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The Quaternary of the Urals: Global trends and Pan-European Quaternary records

Четвертичный период Урала: глобальные тенденции и их отражение в общеевропейской четвертичной летописи

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THE QUATERNARY OF THE URALS: global trends and Pan-European Quaternary records

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Ч52 **Четвертичный период Урала: глобальные тенденции и их отражение в общеевропейской четвертичной летописи :** материалы международной конференции INQUA-SEQS (Екатеринбург, Россия, 10–16 сентября 2014 г.). – Екатеринбург : УрФУ, 2014. – 228 с.
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В книге представлены материалы международной конференции INQUA-SEQS 2014, проводившейся в Екатеринбурге (Россия). Сообщения касаются широкого спектра вопросов, связанных с исследованиями четвертичного периода (2,6 млн лет) в Европе и Азии. На основании результатов локальных и региональных исследований авторы рассматривают проблемы стратиграфии и корреляции четвертичных отложений Уральского региона и Европы и обсуждают вопросы интеграции общеевропейских и евразийских стратиграфических схем. Особое внимание уделено вопросам палеонтологии, палеоклимата и палеосреды четвертичного периода Европы и Азии.

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The Quaternary of the Urals: global trends and Pan-European Quaternary records : International conference INQUA-SEQS 2014 (Ekaterinburg, Russia, September 10–16, 2014). – Ekaterinburg, 2014. – 228 p.
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The book presents the proceedings of the International Conference INQUA-SEQS 2014 held in Ekaterinburg, Russia. Reports concern a wide spectrum of issues connected to the study of the Quaternary Epoch (2.6 Ma) in Europe and Asia. Based on the results of local and regional Quaternary studies the authors focus on Quaternary stratigraphy and correlations across the Ural region and Europe and discuss the integration of pan-European and pan-Eurasian stratigraphical frameworks. The special attention is given to palaeontological, palaeoclimatological and palaeoenvironmental issues from the Quaternary of Europe and Asia.

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Thus, introduction in the GSC structure for the Quaternary of one new unit — subdivision will ensure compliance with the ISC units for the Quaternary system, which is important when working under international programs and in compilation of international general maps.

The questions raised have to find their answers in the near future because this is due to the pressing needs of geological and cartographic production.

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EVOLUTIONARY PATTERNS IN THE DENTITION OF ARVICOLINAE (CRICETIDAE, RODENTIA)

Key words: arvicoline rodents, teeth, phylogeny, ontogeny

Original and previously published data on dental variation in living and extinct arvicoline rodents are summarized.

Fossil record is the only source of evidence for the reality of macroevolution. At different sequential time slices there could be found the taxa, which represent the sequential steps in the formation of trait combinations inherent to the terminal taxa. Thus, we know the emergence time and sequence for particular traits and their combinations on a paleontological timescale. On the other hand, for a particular representative of a taxon (i.e., for an individual) the combination of traits is determined by preceding evolutionary stage and is formed during ontogenesis; particular traits (and/or their groups) develop non-simultaneously.

For the first time in arvicolines, the ontogenetic background of evolutionary changes in the lower incisor development and position in the mandible is revealed. Lingual position of the lower incisor relative to the tooth row in *Lemmini* and *Dictostonichini*, which distinguishes them from other arvicilines, could be regarded as a mere parallelism. Differences in the position and extent of development of incisors and lower third molars (m3) between voles and lemmings are determined by the advanced development of the m3 alveolus in *Lemmini* and *Dictostonichini*, which sets the direction for development of the incisor's alveolus along the tooth row, whereas advanced growth of incisor in

voles precedes the development of m3 and causes the lingual development of m3 alveolus.

Development of a hypselodont tooth (roots are not formed) could be considered as a result of retardation at one of the stages of crown development (Fig. 1). Occlusal outline and shape depend significantly on the ontogenetic stage, at which this retardation starts (in upper, middle or lower portion of the crown). For example, the simplification of occlusal surface of teeth in mole voles (*Ellobius*) could be regarded as the development of a hypselodont tooth pattern, which may have resulted from the retardation of lower (basal) portion of the tooth crown.

Complication of the occlusal outline could be achieved by addition of either a new module of a crown or a new element of the same module.

An analysis of relationships between cement distribution and formation of dentin tracts in different arvicoline lineages achieving hypselodonty suggests that both cement buttresses in re-entrant angles and dentin tracts are formed at rhizodont stage of the phylogeny. Neither cement in re-entrants nor dentine tracts could be developed after the phylogenetic transition to a hypselodont tooth pattern (when the development of roots is excluded from the ontogeny).

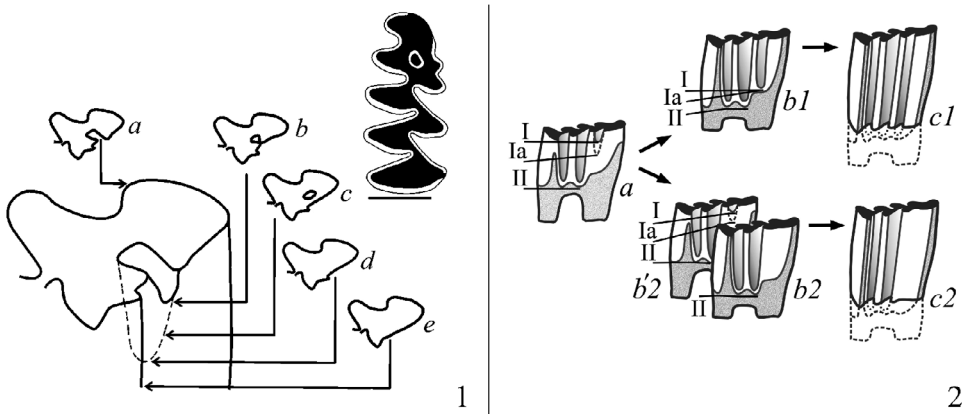

Fig. 1. A scheme of outline changes in the anteroconid portion of the first lower tooth related to the crown wear stage in *Mimomys* vole (1) and different pathways underlying the development of a hypselodont tooth in arvicolines (2), which are related to the early (*b1-c1*) or the late (*b'2-c2*) stages of crown development.

1 — The lines represent the levels of the cross-sections (stages of wear): a — the enamel fold is not closed in the islet; b-c — the stages at which the enamel islet is closed; d — the islet is worn out but the *Mimomys* fold still persists; e — "secondary simplified" anteroconid: no enamel fold and no islet is present; 2 — I — the stage of the islet closing, Ia — the stage of the islet wear, II — the lower border of the crown; *a→b1→c1* — the pathway towards hypselodonty accompanied by the complication of occlusal surface, *a→b2→c2* — the pathway towards hypselodonty accompanied by the simplification of occlusal surface; dashed line — the stages of tooth development excluded during phylogeny from the tooth ontogenesis

Based on the analysis of ontogenetic and phylogenetic pathways from a brachiodot to a hyspelodont tooth, the system of rules and constraints might be established as follows:

– Increasing hypsodonty is the one-way process with no possibility to retrieve the excluded morphogenetic stage of root development, but the occlusal surface may undergo secondary simplifications at the rhizodont stage;

– Presence of cement in re-entrant angles along with the number and position of dentin tracts is defined at the rhizodont stage and could not be changed after the transition to hypselodonty;

– Complexity of the occlusal surface could be related with the enamel folding within the same ontogenetic module of a tooth or it could be determined by the number of ontogenetic modules;

– New ontogenetic module might be developed as an additional element of the already existing tooth.

Combination of patterns underlying the formation of structural and histological elements of a tooth determines the scenario of dental evolution within the arvicoline tribes and within the particular phyletic lineages. The scenarios might be divided into the general for a subfamily (common traits for all arvicolines, which might be differently expressed in particular lineages and species) and specific scenarios inferred for a particular lineage or taxa. The former reflect the evolutionary constraints and the latter reflect the phylogenetically driven interconnections in tooth development.

Lemmini and *Dicrostonichiny* are the examples of the earliest transition to the hypsodonty and hypselodonty, which distinguishes them from other arvicolines and dates their origin back to the Pliocene. However, they show extremely different patterns of complication of the dentition, of enamel differentiation, and cement distribution. Another unique combination of traits related to hypsodonty and occlusal complexity is the tribe *Clethrionomyini*, which also differs from other arvicolines by the age of its origin. If we accept that the ancestor for all the other lineages is the genus *Promimomys* (no cement, relatively low crowns), then the two groups should be established including *Lagurini* and *Ellobius* (no cement in re-entrant angles) and *Arvicola* and *Microtus* (cement is present in re-entrant angles). Classification of arvicolines based on the scenarios of dental evolution shows similar topology with the classifications based on molecular markers.

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GENETIC VARIABILITY OF BURBOT, *LOTA LOTA*, AND THE CONNECTION OF THE MAIN HOLARCTIC RIVER BASINS IN THE QUATERNARY

Key words: Lota lota, mtDNA control region, climate change, Ob River, Irtysh River

Climatic oscillations during the Pleistocene ice ages affected species' geographical distribution and abundance, which could be expected to have genetic consequences (Hewitt, 2004). Burbot (Lota lota, Linneus, 1758), the Holarctic freshwater gadoid, was restricted within glacial refugia peripheral to the ice sheets and depended on aquatic habitats during post-glacial dispersal, and, therefore, serves as an excellent model to study the impact of glaciations. The distribution of burbot mitochondrial haplotypes, revealed in previous studies, suggests that Western Siberia most likely was a transit region, through which burbot could spread from Europe to Siberia during the post-glacial period (Van Houdt et al., 2005). Previously, it was suggested that the distribution of burbot in Siberian rivers began after the Dneprovsk glaciation dated to 300,000–250,000 BP (Svetovidov, 1948; Tyulpanov, 1967). Indeed, paleontological data points to the importance of Western Siberia as one of the key regions in the formation of Eurasian biota during the Quaternary period (Borodin et al., 2001; Borodin et al., 2013). Importantly, the finding of burbot ancient bones at Chembackchino-94A (lower reach of Irtysh River, TL age — 650,000±110,000 years) (Borodin et al., 1998) is one of the oldest findings ever made in Eurasia. This therefore indicates that the Ob-Irtysh River basin could play much more important role in the formation of Lota biodiversity compared to the mere extrapolation of genetic data, obtained for the localities in Eurasia and North America.

The objective of the present study was to determine the diversity of the non-coding mtDNA control region among burbot populations inhabiting Western Siberia.

The left half of the mtDNA control region was sequenced for 116 burbot samples from several localities of the Ob-Irtysh River basin including the Irtysh River at Tobolsk, Severnaya Sosva, Voykar, Sob, Khodyta (tributaries of the Ob River), the Taz River and the Ob River at Karantinskiy island. Sequencing has revealed that the mtDNA control region is highly variable in this species. Indeed,

28 haplotypes were observed in the 116 individuals analyzed. Fig. 1 represents median joining network covering burbot control region haplotypes from two lineages, L. l. lota and L. l. maculosa, together with sequences, derived from the Western Siberian localities. Most of the control region haplotypes, revealed in the Ob-Irtysh River basin, fall into Eurasian and Beringian haplogroups. Our data show that 78 out of 116 control region sequences represent haplotypes, revealed earlier, such as EB30, EB35, EB43, EB44 and EB41 (Van Houdt et al., 2005). Not surprisingly, the majority of samples belong to the EB30 haplotype (55 samples), which is one of the central Eurasian haplotypes and the habitat of which covers not only European (the Isar, the Vistula), but also Asian (the Lena) rivers, as well as Lake Baikal. The ratio of this haplotype is 47%. Besides, 11 samples have Beringian haplotype EB41, which is found in the Kurenjoki and Porkkala Bay in Finland. This haplotype, also named as Xi1, was observed in large quantities in the Irtysh River in the North-Western China (Fang et al., 2013). 21 new haplotypes from the Ob-Irtysh River basin were named as WS 1–21 (Western Siberian). Among 21 new haplotypes, WS1, is the most widely distributed and was found in samples from the Sob River (3 sequences) and the Irtysh River at Tobolsk (4 sequences). This haplotype, together with its derivative haplotypes, WS2, WS3 and WS21, form a separate haplogroup. 17 sequences demonstrated singular haplotypes. The distribution of separate haplogroups coincides with major river basins (Fig. A5, Appendix 4). It is best shown for the haplotypes from the Mississippi, Missouri and Amur. However, also in Eurasia and Alaska a group of haplotypes are specifically found only in separate river basins, which reflects the Quaternary history of the species.

Our data indicate that studies on burbot phylogeography are incomplete and require further research, focused on genetic analyses of burbot inhabiting central part of Eurasia, in particular the Western Siberian Plain and the Eastern European Plain.

REFERENCES

Hewitt, G.M. Genetic consequences of climatic oscillations in the Quaternary // Philosophical Transactions of the Royal Society B-Biological Sciences. Vol. 359. P.183–195. 2004.

Van Houdt J.K.J., De Cleyn L., Perretti A., Volckaert F.A.M. A mitogenic view on the evolutionary history of the Holarctic freshwater gadoid, burbot (Lota lota) // Molecular Ecology. Vol. 14. P. 2445–2457. 2005.

Svetovidov A.N. The gadoid species. // Fauna of the USSR. Fishes. Volume IX. Issue № 4. Academy of Sciences of the USSR. 221 p. 1948.

Tyulpanov M.A. The history of burbot distribution within freshwater bodies // Problems of Ecology. Tomsk. P. 185–196. 1967.

Borodin, A.V., Strukova, T.V., Trofimova, S.S., Zinoviev, E.V. // The World of Elephants: Proc. of the 1st Intern. Congr. Roma. P. 267–271. 2001.

Borodin A.V., Markova E.A., Zinovyev E.V., Strukova T.V., Fominykh M.A., Zykov S.V. // Quaternary International. V. 284. P. 132–150. 2013.

Borodin A., Kosintsev P., Zinoviev E., Trofimova S., Nekrasov A. // Mededelingen Nederlands Instituut vor Toegepaste Geowetenschappen. № 60. P. 353–374. 1998.

Fang H., Zhang J., Song N., Qian L., Gao T. // Russian Journal of Genetics. V. 49. № 10. P. 1047–1056. 2013.

with small mammal materials can help with the distinguishing of the age of the localities. The morphological diversity of *Allophaiomys* teeth which widely used by Western and Eastern European palaeontologists is very important. However sometimes the localities with very few remains of this species compared against each others what could be resulted in wrong conclusions.

Analysis of Early — Middle Pleistocene small mammal remains, particularly Arvicolinae, gives the unique material, which helps to elucidate the evolution in different phylogenetic lineages, to date the deposits which includes the bone localities (what is very important to this interval for which practically unknown absolute dates), to compare the faunas from the different region of Europe and also to help to reconstruct the paleoenvironments.

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SMALL MAMMALS AS INDIRECT BIOTIC MARKERS FOR CLIMATE DYNAMICS ASSESSMENT IN THE CENTRAL PART OF NORTHERN EURASIA

Key words: Micromammals, palaeoecology, Late Pleistocene, Holocene

We summarize the clues which the micromammal fossil record offers to climate-driven biotic shifts in the central part of northern Eurasia during the Late Pleistocene — Holocene and give some results of neontological studies aimed to increase the quality of palaeoecological reconstructions based on small mammals. Spatial and temporal dynamics of environmental conditions in the central part of northern Eurasia from the Late Pleistocene to the present day is considered on the basis of the analysis of micromammal assemblages from about 60 cave sites in the Polar, Northern, Middle and Southern Urals (see Borodin et al., 2013 for the list of localities). Comparisons to the present-day fauna are made using the zoological specimen database (museum of the Institute of Plant and Animal Ecology UrB RAS). In this study we primarily focus on arvicoline rodents because of their wide distribution, high abundance and the most complete fossil record in the study area (as compared to other micromammal groups).

During the time span chosen for analysis the arvicoline fauna of the study area has been represented by living species. To establish ecological groups of arvicolines (17 species known in the study area from the Late Pleistocene to the present day) we undertake an analysis of ecological requirements across the species' ranges (thermoneutral temperature intervals, dietary adaptations, and habitat requirements for nesting, breeding, survival and dispersal — based on published data) and compare the results to the existing classifications of arvicolines used for palaeoecological purposes. Physiological data suggest that intraspecific variability of thermoneutral zones, effectiveness of thermoregulatory mechanisms and similarity of critical temperatures among the arvicoline species make it not possible to use temperature features for palaeoecological inferences. Ecological data suggest that across the modern ranges the most stable (conservative) requirements of arvicolines are the characteristics of nesting and breeding microhabitats, which could be described in terms of humidity and vegetative cover. For some species, dietary adaptations might be used to specify the vegetative cover (when a particular plant group is known to limit the distribution or seasonal survival of a species). The 17 arvicoline species might be considered as indicators of 10 types of microhabitat, which differ by humidity, openness and vegetative cover (Fig. A8, Appendix 7).

To reveal the spatio-temporal variability of the microhabitat conditions in the Southerm, Middle, Northern and Polar Urals we calculate the occurrence of the microhabitat groups of arvicolines in the fossil datasets (divided into the Early, Middle and Late Holocene subsets) and in the modern dataset represented by the live trapping data for the last 50 years (about 350 capture locations). Only presence-absence data are used for analysis; relative frequencies and repeated sampling data are excluded from consideration to avoid biases related to sampling effort.

The figure shows that in the Urals from the Early Holocene to the present the proportion of mesophyte habitats (the species of both open (groups 4–5) and closed habitats with arboreal vegetation (groups 6–7)) has significantly increased. The proportion of species related to open wet habitats (group 1) shows a slight increase towards the present day, whereas the proportion of the inhabitants of open xeric habitats (groups 8–10) has drastically decreased. The figure also illustrates a steep decline in the abundance of the species related to moss-cover (group 3).

The results presented here confirm that arvicoline rodents may serve as indirect markers of climate-driven biotic shifts in time and space and clarify the biotic parameters, which might be reconstructed based on the ecological requirements of the modern species. Novelty of the approach is determined by setting the classification criteria narrower than usual. Biome affinities (e.g. 'tundra species', 'steppe species') and direct interpretations of the preferred climatic variables (e.g. 'cold-loving species') are excluded from the classification in favor of the direct microhabitat characteristics related to a combination of

humidity and vegetative land cover, which limits the present-day distribution or survival of a particular species.

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REFERENCES

Borodin A., Markova E., Zinovyev E., Strukova T., Fominykh M., Zykov S.V., 2013. Quaternary rodent and insect faunas of the Urals and Western Siberia: connection between Europe and Asia. Quaternary International. Vol. 284. P. 132–150.

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STRATIGRAPHY OF THE LAST PLEISTOCENE GLACIAL PERIOD IN POLAND

Key words: Weichselian, climate, ice wedges, Glacial episodes, loess, Poland

Interpretation of climate change during the last glacial stage of Late Pleistocene in Poland has been mostly focused on glacial/periglacial phases and intervening warmer episodes (interstadials) indicated mostly by fluvial deposits or rarely, by biogenic sediments. Much less climatic information has been known for the most severe episodes of Early and Middle Vistulian (Weichselian) in a non-glacial area. It has not been until recently when this information gap started to be partly filled up with substantial data. In general, the last glacial stage in Poland has been traditionally subdivided into two cold intervals (Lower and Upper Plenivistulian, roughly corresponding to MIS 4 and 2), preceded by Early Vistulian (MIS 5d-a) and separated by Interplenivistulian (MIS 3), the last one characteristic for its milder but instable climatic conditions.

The most complete sequence of deposits of the last glacial stage is best known from the Lower Vistula valley region that is a type area of the Weichselian in Europe. In this region the Eemian marine deposits (MIS 5e) are overlain by 4–5 tills that have been ascribed to different glacial phases within the last cold period. Based on recent investigations most widespread of these glacial episodes were correlated with Late Weichselian Glaciation, comprising Leszno (Brandenburg), Poznań (Frankfurt) and Pomeranian ice sheet advances and dated at 24, 20 and 16 ka BP respectively (Marks, 2012). They were preceded by

the sites of the same age on the border of modern forest-steppe and steppe and coniferous subtaiga where similar regularities were pronounced.

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FOSSIL FINDS AND MOLECULAR PHYLOGEOGRAPHY OF THE SIBERIAN FLYING SQUIRREL (*PTEROMYS VOLANS* L., 1758)

Key words: Holocene, Late Pleistocene, mtDNA, phylogeography, Pteromys volans, fossils

The presence of species with well-defined ecological characteristics in fossil assemblages is widely used as an indicator for indirect verification of the Quaternary paleoenvironmental and paleogeographic reconstructions. One of such indicator species is Siberian flying squirrel (*Pteromys volans* L., 1758), which inhabits spruce-dominated boreal forests throughout the whole coniferous forest zone of Eurasia from Finland and the Baltic Sea to the Eastern Siberia and Korean Peninsula, Sakhalin Island and Hokkaido Island (Nowak, 1999). The data on origin of modern *P. volans* and on its expansion in coniferous forest zone of Eurasia are scarce.

Remains of *P. volans* in paleontological materials, as a rule, are not numerous, which is determined by ecological characteristics of the species. Finds of *P. volans* greatly vary in age. Appearance of flying squirrels on considerable territory (Belarus, the Urals, Western Siberia, Yakutia) is associated with time of formation of the modern coniferous forest zone in the second part of the Holocene, which was confirmed by ^{14}C dating (Kosincev, Bachura, 2013; Yakovlev et al., 2005; Smirnov, 1994; Boeskorov, 2005). Known finds of *Pteromys* in Far East and in Pre-Baikal region are older: 30–24 kyr ago and 13.8–14.2 kyr ago (Panasenko, Tiunov, 2010), as well as 33 kyr ago (Ovodov, 2003). Remains of *P. volans* in Late Pleistocene sediments were found together with those of the species, which disappeared from this territory in the Holocene. The most ancient finds of flying squirrel are known from Altai caves, which are famous due to the finds of Denisova hominin: from 24 to 34.5 kyr, layer 2 in Logovo Gieny

Cave (Chikisheva et al., 2007); 29200±36 — 50000±12000, 69000±17000; 171000–282000 layers 11, 14.2, 19.1, 22 in Denisova Cave (Derevyanko et al., 2003). Even if we exclude the oldest radiothermoluminescent dates obtained for the layers 14 and 22 due to their uncertainty (http://antropogenez.ru/location/240/), the age of the finds exceeds 40 kyr.

Development of molecular-genetic methods has promoted the phylogeographic approach for reconstruction of species history and for exploration of population differentiation (Oshida et al., 2000, 2005; Lee et al., 2008). However, until recently no molecular-genetic data on *P. volans* from significant territory of the central part of the species range (the Urals and Western Siberia) were available for analysis of the species' phylogeographic structure.

We identified 4 haplotypes (cyt b) of *P. volans* in the Middle Urals (on the western mountainside and two localities on the eastern mountainside) and compared the existing phylogeographic data, including our own materials, with the paleontological data on the distribution of this species.

Haplotypes of *P. volans* from the Middle Urals fit into Northwestern Eurasia subclade of Northern Eurasia clade (Oshida et al., 2000, 2005). Obtained results are in agreement with the latest phylogeographic inferences on *P. volans* (Lee et al., 2008): the center of species origin was in Southeastern Asia (high genotypic diversity of *P. volans* in this region and the presence of haplotypes of nearly all phylogroups). The Hokkaido clade is well differentiated that might be a result of the earlier isolation of the island population. The divergence within Northern Eurasia clade took place later. Finally, Northwestern Eurasia subclade diverged in a short time to spread out over the large territory from the Baikal Lake to the western boundary of the present day species range.

According to paleontological and molecular-genetic data, the common tendencies of higher haplotype diversity and the earliest dating of the fossil finds of *P. volans* near the hypothesized center of species origin (Southeastern Asia and Far East) could be revealed. However, the age of the earliest fossil remains of flying squirrels found in Altai contradicts the age of the Altai population of the flying squirrel inferred from the molecular data. Modern *P. volans* in Altai and in the Urals belong to the same subclade, Nothwestern Eurasia, which is genetically homogeneous and is supposed to be the youngest one. This contradiction is possibly concerned with the absence of genetic succession between modern *P. volans* and *Pteromys* found in the Pleistocene faunas of Altai and Baikal region. The obtained results suggest that there were several waves of expansion of *P. volans* in Northern Eurasia. Modern species range (at least in its western part) is a result of the last wave of expansion and was formed in a single moment on a geological time scale (during the last 6 kyr). If this suggestion is confirmed, the presence of *P. volans* in the fossil assemblages of some geological periods in Altai, Baikal region and Far East might be considered as an indicator of the faunal exchange between these territories and the Southeastern Asia. Future investigations in this area of research are important for inferring environmental

circumstances, faunal interrelations and early human migrations among the regions of Asia and within the Northern Eurasia, and also for verifying the hypothesis of migration of Denisova hominins from Southeastern Asia to Altai.

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THE MAIN MATTERS OF STRATIFICATION FOR LOWER VOLGA NEOPLEISTOCENE, RUSSIAN FEDERATION

Key words: Pleistocene, Lower Volga, stratigraphy

The study area is located in the south-east margin of the Russian Platform. Sea basins, existed within the territory of present-day Caspian Sea, had been developing for Cenozoic in a transgressive-regressive regime there.

The Lower Volga Neopleistocene sections have been attracting geologists' attention for 100 years. They are easily accessible, well exposed along 350 km and contain fossils of large and small mammals, amphibians, molluscans, seeds and palynoflora, with isotopic and paleomagnetic data.

The sections were studied by a number of researchers (Pravoslavlev, 1903–1939; Zhukov, 1945; Gromov, 1935; Grichuk, 1952–1954; Fedorov, 1957, 1978; Vasilyev, 1961; Moskvitin, 1962; Goretsky, 1966; Shkatova, 1973; Sedaykin, 1988; Schepetnov, 1989; Svitoch and Yanina, 1975–2009). Over the last years the sequences exposed there were correlated with isotope-oxygen stages (Shkatova, 2006; Yanina, 2009).

At the present time FGUP "VSEGEI" carries out geological mapping works of 1:200 000 scale within L-38-XI, XII map sheet where these classic Neopleistocene sections are situated. It is worth noting the stratigraphic scheme of Quaternary successions of Lover Volga Region was established by the Interdepartmental Stratigraphic Committee (ISC) of USSR in 1980's, thus, there is necessity in making upgraded stratigraphic basis for improving of geological certainty and quality of Quaternary deposits maps.

APPENDICES
(COLOR FIGURES)

ПРИЛОЖЕНИЯ
(ИЛЛЮСТРАЦИИ В ЦВЕТЕ)

GENETIC VARIABILITY OF BURBOT, *LOTA LOTA*, AND THE CONNECTION OF THE MAIN HOLARCTIC RIVER BASINS IN THE QUATERNARY

Y.Y. Khrunyk, A.R. Koporikov, V.D. Bogdanov, A.V. Borodin (p. 51)

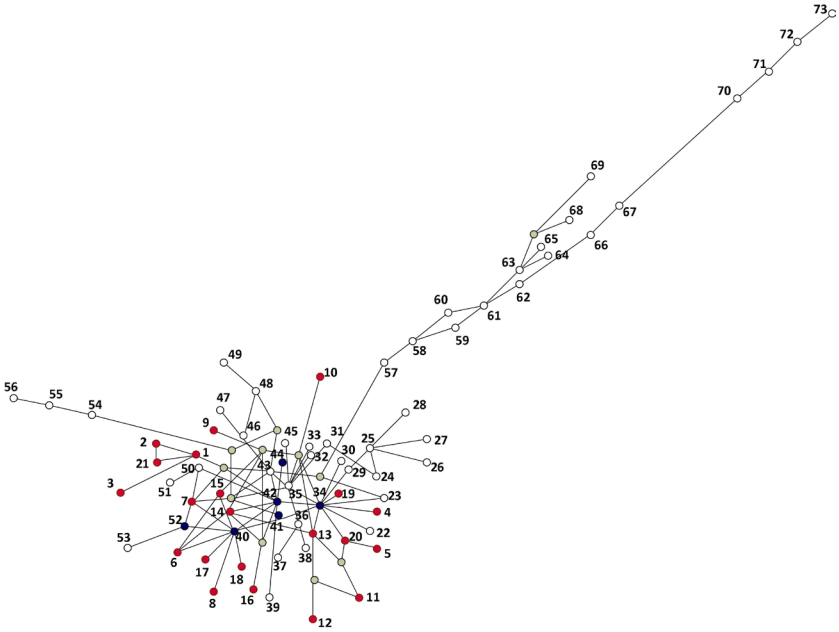

Fig. A5. Median joining network representing the genealogical relationships between 73 mitochondrial control region haplotypes of burbot (*Lota lota*). Lengths of lines are proportional to genetic distances between haplotypes. 21 new haplotypes (WS1-WS21), revealed in the Ob-Irtysh River basin, are highlighted in red and marked by numbers 1–21, respectively. Hypothetical haplotypes are shown in grey. Blue circles demonstrate haplotypes from the NCBI, which were revealed in the Ob-Irtysh River basin. White circles show the rest of NCBI haplotypes, used in this analysis. Together with new WS haplotypes, the star-like Eurasian cluster includes Western European haplotypes EB00, EB02, EB03, EB04 (numbers 25, 28, 26 and 24, respectively), Northern European haplotypes EB10, EB11, EB12, EB13, EB14, EB15, EB16, EB17 (numbers 35, 45, 33, 31, 32, 36, 37, 38, respectively), Beringian haplotypes EB41, EB43, EB44, EB45, EB20, EB21, EB22, EB23 (numbers 40, 52, 44, 39, 46, 43, 47 and 48, respectively), Eurasian haplotypes EB30, EB32, EB33, EB34, EB35 (numbers 34, 30, 22, 23, 41, respectively), and Alaskan haplotypes EB42, EB50 (numbers 50 and 53 respectively). Five more NCBI haplotypes, which belong to the Eurasian cluster, are marked by the following numbers: 27 (the Seine River), 29 (the Vistula River), 42 (from Russia), 49 (Lake Constance) and 51 (Xj3 haplotype from the Irtysh River in China). The Amur cluster includes three haplotypes Amur 1–3 (numbers 54–56), found in the Duobuku'er River, which is the tributary of the Amur River. Another cluster corresponds to *L. l. maculosa* lineage and includes Mississippi (numbers 57–65, 99, 102), Missouri (numbers 95–98) and Pacific (numbers 110, 111) haplotypes

SMALL MAMMALS AS INDIRECT BIOTIC MARKERS FOR CLIMATE DYNAMICS ASSESSMENT IN THE CENTRAL PART OF NORTHERN EURASIA

E.A. Markova, T.V. Strukova, A.V. Borodin (p. 98)

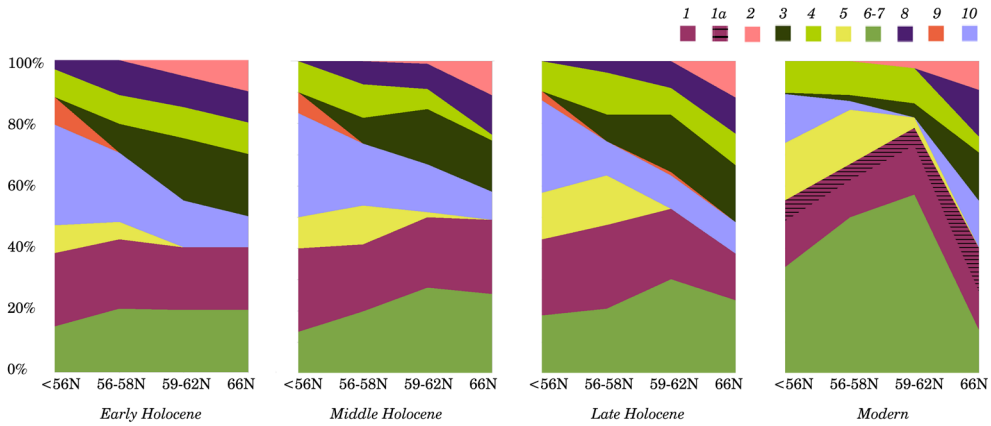

Fig. A8. Latitudinal and temporal occurrence (in percentage) of the microhabitat groups of arvicoline rodents in the Ural Mountains based on the analysis of the databank of fossil assemblages from the cave sites (see Borodin et al., 2013 for the list of localities) and the database of modern arvicolines captured during the last 50 years (zoological museum of IPAE UrB RAS). Latitudes: 51–56° N — Southern Urals, 56–59° N — Middle Urals, 59–62° N — Northern Urals, 66–68° N— Polar Urals. Radiocarbon dates: Early Holocene — 8100–10600 years BP, Middle Holocene — 7380–3060 years BP, Late Holocene —1470–612 years BP). 1–10 — microhabitat groups according to humidity/openness/vegetative cover: 1. Wet to wet-mesic (intrazonal)/open to semi-open/ herbaceous cover (1 — native species *Arvicola terrestris* and *Microtus oeconomus*, 1a — *Ondatra zibethicus* introduced in 20th century); 2. Wet-mesic to mesic/open to semi-open/herbaceous cover (*M. middendorffi*); 3. Wet to mesic/open to closed/moss cover (*Lemmus sibiricus, Myopus schisticolor*); 4. Mesic to wet-mesic/open to semi-open/swardy or tussocky herbaceous cover (*M. agrestis*); 5. Mesic/open to semi-open/ herbaceous cover (*M. arvalis obscurus, M. rossiaemeridionalis*); 6. Mesic/closed or semi-closed/woody cover (*Clethrionomys rutilus, C. glareolus*); 7. Mesic to dry-mesic/closed or semi-closed/woody cover (*C. rufocanus*); 8. Xeric to mesic/open to semi-open/ grass-and- shrub cover (*Dicrostonyx torquatus*); 9. Xeric to mesic/ open to semi-open/ sagebrush cover (*Eolagurus luteus*); 10. Xeric/open/herbaceous cover (*Ellobius talpinus, M. gregalis, Lagurus lagurus*)