of this syndrome are need further elaboration.

The aim of this study was to study SM in the population structural dynamics; in particular, to estimate the association with age and functional status of animals using the example of bank vole (*Clethrionomys glareolus* Pall.) in different areas of Ural region with reduced technogenic pressure and recreation. The observations in different areas lasted for 5–30 years. More than six thousand individuals belonging to ten species of mouse-like rodents were trapped. We did entrapments and preparation of animals using standard techniques with the verification of species, sex, reproductive and morphological and physiological status. Age was determined from age markers, such as age-related changes of teeth, also accounting for animals’ functional condition (Olenev, 2009; Kolcheva, 2011).

The association of spleen seasonal and age changes with the energy metabolism rhythm, which was related to maturation, growth and reproduction of mouse-like rodents was shown earlier (Ivanter et al., 1985). The introduction of “Norm – SM” parameter (Olenev, Pasichnik, 2003) and use of functional-ontogeny approach (Olenev, 2002) allowed to consider high variability and registration of pathological spleen enlargement from the point of view of functional structure of population. SM is first is typical for breeding population (1 and 3 physiological functional groups – PFG), that it is present in animals with high level of metabolism, mainly overwintered animals. Small SM prevalence is also constantly registered among nonproductive young of the year (2 PFG), despite low metabolism. Comparison (Mann-Whitney test) of absolute and relative spleen weight in animals of different PFGs discovered significant differences between breeding and nonbreeding individuals.

The absence of clear linear dependence of spleen weight from age confirms the qualitative nature of the SM phenomenon. Spleen increase up to super-normal values is more important than the scale of this increase, which are possibly individual-related or connected to species specificity. The relationship of age and SM probability is clearly visible in the analysis of age-related SM prevalence. With increasing age, the prevalence of SM also rises. We, therefore, conclude that there is a considerable impact of age on SM syndrome probability in small mammals.

Thus, the general laws of physiological and functional groupings remain. (1) The lowest relative prevalence of SM was found in nonbreeding young of the year (2 PFG). (2) Breeding animals (1 and 3 PFGs) showed much greater SM prevalence, with highest readings in the “oldest” overwintered individuals (1 PFG). (3) The age is recognized a significant factor, that is, SM probability by the end of life is 10 times greater.

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POPULATION OF *ANSER FABALIS* BEAN IN THE AMUR REGION

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Among Bean subspecies, *Anser fabalis serrirostris* and *Anser fabalis middendorffii* arrive from the southern regions of the Asian part of the Palearctic seen in the first half of spring. These taiga subspecies have latitudinal migrations. In addition, *Anser fabalis rossicus* is registered in the end of spring migration. Migration time and spatial distribution show that birds fly along the longitude line from south to north. Such increase in the length of the route eastwards probably occurred not so long time ago, because researchers earlier claimed it did not exist in the Far East before.

We defined subspecies and their proportions during the spring migration. Based on generally accepted systematic signs of Bean species (Syroechkovsky et al., 2011), we analyzed 42 individuals legally hunted in the Amur Region in the last 2 years. We have also analyzed individuals photographed throughout the region over the recent years. Based on the available material, we hypothesize that *Anser fabalis rossicus* is a subspecies, flying to the Amur Region at later stages of migration. Today it has a large share (nearly 30%) in flocks of Bean migrating here (Sandakova, Toushkin 2015).

In the study area, the Bean was observed in almost all districts of the Amur region during spring migration. The greatest concentration was achieved in Konstantinovsky, Tambovsky, Mikhailovsky and Blagoveschensky districts, where their count ranges from 5,000 to 10,000 individuals in different years.

Bean’s flying trajectory varies with years, which is mostly affected by climate. Geese get together on the fields of the south after snowy winters and in years with wet spring, where numerous bays and vast estuaries are formed at a time of fly. During these years, geese rest in temporary ponds and feed near the fields with the last year's harvest remains. Corn, soybeans and wheat grown here is main food for birds in these fields. This field in the area between the Amur and Zeya are key habitats during migration in such years.

All that changes dramatically in drought years. Arrived geese stay on the spits of Amur River to rest, where it feeds on fields with lower disturbance level due to limited availability for hunting in the border zone. From there they fly away to taiga lakes in the central part of the region along the River Zeya. Goose concentrates near the lakes, where after deep freezing, concealing ice pops and raises silt sediments rich in shellfish and amphibians. Another important source of food is caltrop growing here or floating water chestnut from last year *(Trapa natans)*.

We note that the timing and space for geese concentration during migration are more or less stable in the flood plain of the Amur River and in the central part of the Province. In other areas, it depends on the year, or on the edge effect of the migration corridor.

Over the last 30–40 years, timing of arrival and departure of bean in the Amur region shifted to 10–15 days earlier on average. Nowadays, Bean arrival in Amur Region starts in late March or early April. Intense fly-through occurs from April 15–20 until May 1–5, ending on May15–20.

POSSIBLE ADAPTIVE MEANING OF POPULATION GENETIC STRUCTURE IN THE EURASIAN LYNX

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Due to their high mobility, large terrestrial predators are potentially capable of maintaining high connectivity, and therefore low genetic differentiation among populations. However, previous molecular studies have provided contradictory findings in relation to this. To elucidate patterns of genetic structure in large carnivores, we studied the genetic variability of the Eurasian lynx, *Lynx lynx* throughout north-eastern Europe using microsatellite, mitochondrial DNA control region and Y chromosome-linked markers. No polymorphism for the cytochrome *b* and *ATP6* mtDNA genes and Y chromosome-linked markers were found. Using SAMOVA we found analogous patterns of genetic structure based on both mtDNA and microsatellites, which coincided with a relatively little evidence for male-biased dispersal. Lynx inhabiting a large area encompassing Finland, the Baltic countries and western Russia formed a single genetic unit, while some marginal populations were clearly divergent from others. The existence of a migration corridor was suggested to correspond with distribution of continuous forest cover. Lynx from the Kirov region (Russia) showed the highest diversity of mtDNA (8 haplotypes) and microsatellite allelic richness (4,4). The lowest variability (in both markers) was found in lynx from Norway and Białowieża Primeval Forest (BPF), which coincided with a recent demographic bottleneck (Norway) or high habitat fragmentation (BPF). The Carpathian population, being monomorphic for the control region, showed relatively high microsatellite diversity, suggesting the effect of a past bottleneck (e.g. during Last Glacial Maximum) on its present genetic composition. Genetic structuring for the mtDNA control region was best explained by latitude and snow cover depth. In contrast, microsatellite structuring correlated with the lynx's main prey, especially the proportion of red deer (*Cervus elaphus*) in its diet. We conclude that Eurasian lynx are capable of maintaining panmictic populations across eastern Europe unless they are severely limited by habitat continuity or a reduction in numbers. Moreover, the correlations of genetic differentiation with climatic and ecological factors suggest the occurrence of populations specifically adapted to local conditions in terms of prey availability and climate severity, which may contribute to genetic isolation. Also, due to different correlations of mtDNA and microsatellite population divergence patterns with climatic and ecological variables it is possible that separate selective pressures are acting on males and females in this solitary carnivore.

BIOTIC COMMUNITY LINKS OF WOLF IN YAKUTIA

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Wolf count in Yakutia is not stable (Romanov, 1941; Labutin, 1960). It was high in the beginning of 1950s. Activities on its depopulation started in 1958, and 3117 wolves were exterminated during the next 6 years (957 individuals in 1958, 680 in 1958, 538 in 1960, 431 in 1961, 295 in 1962, 216 in 1963 (Paulin, 1965). It was followed by a significant reduction of damage to the domestic reindeer, horse and cattle herds. For example, from 1954 to 1958, wolves killed 24000 reindeer, while in 1959 to 1963 only 11400.

According to broad-brush estimates, wolf population size in Yakutia was up to 500–700 individuals (Egorov, 1965) in 1963–1964, 2000 in 1978–1979 (Labutin, Vschivtsev, 1985), and 3000 in 2000–2015 (Okhlopkov et al., 2005; Sedalishchev, 2013; Stepanova, Nikolaev, 2015).

The wolf food connections in Yakutia vary widely (Labutin, 1960; Mammals of Yakutia, 1971). Prior to 1970, tundra and forest-tundra wolf mainly hunted domestic reindeer. The elk and red deer dominated (78%) in the wolf's forage in the South of Yakutia, whereas hare (70–80%) was the principal forage in Central, Western and North-Eastern Yakutia.

However, since the end of the 1960s in Central, Western and North-Eastern Yakutia hare population decreased steadily apparently due to anthropogenic factors (Prokopiev, Sedalishchev, 2009; Sedalishchev, Anufriev, 2002). Degradation of wolf forage in recent years was registered in South Yakutia as associated with the elk population overhunting and decrease since the beginning of 1990s (Sedalishchev, Popov, 2002; Prokopiev, Sedalishchev, 2009). Therefore, wolf in these parts of Yakutia switched to domestic reindeer and cattle as forage.

According to data of the Ministry of food and agriculture of Yakutia, in 2011–2013 wolves annually killed from 10000 to 15000 domestic reindeers and about 1500 horses. Monetary equivalent of that damage was more than 100 million rubles (Stepanova, Nikolaev, 2015). According to Nikolayev et al. (2014), the analysis 1000-wolf stomachs from various regions of Yakutia in 1981–2013 confirmed the presence of domestic animals remains in 800 animals, the remains of wild animals including reindeers (40%), hares (20%), elks (15%), roe-deer (15%), and red-deer (10%) in 200 wolves' stomachs.

In order to reduce the damage to domestic reindeer, horse and cattle herds, and to promote wild ungulates population increase, wolf count should be brought to the level of 1963–1964s, i.e. to raise hunting pressure on mature animals 2,0–2,5-fold (Sedalishchev, 2013).

In the study of 74 wolves from five regions of Yakutia, we found 10 species of helminths, including three species of trematode *Plagiorchiselegans* (Rudolphi, 1802), *Euparyphiummelis* (Schrank, 1788), and *Alariaalata* (Goeze, 1782); four species of cestodes *Taeniahydatigena* (Pallas, 1766), *Taeniakrabbei* (Moniez, 1879), *Multicepsserialis* (*Gervais*, 1847), and *Echinococcusgranulosus* (Leuckart, 1863), and three species of nematodes *Ancylostomacaninum* (Ercolani, 1859), *Taxascaris leonine* (Linstow, 1902), and *Trichinellanativa* (Britov et Boev, 1972). The overall wolves' contamination with helminths was high and reached 82,4%. We also found some specific features of wolves' contamination in different regions of Yakutia, therefore their helminth species composition was largely determined by the wolves' trophic links.

PATTERN OF FEEDING BEHAVIOUR OF A FIELDFARE *TURDUS PILARIS* L. IN KALININGRAD CITY

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The study of fieldfare (*Turdus pilaris*) feeding behaviour was carried out in Kaliningrad in 2012–2015.

We found that in Kaliningrad, during the nesting period fieldfares is foraged mainly on the ground: on lawns, which are sites with low vegetation thinned due to the man-induced impact (57,8%), and less frequently on lawns with thick vegetation (21,1%). Other sites are used with a frequency of 7% or less. In autumn and winter, fieldfares in Kaliningrad prefer to feed on trees and shrubs in parks and gardens, roadside alleys (85,3%), less frequently on lawns and paths, as well as lanes (14,7%).

When foraging a fieldfare in Kaliningrad moves by a series of 3 to 8 jumps or by runs alternating them with looking around and ripping (ripping the forest floor, digging feed from soft soil). In 1 minute a fieldfares makes 5 to 25 jumps, 10 to 17 pecks, 5 to 10 ripping motions, 3 to 9 looks around (average duration is 9,13 ± 10,7 seconds, n = 145, reaching 30 to 45 seconds, in singular events more than 60 seconds). The bird makes a peck primarily after motion (0,54), less frequently after looking around (0,17) or ripping (0,17) or a peck (0,12). After the peck, a bird of this specie looks around most often (0,56), less frequently jumps, runs (0,24), sometimes rips ground (0,1) or makes next peck (0,1). In autumn and winter, peck frequency increases, the bird flies to other places along with other foraging types. During feeding on the ground, ripping frequency, as well as peck frequency, increases, when a fieldfare forages from under snow and leaf litter.

During nesting, fieldfares mainly use earthworms for food, and other invertebrates less frequently. In autumn and winter, fieldfares mainly feed apples, berries of mountain ash, hawthorn, snowberry etc. No observations were made in Kaliningrad as per fieldfare foraging by anthropogenic feed, although there is an additional available forage base, such as the wastes of human activity (which is used by black thrushes) and according to literature data (Lübcke, Furrer, 1985; Telpova, 2006), fieldfares forage unusual feed types (small fish, meat and fat, forage at landfills in other cities).

Thus, compared with the forage behaviour of natural fieldfares populations (Baranovskiy et al., 2007) in Kaliningrad, urban population of this species is noted for increased frequency of feed actions, such as movements before peck and looking around frequency as well as looking-around period after a peck. These peculiarities are defined by both bird’s attitude (suspicion) to humans and attributes of feeding habitats in Kaliningrad.

GENETIC DIVERSITY *MICROTUS ARVALIS* OBSCURUS AND POSSIBLE WAYS OF ITS FORMATION IN THE URAL REGION

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We analyzed variability of two mitochondrial DNA markers (cytochrome *b* gene and control region of mtDNA) in the populations of common vole (*Microtus arvalis* Pall., 1778 form “obscurus”) in the Ural Mountains and adjacent plains. We also considered possible ways of how modern genetic diversity in *M. arvalis* “obscurus” in the Ural region was formed.

The material was collected in 25 localities in the Urals, Pre-Urals, and Trans-Urals (51°07′–60°38′ N; 48°38′–66°33′ E). A total of 128 sequences of cytochrome *b* gene and 111 sequences of mtDNA control region was included in the analysis. In addition to original data, we used cytochrome *b* gene sequences of *M. arvalis* “obscurus” from other regions (Haring et al., 2000; Hayens et al., 2003; Tougard et al., 2008; Tougard et al., 2013).

Analysis of cytochrome *b* gene sequences showed that all individuals of common vole in the Ural region belonged to the previously described Sino-Russian clade (Tougard et al., 2013), which inhabited the greater part of the area of *M. arvalis* “obscurus” (from northeastern China to Crimea). Phylogeographic analysis of Sino-Russian clade in general allows to describe four groups of geographically localized haplotypes and a widespread group of poorly differentiated haplotypes which are common in the central (Urals region) and eastern parts of the distribution range of Sino-Russian clade. Within the Urals and the adjacent plains, three groups of haplotypes were found, including northwestern, southwestern and South-Uralian. Fourth group, the southeastern group, inhabits the northwestern China and the upper reaches of the Irtysh River. Incorporation of the data on the variability of mtDNA control region in the analysis of common voles in the Ural region confirmed that at least three mitochondrial lineages existed in the region. These mtDNA lineages corresponded to cytochrome *b* groups. Based on the analysis of mtDNA sequences, the greatest genetic diversity was found in populations of common vole in the Southern Urals. The lowest genetic diversity was found in populations in the Middle and Northern Urals and northern Pre-Urals; however, a separate group of haplotypes (the northwestern group) inhabited the northern Pre-Urals.

To analyze the history of modern genetic diversity in *M. arvalis* “obscurus” within the Ural region we used groups of data, including geographical distribution of various mitochondrial lineages in the Ural region; genetic distances between mtDNA sequences of animals from different localities; demographic analysis of mtDNA sequences; and paleontological findings of species in the Ural region. The results indicate that *M. arvalis* “obscurus” might have experienced several colonization phases in the Ural regions. Perhaps, colonization of the Pre-Urals might have started earlier than in the Trans-Urals.

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DYNAMICS OF ETHOLOGICAL STRUCTURE WITH THE CHANGES OF POPULATION COUNT IN AN ISLAND POPULATION OF THE FERAL HORSE

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The natural social structure of an island feral horse population of the "Rostov" State Nature Biosphere Reserve consists of harem, bachelor, and mixed groups (Spasskaya, Shcherbakova, 2006; Spasskaya et al., 2010; Spasskaya, 2016). Both the way of formation of social structure and presence of bachelor groups distinguish this population from those of the native breeds maintained in a wild herd-drove manner. The above three social units are stable to a different extent: during the study, harem groups did not change their composition dramatically for 6 years, while the groups of other two types remained stable for two to three years.

The population number in 2006–2010 was fluctuating within a wide range (72 to 419 individuals) because of two catastrophic losses in 2007/2008 and 2009/2010; population count decreased by 33,2% and 79,8%, respectively. In 2008, the population counted 307 individuals in total, and all main types of groups persisted, with the harem, bachelor and mixed groups containing 58,2%, 15,4%, and 25,8% of the total number, respectively (Spasskaya et al., 2010). Compared to 2006 data (corresponding precise figures for 2007 are not available), the quantitative ratio of these groups changed, i.e. the size of harem groups decreased by 16%, while size of bachelor and mixed groups increased by 7,7 and 8,4%, respectively. In 2010, the social structure appeared to be completely reformed: new harem and bachelor groups were formed, while mixed groups were not. In total, 87,5% of population count was part of 16 harem groups, and 12,5% remained in 3 bachelor groups.

In 2012, 2013, and 2015, the Reserve administration conducted regulatory measures (though the last two captures were undertaken without scientific rationale). Twelve animals born in 2012 and 2011 were captured in 2012, while 13 animals of various age were captured in 2013, therefore population number decreased by 8,2% of the entire population count in both instances. In 2012, they captured young animals that occupied the lowest positions in the group hierarchies, so they did not play any role in the intergroup relations. However, capturing of 8 adult and young bachelors in 2013 led to a complete reformation of the bachelor groups. As a result, the remaining bachelors formed two harem groups and a mixed group with two stallions. A new mixed group was formed for the first time since 2009 to include 2,2% of the total population count (180 animals in 2014); 87,8% of the total population amount was belonged to 19 harem groups, and the remaining 10% were 5 or 6 bachelor groups.

Because of capture and slight loss during autumn and winter 2015/2016, the population number decreased by 25,8% (55 animals, including 39 stallions and 16 mares). Among the remaining animals, 23,5% were adults (over 5 years) and 74,5% were 1 to 4 years old. Subsequent restructuring in the population social structure happened: new harem groups and a mixed group were formed; 2 mixed groups (with two adult stallions in each) turned into harem ones (the "extra" stallions turned to be bachelors). One harem group ceased to exist and two harem groups disbanded because of capture of their stallions. In April 2016, with total population being 178 individuals, 18 harem groups made 87,6% of the total count, while three mixed and three bachelor groups each contributed 6,2% and 5,6% to the total count.

We conclude that harem groups (up to 88% of the total population amount) and bachelor groups constituted the basic social structure of the feral horse population studied. Mixed groups appeared to be the most unstable social elements. Fluctuations in population number mainly due to mature individuals, caused by natural or anthropogenic effects, resulted in instability of an established social structure, which, in their turn, led to disappearance/appearance of mixed groups and to changes in the quantitative ratio of the groups of different types.

EPIZOOTOLOGY SITUATION WITH TULAREMIA IN THE MIDDLE OB (IN PHASE OF DEPRESSION MANNING WATER VOLE)

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Natural foci of floodplain-river type are typical for Khanty-Mansiisk Autonomous District – Yugra. *Arvicola amphibius* is considered the main reservoir and source of massive tularemia infection. An outbreak of tularemia that involved 1005 people (Ostapenko, et al., 2014) was registered in Ugra in July and October 2013. Thorough study of small mammals and amphibians as potential carriers of tularemia infection was conducted in Khanty-Mansiisk district and the city of Khanty-Mansiisk from May to September 2015 and in June and July 2013, and September 2014. We also examined floodplain habitats of the Middle Ob and the surrounding areas.

In 2013, *A. amphibius* was part of the dominant species in virtually all riparian biotopes near the city of Khanty-Mansiisk. In autumn 2014, there were only few individuals floodplain biotopes of the natural monument “Lugovsky mammoths” 37 kilometers west of the city of Khanty-Mansiisk. In the snow-free period of 2015, we did not find *A. amphibius* near Khanty-Mansiiskas did the staff of the Center for Hygiene and Epidemiology in KhMAO-Ugra that may be a sign of deep depression and almost its complete absence. On the territory of tularemia focus in the confluence of rivers Ob and Irtysh, we found 12 species of parasitic gamasid mites on small mammals. In 2013, parasites were mainly represented by specific parasites of *A. amphibius Laelaps muris* and *Hyperlaelaps amphibius*. They were absent in 2015, *Alexandromys oeconomus* dominated among animals, whereas *Laelaps hilaris* was a dominating species among gamazid (73–80%, using cones and mashers). The vast majority of ticks (*Ixodes persulcatus*) were found in small mammal biotopes in the floodplain terraces. In 2015, the causative agent of tularemia in the water was not found (10 samples). Of all samples of small mammals and amphibians (573 spleens), tularemia DNA was identified only three animals of *Myodes rutilus* (terrace above the floodplain). The employees of the State Scientific Center of Applied Microbiology and Biotechnology (Obolensk, Moscow Province) carried out the analysis.

Thus, restructuring of zoocenosis in floodplain habitats occurred near Khanty-Mansiisk in 2015 as compared to 2013. *A. amphibius* as a massive source of tularemia infection was eliminated from the pool of small mammals. Core community of the floodplain complex of small mammals comprised four species, including *A. oeconomus*, *M. rutilus*, *Sorex araneus*, and *S. minutus*. In 2015, we observed a sluggish current epizootic of tularemia among small mammals in the floodplain and biotopes bordering floodplain. Of all surveyed small vertebrate, tularemia DNA was confirmed only in the spleens *M. rutilus*, which accounted for 0,5% of the number of isolates in the bioassay. There is no doubt that *M. rutilus* contacted the inhabitants of amphibious organisms in floodplains in tularemia years previously (2013 and 2014). Our studies have confirmed that *A. amphibius* is the main source of tularemia in the floodplain-river type of focus. When epizootic range expands, it involves a number of amphibious organisms, including *A. oeconomus*, *Ondatra zibethicus*, and the *Myodes*, shrew, other small mammals and their ectoparasites, such as ticks, gamasid mites, fleas, lice, mosquitoes, horseflies and others.

In 2015, prerequisites for the occurrence of acute tularemia epizootic in the study area were not found.

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LONG-TERM POPULATION DYNAMICS OF TAMARISK GERBIL UNDER HUMAN-INDUCED LANDSCAPE CHANGE

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Rangeland ecosystems are the most sensitive to environmental changes and they easily transit from one state to another. As the result of overgrazing, the only anthropogenic desert in Europe was formed in Kalmykia by the end of the 80s. Livestock population demonstrated a significant and rapid decrease due to the economic reforms in the early 90s. This triggered recovery of degraded rangelands and favored steppe expansion. Such human-induced landscape transformation provided an opportunity to study species-specific response to environmental change. We have analyzed the population dynamics of tamarisk gerbil (*M. tamariscinus*) during the period from 1994 to 2015. Tamarisk gerbil is a mesophilic folivorous species, which prefers to inhabit sites with compact soil and saltwars, bushes and shrubs. Distribution and abundance of tamarisk gerbil increased concurrently with rangeland recovery, but further steppe expansion led to fragmentation and reduction of suitable habitats. Its population drastically declined in 1998, remained low until 2004 and has not been registered henceforth. Thus, the population of tamarisk gerbil transited into unstable state and went extinct. Intriguingly, the population of a psammophilous granivorous midday gerbil (*M. meridianus*) also decreased in 1998 but rapidly restored. The population had a sudden shift into a state with low abundance in 2003 and remains in this state until now. The inert response to human-induced landscape change demonstrated by *M. meridianus* in contrast to *M. tamariscinus* can be attributed to its ecological generalism.

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ECOLOGICAL ADAPTATIONS OF BACKGROUND SMALL MAMMALS SPECIES IN AGROCENOSES IN THE REPUBLIC OF MOLDOVA

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Being aware of the laws and the ways of mammals' adaptation to different environment conditions and, particularly, to the anthropic landscape, dynamic in nature, represents one of the main directions of the contemporary mammalogy. A possible solution to this problem is only systematic and detailed study of the species population's structure in different ecological conditions and at different phases of the dynamics of the number of population.

In the '80s of the last century, the wood mouse (*Apodemus sylvaticus*) exceeded in number the mound-building mouse (*Mus spicilegus*) and the common vole (*Microtus arvalis*) species, accounting for more than 50% of all the rodents that populated the agrocenoses of the Republic of Moldova (Munteanu, Savin, 1986, 1988, and 1990). At the same time, another species, the striped field mouse (*Apodemus agrarius*), was almost totally dispersed from the fields and the bright forest strips. Some essential changes arouse in the dynamics of rodents' number as well. The 3–4 years cyclical oscillations were not typical of common vole species as it was registered in other parts of the area (Sytnic, 1999). It is possible that the intensification of the anthropic pressure on rodents reflects on the type of the number dynamics too. During years of mass reproduction and rapid increase in number, the vole invoked huge damage to agriculture, particularly to crops of alfalfa, clover, wheat, etc. In relation to this, there is a problem with managing animals number based on studying adaptation and control of the number in the variable landscape.

The species enumerated above are background species in the Republic of Moldova's agrocenoses. The other species in the agrocenoses are less numerous, for example the yellow-necked mouse (*Apodemus flavicollis*), the bank vole (*Clethrionomys glareolus*), the striped field mouse (*Apodemus agrarius*), and also the European hamster (*Cricetus cricetus*), and *Cricetus migratorius*. Four species, i.e. the wood mouse, the mound-building mouse, the common vole, the apodemus uralensis, had almost synchronized multiannual oscillations of the number.

In recent years, under the strong influence of the drought *M. spicilegus* adapted insignificantly to ecological conditions and accounted for 13,7%, while another species, *Ap. sylvaticus*, showed strong ecological valence (Savin, Munteanu et al., 2009). This species quickly adapts to changes of conditions and its abundance equals 40%. *Ap. agrarius*' abundance rose from 2,1% to 17,8% and its presence was permanently accounted for in agrocenoses as well as in forest cenoses. *Cl. glareolus* was more frequently captured in the reproduction period in the fields with multiannual forage grasses at a distance of 150–200 m from the forest. *Ap. flavicollis* was found to have an abundance of 5–8%. Due to the reduction of the multiannual forage grasses fields, which resulted from their privatisation and the emergence of a number of fragmentary raw agricultural land there is no cyclicity in the plant feeder species, *M. arvalis* and *M. rossiaemeridionalis* (Sytnic, 2016). Under these conditions, their abundance rose insignificantly from 7,2% to 9,7%. These species were in the growth phase but they did not reach the peak phase.

The strategic reproduction peculiarity of *M. arvalis* resides in females' domination and increase in duration of reproduction period. *Ap. sylvaticus* individuals who wintered usually lay eggs but rarely three batches. Spring generations lay 1–2 batches of eggs. During peak years, this species stops reproducing at the end of summer, while in the depression phase, and with an average population count, reproduction period continues by the middle of autumn (Savin, 1999). The role of age groups of the studied species was determined in control of the population number. During the year with bad population, the contribution of individuals of the current year is on the rise, while during the year with optimal conditions, the number of individuals who wintered is on the rise.

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THE ADAPTIVE ROLE OF INDIVIDUAL VARIABILITY INDICATIVE OF THE SKILLS OF THE CHILS BARABA GALL (*LARUS BARABENSIS*)

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At an early age Chicks of Baraba gull (*Larus barabensis*) have a high risk of infanticide and cannibalism compared to the smaller Chikovani. The territorial aggressiveness of the parents is an effective protection against the attacks of neighbors, but at the same time, limits the movement of Chicks by the area limits. And the risk of attacks by cannibals during the absence of parents makes the Chicks hide in shelters on the nesting site. In these circumstances, there are various ways of development of the indicative skills of the juveniles, which depend on their basic cognitive abilities. The aim of this work was to evaluate a variety of indicative personal skills of the Chicks and their adaptive value in terms of breeding colonies.

The first week of life in gulls is critical to survival, so we measured the mass and length of the heads of the Chicks in the 1st and 8th days of their life. The level of cognitive development was evaluated for every chick. It was offered the orientation task in the experimental construction “Labyrinth”, adapted for the gull Chicks. To check the learnability of the Chicks a pairwise pairing was performed: the Chicks which did not solve the task, were tested in combination with those hatchlings who successfully found their way. After 15 days, a single test to assess the influence of the environment on nestling development was repeated.

The ability of the Chicks to solve the problem of orientation in the labyrinth was different at an early age and has varied over time. After the first test the groups of birds were defined which were distinguished by the way of solving the problem. After re-testing, the elements of teaching the Chicks were found, which formed a “cognitive map” of all the signs of “labyrinth”. The use of such map does not affect the fact of solving the problem, but it affects the efficiency of solving the problem, which was estimated by the time of the experiment and the number of mistakes made

We believe that in terms of developed territorial behavior of adult birds and high risk of cannibalism a certain set of personal characteristics among the birds is implemented. In addition, the estimated skills develop in Chicks due to the need to monitor their own safety independently. The dependence of the adaptive values of the personalities on the original dimensions and the strategy selected by parents for the education of the young was shown.

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UNGULATE POPULATION STRUCTURE IN THE OLYEKMINSKY RESERVE

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We collected material describing the state of prey in the reserve from 1985 to 2016 including annual surveys covering different habitats MFP, monitoring and accounting for solonetzes during rutting red deer males account on (roar). The release date of calves their number, sex and age composition were determined visually by animals and encounters on the trail, as used camera traps.

Moose (*Alces alces* L.). Population count and density were estimated using aerial surveys (Revin, 1989), as well as our data of 1990–1993, and the results of SCM of 1989–2016, undertaken in the Reserve and adjacent hunting grounds. Moose population density in the Basin of Olekma River was 0,2 birds/10 km² on average, being twice less than in the basins of Amga and Tuolba (0,4/10 km²). According A.A. Krivoshapkina (2004), sex and age structure of the moose is severely impaired. The predominance of females in the population of (1,7: 1) resulted in an increase barrenness of moose (40,8% of all females encountered). In males, young 2–3 year olds who do not participate in the rut, prevailed, which was indicative of the rejuvenation of the herd. According to O.V. Yegorova (1970), male to female ratio was 1:1 in the 1960s, and barrenness among elk was negligible.

Red Deer (*Cervus elaphus* L.). Studied in the protected zone showed a number of regional attributes in the distribution, related to both periodic seasonal migration of large groups from one location to another, and long-term changes in their count. The population is going through a period of depression; this is due to an increase the wolf count and more intense shooting in the neighboring territories. However, beginning in 30s of the XX century, this species population area expands northwards. The reserve, being the largest reserve in the north of species areal with the average density of 2,5–3,0 ind./100 km², is inhabited by 250–300 red deer in the adjacent areas as of SCM data, with the density close to the reserve (2,2–2,8 ind./100 km²).

Reindeer (*Rangifer tarandus* L.). Can be found throughout the geomorphological terrain profile from the bottom of the intermountain basins and low flood plain to the heights of the local watershed within the boundaries of the reserve and adjacent territories. The mean population density is 4 ind./100 km^2 in South Yakutia, and about 5,5 ind./100 km^2 within the reserve’s territory. The total population is 400–450 individuals.

Roe Deer (*Capreolus pygargus* Pallas). The traces of the Siberian roe deer are rarely observed in summer and autumn only in the Basin of Olekma River. However, the area is surrounded by sites of permanent and relatively old habitat of this species all over. Although the formation of a viable permanent population of roe deer on the territory is unlikely, sporadic penetration of single animals occur regularly.

Siberian Musk Deer (*Moschus moschiferus* L.). In the Basin of Olekma River, musk settles on upland terraces and steep sides of the valley with sloping land occupied by dark coniferous forests and rock outcrops. In the Basins of Tuolby and Amga Rivers, musk deer occurs periodically every year, and in the absence of sludge and rocks, it prefers cluttered areas of taiga, covering it from predators to some extent. In the event of sharp depletion of food, the animals leave their place (in particular, as a result of forest fires) and re-populate that territory after the partial recovery in a few decades. By extrapolating the mean population density index, calculated from different parts of the Basin of Olekma River (2 ind./100 km^2), the total population is estimated at 200–250 individuals.

SABLE POPULATION GENETIC STRUCTURE (*MARTES ZIBELLINA* L.) IN TOMSK PRIOBYE

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The contemporary sable groups in Tomsk Priobye are traditionally considered descendant of acclimatized eastern Siberian animals (Monakhov, 2006). Intense hunting commenced with founding of Tomsk in 1604 resulted in dramatic reduction in the aboriginal species. By the beginning of the XX century, population count was critically low. Its areal from a homogenous turned into groups of isolated spots. In Tomsk Priobye, by the time of ban on its hunting in 1935, it only inhabited difficult-to-access habitats near Bakchat swamps (upper course of Chaya River), in the Basin of Vasugan River, and on the right shore of Ob in the upper course of Rivers Ket and Chulym (Laptev, 1958). These negative trends resulted in reacclimatisation. 1347 wild sables were introduced to Tomsk Province from Irkutsk Province and Burat ASSR from 1940 to 1957 (Pavlov et al., 1973). As a result, this species inhabited all suburb habitats by the end of the XX century, whereas high count allowed for intense hunting. Contemporary sable population in the southeast of West Siberia is very much diverse as of both morphological attributes (Ranyuk, Monakhov, 2011) and fur color (Tyutenkov et al., 2010). The aim of this study was to determine modern genetic diversity of sable population in light of its recent rearrangement.

This report is built upon the analysis of 65 specimens collected in sables' groups, inhabiting the Basins of rivers Vasugan, Tym and Chaya. We used mtDNA control locus fragment with a length of 495 pn (Rozhnov et al., 2010) as a marker. Compared to other areas (Pischulina, 2013), Tomsk sample is noted for low genetic diversity ($H = 0{,}89 \pm 0{,}02$, $\pi = 1{,}16 \pm 0{,}63$). This is characteristic of populations, founded by a small number of ancestors.

Median net, which we built, combining all variants of mtDNA in our analysis, confirmed two clearly marked mytogroups on the territory of Tomsk Priobye, which highlights two ancestor lines, such as aborigines and acclimatized animals. 55% of group 1 ($n = 22$) was sable from the Basin of River Tym, having their phenological traits very close to imported "Barguzin" animals. 47% of group 2 (43 specimens) were animals from the Basin of River Vasugan, morphologically close to autochthonous animals. This ratio may witness animal exchange between various sable groups with homogenous special areal present in Tomsk Priobye.

Small distance between mytogroups (8 nucleotide replacements), poor nucleotide and haplotypical diversity are indicative of the modern population as a result of recent junction of several groups, isolated previously. Those groups initially were not numerous, because the number of founders (allochthones) was small or because populations passed through a long-term demographic "bottleneck" (autochthones). Thus, modern genetic structure of sable population in Tomsk Priobye reflects its transformation resulting from intense hunting, biotechnical and nature preservation activities.

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GEOMETRIC MORPHOMETRICS IN POPULATION ECOLOGY: THE NEW POSSIBILITIES AND SCIENTIFIC OUTLOOKS

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At the end of the XX century in biology, a new way of multidimensional morphological analysis (2D and 3D) allowing to characterize size and shape variability of the same morphological structure was independently developed (Rohlf, Slice, 1990; Bookstein, 1991), so-called geometric morphometrics – GM. The main task of the GM was to describe the variability of shape as such, excluding the impact of size component, and comparing representatives of different groups. In recent years, GM is widely used in various fields of biology, including taxonomy, paleontology, and anthropology as well as in archeology, criminalistics, medicine and other areas (Adams et al., 2013.). However, in dealing with population-ecology problems methodical apparatus of GM and its opportunities are obviously underutilized (Zelditch et al., 2004; Anderson et al., 2014).

GM allows morphogenetic interpretation of the shape changes (Zelditch et al., 2004; Vasil’ev et al., 2013) and facilitates biological interpretation of these modifications with the use of visualizing techniques (Klingenberg 2013). Using of GM-methods permits, thus, essentially expand the methodological potential of population ecology. All this makes GM an extremely efficient and universal approach to solve not only the problems of population ecology, but those of population synecology too (Vasil’ev et al. 2014, 2016; Vasil'ev et al., 2015).

We aimed to present scientific perspectives of GM to solve number of population ecology problems and demonstrate new methodological possibilities of this technique using specific examples.

This study is based on the results of multiyear research of the authors and their colleagues at the Laboratory of Evolutionary Ecology (IPAE, Ural Branch of RAS) undertaken on model species of rodents and shrews. The report presents the original approach of authors, including “geometric phenogrammetry” method based on converting of homologous phenes of non-metric traits in phenogram and allowing phenetic ordination based on GM technology, as well as the method for estimating within-group morphogenetic diversity by analyzing the pattern of the nearest neighboring points within scatter-plots of shape variation. The applicability of morphological and functional mandible indices are shown (Anderson et al., 2014). We present examples proving the feasibility of “compensation principle” developed by Acad. Yu. I. Chernoff within populations, as well as demonstration of population morphogenetic effects of non-selective elimination in populations of forest voles.

We propose to make greater use of GM methods in population ecology to mine information on individuals’ morphogenetic reactions, as well as within- and between-population groups at different constellations of climatic and biotic conditions, all this will significantly complement the possibilities of interpreting population phenomena, linking them with the morphogenesis of animals. In this sense, the GM-approach is a multi-dimensional analogue of a well-known method of morphological and physiological indicators developed by Acad. S.S. Schwartz (et al.), as well as population-ecological and physiological methods for stress evaluation, which were developed by Acad. I.A. Shilov.

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INFLUENCE OF CITY IMPROVEMENT ON STRAY DOGS POPULATION DENSITY IN YAKUTSK

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With regard to stray dogs, two polar (very biased) points of view exist among people. On the one hand, part of human population consider stray dogs a clearly negative element of the urban environment, source of potential danger, polluting waste producer and source of noise. From this point of view, complete elimination of stray dogs would be the ideal solution. On the other hand, part of the population, including animal protection organizations, actively fight against cruelty towards stray dogs, prioritizing the moral and ethical aspect of the problem, considering primarily the interests of individual dogs. At the same time, the assessment on the population level does not exist, where they would evaluate both the role of stray dogs in in life urban ecosystems and urban social life. In both cases, the role of stray dogs is very high, since it is the largest, massive and significant mammal in the city.

Yakutsk is noted for the absence of clear industrial development zone as a whole, since existing industrial enterprises are located in different parts of the city interchanging with residential neighborhoods. Therefore, we counted dogs in a residential area, also considering buildings profile.

We used a modified selective method of counting in the test areas (SA Vereshchagin, Poyarkov AD Goryachev KS 1999; Chelintsev NG, 2000), located in two main types of urban environment (residential 1–2-storey buildings and residential multi-storied buildings). Fourteen sites in total were selected with a total area of 2,325 km^2. In each site, we counted tall visible dogs walking around the site three times. For the purpose of proper identification, we photographed each dog to be included in the database.

In general, for the period from 2011 to 2016 we found sharp fluctuations in the number and density of stray dogs' population, both in time and space. For the entire period, the mean count was 2907 individuals with the lowest in 2011 and peak in 2013 (5599 individuals). We also noted season dogs' count fluctuations. In summer, urban stray dogs disperse in the outskirts of the city and suburban arrays, resulting in lower counts; and in winter the number of dogs in the city increases. Higher rates of population density in winter are typical for 1–2 storied building neighborhoods, because of the presence of places that serve as shelters of poor modernization, which facilitates foraging.

Black & brown (52,6%) was the predominant type of color in stray dogs of Yakutsk. Medium-sized dogs (80,25%) dominated, which may be indicative of selection against very small and very large specimens.

In the city of Yakutsk, we found small proportion of sedentary individuals (38,2), while migrating and aliens showed 28,9 and 32,9% prevalence respectively. This is an indication of high mobility of local population, a high proportion of individuals moving from "possessory" category into the "neglected", and, perhaps, due to the high mortality rate. At the same time, residential quarters of 1–2-storey showed higher prevalence of sedentary individuals, whereas in the high-rise building neighborhoods we found more migrants and newcomers, indicating the dogs' population instability in this type of environment and indirectly confirms our view of being less favorable for the stray animals.

CHROMOSOME VARIABILITY IN RODENT POPULATIONS NEAR THE RANGE BOUNDARIES IN THE URALS

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Ecological-genetic studies at the boundaries of species ranges are crucial when estimating stability and adaptive potential of populations in the varying environmental conditions, and when clarifying the factors that determine the species distribution limits. We present the analysis of chromosomal variability in three widely distributed rodent species: common vole (*Microtus arvalis* obscurus), striped field mouse (*Apodemus agrarius*) and yellow-necked field mouse (*Sylvaemus flavicollis*). The study was done in the Urals. The boundaries of the ranges of these three species pass through the Ural region (northern boundary of *M. arvalis* obscurus and *A. agrarius* ranges pass through the Northern Urals; and eastern boundary of *S. flavicollis'* range is in the Middle Urals). In *M. arvalis* obscurus, we analyzed the presence of chromosome polymorphism in the fifth chromosome pair (subtelocentric or acrocentric variant, the former predominates all over the species range) and X-chromosome monosomy in females. In both mouse species the presence of additional chromosomes (B-chromosomes) in karyotype was estimated. In *A. agrarius* we also analyzed metacentric autosomes count, the number of which is 8 in the standard karyotype but varies from 6 to 10 chromosomes in single individuals in certain populations, and the morphology of four largest acrocentric autosomes, for which the cases of substitution by subtelocentric are known.

Karyological analysis of 567 *M. arvalis* obscurus from 16 localities along the south-north gradient up to the northern limit of the species distribution in the region showed no genetic specificity in peripheral populations. We identified no carriers of an acrocentric variant of the autosome 5, the frequency of which in general is low in the Uralian populations of *M. arvalis* obscurus. X-chromosome monosomy, which was found in one female from the northern localities, was also detected in other studied populations in the Urals.

In 180 *A. agrarius* from 12 localities in the Southern, Middle and Northern Urals, the considered types of chromosome variability were not detected. All individuals had normal karyotypes ($2n = 48$, $Nfa = 54$). A departure from standard karyotype was shown only in one male in the Southern Urals in the locality exposed to significant chronic radiation (zone of the East Urals Radioactive Trace from Kyshtym accident in 1957). Among 50 analyzed cells of this male, 2% had normal karyotype; 19% had 47 chromosomes (one of the acrocentrics was absent); and 79% of the cells had, along with 47 normal chromosomes, a morphologically modified one of very small size.

In 7 *A. flavicollis* from a population at the northeastern species distribution limit, B-chromosomes were not detected, although it is known that B-chromosomes are present in almost the entire species' range. However, taking into account that additional chromosomes frequency is very low in certain populations, small size sample does not allow excluding the presence of B-chromosomes (with low frequency) in the studied peripheral population.

Thus, our study of chromosome variability in three rodent species near the boundaries of the species ranges in the Urals demonstrated no cytogenetic differentiation of the peripheral populations. Presumably, the studied peripheral populations of *M. arvalis* obscurus, *A. agrarius* and *S. flavicollis* are not isolated from the core populations and live under environmental conditions, which are not ecologically marginal.

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COMPRABILITY OF LIZARD AGE DETERMINATION OF USING TRANSVERSE SHEAR AND LONGITUDINAL SECTION

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Absolute age determination is an essential requirement for modern research in reptile demography. Sceletochronological method is the one most widely used is based on growth stoppage lines calculation (agglutination lines – AL) in the bones. Two major technical ways to visualize and calculate AL in the bones exist to date: 1 – making transverse dyed shears (Smirina, 1989; Castanet, 1994); 2 – making thin light longitudinal sections with the consequent microscopy in polarized light (Kornilova et al, 1996). The latter requires less effort to prepare material, leading to higher productivity to in screening more samples. However, AL calculation using transverse shear is more reliable because it enables to visualize structure in more detail and assess bone tissue resorption.

Age determination using longitudinal section was validated on grass frog *Rana temporaria* (Kornilova et al, 1996), and tested in reptiles on nimble lizard *Lacerta agilis* ($n = 10$) with the consequent use for age determination of lacertide of the Southeast of Western Siberia (Bulakhova, 2004). Due to limited use of this method, its applicability is still questionable.

We studied a sample of viviparous lizard *Zootoca vivipara* ($n = 14$) from Chudnoe lake (Kuznetsk Alatau, 1170 MASL) from the collection of the department of animal zoology and ecology of Tomsk State University (N.F. Nekratov's expedition samples, 14–16.07.2001). Animal age in this sample was determined using longitudinal section of a hip earlier (Bulakhova, 2004). We also cut femurs on the opposite side from these samples, decalcified them and made transverse shears by spilling sample in paraffin using classic histologic methodology (Exbrayat, 2013). Transverse shears 10 mcm wide were dyed with Carrazi hematoxylin. Preparations were visualized with Axio Lab A1 microscope (Zeiss, Germany). Statistical analysis was done with Statistica 7.0 (StatSoft, USA).

We did not find any statistical difference ($\chi^2 = 3{,}86$; $df = 5$; $p > 0{,}05$) when comparing two methods of age determination using transverse shears and longitudinal section. In 7 cases out of 14 (50%) these two methods in age determination did not meet in consensus. The age of sexually mature females determined with transverse shears was at least 2–6 winters, at least 2–3 winters of males (our data), whereas when sections method was used, the age of both males and females was at least 2–4 winters (Bulakhova, 2004).

Age determined with shears and sections did not coincide for *R. temporaria* in only 18,2% cases ($n = 11$; Kornilova et al., 1996), in 30% for *L. agilis* ($n = 10$; Bulakhova, 2004), in 50% for *Z. vivipara* ($n = 14$). Longitudinal section microscopy biases the age estimation to 1–2 fewer winters. Besides, crumbling lizard thin bones are not good for section, since getting even section from them may be challenging (Smirina, 1989).

Thus, age estimation using bone longitudinal section is less applicable for modern lizards. When using sections for population-based age estimation, control group of animals should also be present to have their age determined with both techniques. This will, however, increase age determination precision in a limited way only.

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HISTOLOGIC ANALYSIS OF TAIL SKIN OF SIBERIAN SALAMANDER *SALAMANDRELLA KEYSERLINGII* (AMPHIBIA: CAUDATA, HYNOBIIDAE), IN WATRE AND GROUND CYCLES

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Most replies of temperate exhibit biphasic cycles, i.e. wintering and most activities occur on the ground, which is ground phase, whereas reproduction occurs in water bodies in spring and makes water phase. Environment change entails pronounced change of extremal morphological attributes. Siberian salamander *Salamandrella keyserlingii* is one of such reptiles. This species males exhibit greater seasonal variability. With this, most noticeable changes happen in the tail, which is an essential reproductive element (Kuranova, Yartsev, 2011). We studied histological attributes of male tail skin belonging to *S.keyserlingii* in water and ground phases in order to better understand tissue mechanisms underlying such changes.

We withdrew 4 specimens of water and ground morphological types of male tail skin from the collection of the department of vertebrae zoology and ecology in Tomsk State University. We used classical methods to make histological preparations (Exbrayat, 2013). Transverse shears of skin from the mid-tail were colored with pycrofuxin using Van-Gizone method and with modified azan. We used Axio Lab A1 microscope with AxioCam ERc 5s camera and ZEN 2012 software (Zeiss, Germany) to photograph preparations. Photos were used to measure epidermis surface (ES), compact dermal surface (CDS), granular gland surface (GrGS) and glandular gland surface (GlGS), emptiness surface (ES) and the total examined surface (TES). Based on these measurements, we calculated mellow dermal surface (MDS), corium surface (CS) and conjunctive tissue surface (CTS). All relative readings were derived, which we compared using Mann-Whitney test in Statistica 7.0 (StatSoft, USA).

Microscopic examination showed that the tail skin composition changed form the inferior part to the superior part of the tail. Histologic attributes of those were compared, and statistically significant difference were found in ES, CDS and CS in males of both water and ground phases ($p \leq 0,05$). Further comparison considered these changes.

Upper segments of male tail skin of water and ground morphological types differed in ES, CDS and CS ($p \leq 0,05$), whereas lower segments differed in all attributes ($p \leq 0,05$), GlGS. Our findings may generally highlight the following trends: 1 – in water phase males epidermis in general and conjunctive tissue are greater compared to ground phase males there, 2 – in ground phase males, granular glands are larger, therefore corium was also larger. When entering water body, much water enters through the skin and then consumed by the intercellular space of the conjunctive tissue, leading to its volume increase and “swallowing”. When males exist the water body and ground morphological type is formed, conjunctive tissue shrinks without water. Epidermis volume also decreases due to partial cornification and upper layers consolidation. Granular gland increase, because some part of them produces protective mucosa toxic components.

Similar findings when studying back skin of *Hynobius nigrescens* of water and ground morphological types (Hasumi, Iwasawa, 1992) were reported, as well as when comparing histologic attributes of *Batrachuperus pinchonii* always residing in water and *H. chinensis* exposed to water only for reproduction (Xiong et al., 2013).

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DOGS’ POPULATION STRUCTURE AND BEHAVIOR IN MOSCOW METRO

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Moscow Metro is a complex engineering structure, which includes transport routes, compositions, stations, underground passages in close proximity with the exit. These structures also serve a temporary or permanent shelter for animals, including dogs. In what way and to what extent the number of dogs in Moscow subway should be controlled remains questionable. What role underground plays in dogs’ lives, as well as how it influences their behavior and what for reason dogs use is an area open for discussion.

To study the structure of stray dogs’ population, we chose six lines of the Moscow Metro including Sokolnicheskaya, Kalininskaya, Arbatsko-Pokrovskaya, Filyevskaya, Zamoskvoretskaya and Kaluzhsko-Rizhskaya, 102 stations in total. We examined stations, lobbies, exits and territory close to entrances (5 to 30 meters around the entrance).

We chose “Yugo-Zapadnaya” station of Sokolnicheskaya line for a detailed study. This station has construction sites, shops, and cafes on its territory. We used tracking methods, audio and video recording along with photographs (Poyarkov, 1991). First, we carefully checked the dogs presence on the platform, then we examined the lobby with the territory around the entrance. We used notebook or tape recorder, and then all that information was tabulated. In case no dogs were found, we interviewed the staff. Tables were analyzed using Microsoft Excel. Time was tracked with minute intervals, and we used Statistica 6.0 for the analysis.

Conclusions

1. In Moscow metro, male stray dogs prevail over female stray dogs with a ratio of 3:1. This was typical both for the experimental stray dogs group at “Yugo-Zapadnaya” station, and all the studied underground lines. There were predominantly adults in the stray dogs’ population of Moscow Metro with very few puppies and old individuals. The groups of Moscow metro dogs mainly consisted of random individuals (70%).
2. Kolcevaya Line stations had five times fewer stray dogs compared to other lines. The mean number of dogs per station within the Kolcevaya Line was 0,84 individuals, being 2 individuals per station outside this line.
3. Sleep was predominant behavioral of stray dogs in Moscow Metro (45%), regardless of the time of the day. The least activity was observed in the morning (17%), which increased closer to the afternoon (33%), reaching its maximum in the evening, which corresponded to the overall human activity profile in the city. Begging (63%) was the predominant way to get access to food for Moscow metro dogs, followed by gathering (33%), and sometimes even hunting (4%).
4. Most of the time (87%) stray dogs spend on the territory close to the underground facilities and use them as shelter from unfavorable environmental conditions. Most often stray dogs stay indoors in the evening.

CONTEMPORARY SPECIES COMPOSITION AND PREVALENCE OF MOUSE-EARED BAT (*MYOTIS*, CHIROPTERA) OF ALTAI AND SAYAN MOUNTAINOUS REGION AND SOUTHERN URALS BASED ON GENETIC ANALYSES

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Molecular and genetic studies in the last few decades introduced significant changes into classification of *Chiroptera* Blumenbach, 1779. Phylogenetic relationships of various taxa were clarified and many cryptic species were found. Yet, a number of questions remain, especially related to species distribution. Due to lacking material from various territories our knowledge on occurrences and co-ocurrences of bat species is still rather patchy. This holds true especially for mouse-eared bats of the genus *Myotis* Kaup, 1829 of Siberia and Southern Urals, which make up the core of these regions Chiroptera fauna and include a number of cryptic species. Precise distribution ranges of Eastern mouse-eared bats: *M. petax, M. sibiricus* and *M. davidii* remain unclear, which were separated from *M. doubentonii, M. brandtii* and *M. mystacinus,* respecitvely (Benda, Tsytsulina, 2000; Kruskop et al., 2012; Matveev et al., 2005).

We collected 34 samples (skintissue from the tail) of mouse-eared bats in the Northern and central Altay and Sayan mountainous regions as well as 23 samples in Southern Urals. In addition we retrieved nucleotide sequences of various Siberian mouse-eared bats from GenBank (http://www.ncbi.nlm.nih.gov) for comparison. DNA isolation was performed using the DNeasy® Blood & Tissue Kit (250) (QIAGEN) following the manufacturer´s protocol. The mitochondrial *ND1* gene was used as a genetic marker. PCR was performed with primers L2985 (5'-CCT CGA TGT TGG ATC AGG-3') and H4419 (5'-GTA TGG GCC CGA TAG CTT-3'). Sequencing of the PCR products was performed by «Sintol» company (Moscow). Sequences were edited in BioEdit v.7.2. (Hall, 1999) and phylogenetic trees were reconstructed using Neigbour Joining (NJ), Maximum Parsimony (MP) and Maximum Likelihood (ML) methods. The TN93 model was selected as the optimal mutation model, according to the Bayes criterion (BCI) (Tamura et al., 2013)

Our data verified the occurrence of *M. petax*, *M. ikonnikovi*, *M. sibiricus*, *M. blythii* and *M. asycneme* in the Altay and Sayan mountains. Thus, the known distribution range of *M. sibiricus* was expanded to the west towards the Northern and central parts of Altay and Sayan mountains. *M. sibiricus* and *M. gracilis* proved to be not differentiated in the *ND1* sequences. Similar results were obtained by Kruskop et al. (2012) based on the mitochondrial *cytochrome b* (*cyt b*) gene.

Phylogenetically, *M. blythii* is of great interest from Altay, where its limited population was found (Strelkov, 1972). It was proposed earlier to treat animals from this territory as a separate species (Dzeverin, Strelkov, 2008). Molecular and genetic analysis based on *cyt b* sequences (Kruskop et al., 2012) showed remarkable (4,27%) intraspecific differences in animals from the Caucasus, Central Asia and Altay. Our data are in concordance with this finding as the animals from Altay analysed in the present study are close to individuals from Kyrgyzstan (p distance 2,1%), contrasting with animals from other locations from Europe, Caucasus taken from GenBank (p distance >5%).

M. daubentonii, *M. dasycneme*, *M. mystacinus* and *M. davidii* were identified in the Southern Urals. The detection of *M. davidii* in the Bolshoy Kizil river is the first report of the species in the Southern Urals, which expands the known northern limit of the distribution range at this geographic longitude (Tsytsulina et al., 2012) by up to 500-600 km.

Thus, this study refined the knowledge on distribution ranges of some mouse-eared bats species. The areal of *M. petax, M. daubentonii*, and *M. sibiricus* with *M. brandtii,* however, remain unclear.

THE ADAPTATION OF PARTI-COLORED BAT *VESPERTILIO MURINUS* L., 1758 (CHIROPTERA, VESPERTILIONIDAE) TO HABITATION IN THE URBAN ENVIRONMENT

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The intense environment urbanization and its man-made pollution forces animals to adapt to such changing environment. Not all species do possess mechanisms to react and adapt to changing environment. One of such species is parti-colored bat which demonstrates the features of synanthropic species all over (Botvinkin, 2001; Ilyin et al. 2003; Starikov et al., 2009; Marnell, Presetnic, 2011). Most probably, its synanthropisation succession is explained by an extended twilight and nighttime activity, wide food availability, as well as high reproductive capacity to produce offspring of 4 pups a year. To what extent should urban environment foster its reproductive potential, which in turn sustains this species existence?

This report is based on the findings from the four *V. murinus* colonies investigation. Two of these were located in the central part of the settlements (city of Tomsk and Shushenskoe village), and the remaining two existed in the suburban areas (Kolarovo village in Tomsk Province and the city of Novosibirsk). There were 2,9 and 2,7 pups per adult female in Tomsk and Chushensk colonies respectfully. Similar indicator in suburban colonies was 1,8. Other investigators (Strelkov, Ilyin, 1990; Snitko, 2001; Pervushina et al.., 2005, Starikov et al., 2009) noted similar productivity patterns of this species outside settlements in the European part of Russia and Western Syberia.

Our data stipulate there exist specific conditions in the urban environment which may impact parti-colored bat’s fertility. Those may be micro- and mesoclimatic conditions. It was demonstrated in various Chiroptera species that higher ambient temperatures in the city and dwellings around them with heat islands can help save energy to keep body temperature stable in regnant females (Racey, 1973; Racey, Swift, 1981); keep them from transiting to anabiosis (Lausen, Barclay, 2006); can help keep pup’s body temperature stable (Hollis, 2004) thus resulting in better survival; and stimulate lactation in females (Wilde et al., 1995). Artificial light retaining insects in certain locations can help save Chiroptera’s energy to procure food, resulting in more pups having access to food. Maximal chemical and noise pollution, on opposite, limits access of bats to food procurement, and suppresses their nighttime activity (Bunkley et al., 2015). We could not find perished animals in Tomsk and Shushenskoe colonies, which contrasted with a few deceased animals in Novosibirsk and Kolarovo colonies.

Thus, urban environment raises the reproduction potential of Chiroptera compared to suburban. This may be related to a reduced energy expenditure for food procurement and keeping stable body temperature with a trade-off for energy saved to reproduction.

AGGREGATION AND OVERLAPPING OF RODENTS’ SITES UNDER ANTHROPOGENIC DESTURBANCES

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Our aim was to estimate the association between the index and density on the disturbed territories. We used Blackman’s aggregation index (1942) for calculations. To assess changes within the aggregations, we evaluated the index of overlapping sites and the relationship between the overlapping sites index and the aggregation.

For bank voles, linear dependence between the index and density amplified due to the heterogeneous landscapes increase. Moreover, these populations became denser.

With regard to the Ural field mice, the association of the index with density on the disturbed territories was weaker. This was because forest disturbed areas became more homogeneous for this species and this species overcame anthropogenic pressure more successfully. The settlements, however, became less populated and the sites got more isolated.

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