New subspecies of the common long-eared bat *Plecotus auritus* (Vespertilionidae: Chiroptera) from the Caucasus

Sergei V. Kruskop & Svetlana S. Zhukova

ABSTRACT. Comparison of the mtDNA sequences and skull measurements indicates the presence of a specific form of *Plecotus auritus* in the Caucasian part of the species range, which we describe here as a separate subspecies *P. a. ponticus* subsp. nov. It differs from other long-eared bats from European Russia by having smaller mean values for 13 of 27 measured cranial characters and approximately 4.9% differences in the *cytb* mitochondrial gene sequence. The described subspecies inhabits the forests of the Caucasus region, as well as, apparently, the northeast of Turkey, and possibly the Rostov region and Crimea. The possibility of identifying other subspecific forms within this wide-range species and the need to study this issue are discussed.

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Новый подвид бурого ушана *Plecotus auritus* (Vespertilionidae: Chiroptera) с Кавказа

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РЕЗЮМЕ. Сравнение последовательности мтДНК и промеров черепа свидетельствует о наличии в кавказской части ареала *Plecotus auritus* особой формы, которую мы описываем здесь как отдельный подвид. Он отличается от ушанов из Европейской части России меньшими средними значениями 13 из 27 измеренных черепных признаков и приблизительно 4.9% различий в последовательности митохондриального гена *cytb*. Описываемый подвид населяет леса Кавказского региона, а также, по-видимому, северо-восток Турции, и, возможно, Ростовскую область и Крым. Обсуждается возможность выявления других подвидовых форм в пределах этого широкоареального вида и необходимость изучения данного вопроса.

КЛЮЧЕВЫЕ СЛОВА: рукокрылые, Plecotini, систематика, морфометрия, генетика, географическая изменчивость.

Introduction

In about a century, known diversity of the Old-World long-eared bats (*Plecotus* s. str.) fluctuated mainly between one or two, occasionally tree or four accepted species (Tate, 1942; Kuzyakin, 1950; Hanák, 1966; Strelkov, 1988; Koopman, 1994; Bogdanowicz *et al.*, 1998). Following the use of the molecular genetic methods, taxonomy of this genus underwent dramatic changes with number of known species quickly raised over 15 (Benda *et al.*, 2004; Juste *et al.*, 2004; Spitzenberger *et al.*, 2006). Since most of the previous-

ly named forms, including those considered synonyms, were elevated to full species, this led P. Strelkov to announce a "crisis in the polytypic concept of species" (Strelkov, 2006).

Nevertheless, in wide-range species with low migratory activity it is reasonable to expect the presence of certain geographical variability, which can be described, besides other, in terms of subspecies. Common long-eared bat, *Plecotus auritus* (Linnaeus, 1758), in its modern understanding, has a vast range covering almost the entire forest zone of Europe from the Iberian Peninsula and the British Isles to the Urals, as well as the Caucasus and Transcaucasia. It inhabits both boreal and mixed forests, as well as the Mediterranean-type forests and forest islands in the steppe zone (Ancilotto & Russo, 2023; Russo & Cistrone, 2023). This species is considered sedentary, making seasonal movements within a few tens of kilometers (Hutterer *et al.*, 2005). However, only two subspecies are currently recognized: *P. a. begognae* de Paz, 1994, endemic to the Iberian Peninsula south of the Pyrenees, and the nominotypical one, inhabiting the rest of the range (Ancilotto & Russo, 2023).

During the work with museum collection materials in the study of interspecific differences in the genus *Plecotus*, it was noticed that common long-eared bats from the Caucasus differ from animals from the European part of Russia. To test this assumption and assess the level of differences, we analyzed the available cranial materials of the long-eared bats from different parts of their range and obtained the genetic sequences of common long-eared bats from the Caucasus.

Material and methods

All the specimens used in the analysis are housed in the collections of the Zoological Museum of Moscow State University (ZMMU) and the Zoological Institute of the Russian Academy of Science (ZIN). A total of 48 museum specimens of P. auritus were used in the morphometric analysis; also 36 specimens of morphologically similar P. ognevi Kishida, 1927 and three specimens of P. macrobullaris Kuzyakin, 1965 were used for comparison. Full list of specimen IDs is provided in the Appendix. The following cranial measurements (abbreviations given in parentheses), were taken: greatest skull length (TL), braincase height without (BCH1) and with auditory bullae (BCH2), condylocanine length (CCL), condylobasal length (CBL), rostral width at the level of the infraorbital foramina (RW), rostral length from anteorbital foramen to the alveolus of the inner incisor (RL), least width of the postorbital constriction (POC), width between the inner margins of upper canines (CC int), palatal width behind M3 (PpalW), width between inner margins of auditory bullae (ACIW), width across outer margins of auditory bullae (ACEW), length of neurocranium from the anterior point of orbit to the condyle (BSL), width across outer points of supraorbital ridges (PPW), length from the lower M3 to the anterior margin of glenoid fossa (M3_CJ), lower jaw length from alveolus of i1 to the posterior extremity of glenoid process (MDL), lower jaw height to the tip of coronoid process (PrCH), distance between tips of coronoid and articular processes (PrA PrC), distance between tips of articular and angular processes (PrA_PrAn), distance between tips of angular and coronoid processes (PrC PrAn), length of the mandibular symphysis (Symph), height of the mandible body at level of m3 (Pdh), depth of a notch between angular and articular processes (AD), width across inner parts of glenoid fossae (Gl Gl), C-M3 length (CM3), maxillary molariform row length (PM3), length of the upper canine cingulum base (C).

To assess the pattern of variation of quantitative characteristics, Principal Component (PC) and Discriminant Function (DF) analyses were performed for the 20 craniodental measurements, using the Principal Component and Discriminant Function analyses and Classification modules of STATISTICA for Windows ver.7.0 (StatSoft Inc., 2004). DF analysis was used to calculate squared Mahalanobis distances between groups and significance of inter-group difference. For external comparison, forearm length (FA), ear length (A), tragus length (Tr), thumb length (D1) and its claw (ung) were used. To ensure that the measurements were comparable, only measurements from collection specimens fixed in alcohol were used.

For DNA analyses, tissue samples were taken from the two alcohol-preserved specimens housed in the GenBank Nos. ZMMU collection, ZMMU S-202310 and S-202311 (PV289749-750) from the vicinity of Utrish, Krasnodar Territory; and also from one specimen ZMMU S-200480 (PV289748) from Feodosia, Crimea, and one specimen ZMMU S-204040 (PV289747) from the middle Volga River (Chuvash Republic). Total DNA was extracted using standard protocol of proteinase K digestion, phenol-chloroform deproteinization and isopropanol precipitation (Sambrook et al., 1989). The cytochrome b gene (cytb, 1140 bp) was amplified with primers previously used by us for Plecotus species; for details of genetic analysis see Artyushin et al. (2021). Polymerase chain reactions (PCR) were performed on a My Cycler BioRAD device. The amplification reaction was carried out under the following conditions: primary denaturation — 94°C for 3 min.; then 35 cycles, including denaturation -94°C for 45 sec., annealing 54°C for 1 min., synthesis - 72°C for 1 min. The final synthesis was carried out at 72°C for 7 min. Amplification control was carried out in 1% agarose gel. PCR products were purified using the Diatom DNA Clean-Up kit and sequenced by genetic analyzer 3500xL Applied Biosystems by third party company (Evrogen, Moscow, Russia). Sequences were verificated using SeqMan Pro v.7.1 (Burland et al., 1999) and aligned with MEGA ver.11.0.13 (Tamura et al., 2021). Preliminary genetic identification was conducted with the use of BLAST (https://blast.ncbi. nlm.nih.gov/Blast.cgi), and then the phylogenetic trees were obtained with the sequences of appropriate species. Additionally, 74 sequences of Plecotus species were taken from GenBank (https://www.ncbi.nlm.nih. gov/genbank/); two sequences of related genus Corynorhinus were taken as outgroup (see Appendix). Reconstruction of the phylogenetic trees was performed using the maximum likelihood (ML) method using the IQ-Tree program v.1.6 (Nguyen et al., 2015). The ModelFinder routine (Kalyaanamoorthy et al., 2017) was used to determine the optimal partitioning scheme and best-fit substitution models. The used substitution models are as follows: TIM2e+G4: 1stpos; HKY+F+I: 2ndpos; TIM+F+I+G4: 3rdpos. Clade stability was inferred using Ultrafast Bootstrap with 10000 replicates. Uncorrected p-distances among haplotypes (Kimura's two-parameter model was used since it make possible to compare with the previously published results) were calculated in MEGA X (Kumar *et al.*, 2019).

Results

Morphology

The results of the Principal Component analysis (Fig. 1) demonstrated a partial separation of the *P. auritus* samples from the European part of the range and the Caucasus according to the values of the First (size-related) Factor, correlated with the skull length, the length of the upper tooth row, the mandible length, and in the version with normalized data, also by the length of neurocranium. Factorization of the data was quite poor, with the first four Factors accounting for only about 59% of the total variance. The specimens from Crimea were more likely associated with those from the Caucasus, although they were located in the morphospace near the area of cloud overlap. The specimens from the steppe regions of Russia fell in part into the area of cloud overlap, and in other part associated with P. auritus from the European part of Russia.

Discriminant Function analysis also separated the samples with little overlap; at least one small individual from the European part of Russia was assigned to the Caucasian population following posterior probabilities. The separation was borderline significant, with *p*-value

about 0.019. Meantime, the separation of P. auritus and the morphologically similar P. ognevi was complete, with a noticeable hiatus. According to posterior probabilities, three out of four Crimean specimens were associated with the Caucasian population, and one occupied an intermediate position. Of the four animals from the steppe regions, two were more likely associated with P. auritus from the forest/forest-steppe zones of the European part of Russia, one is closer to the Caucasian population, and one occupied an intermediate, uncertain position. When including only P. auritus in the analysis, we obtained a single Canonical Variance with a p value of about 0.01. At the same time, posterior probabilities assigned all individuals included in the analysis to "their" population clusters (to which they were initially allocated). Of the four Crimean specimens, three were associated with the Caucasian population, and one with the European populations. The samples from the steppe regions were divided in this version of the analysis: individuals from the Rostov Region were associated with the Caucasian population samples, and those from the Volgograd Region - with the European specimens.

On the average, the skulls of the long-eared bats from the Caucasus are smaller in size than those of specimens from the European part of the range, although there is no hiatus in any of the measurements. Of the 27 measurements, in eight the difference in av-



Fig. 1. Scatter plot showing distribution of 48 *P. auritus* specimens in space of the first two Factors (Principal Component analysis). First factor covers 36.4% of total variance and greatly correlates with TL, CCL, CBL, MDL, CM3 and P4M3; Second factor covers 9.26% and mainly correlates with CC_int and PPW.

erage values appeared to be within the measurement error; in 13 measurements (TL, BCH2, CCL, CBL, RL, RW, POW, ACEW, BSL, MDL, Gl Gl, CM3 and PM3) the difference between the average values for the Caucasian and European specimens exceeded the standard deviation for the latter. Thus, there was a definite trend towards smaller sizes in the Caucasus long-eared bats, but the wide overlap remained. In this case, we are hardly talking about clinal shift of variation, since large- and small-sized European samples were not tied to the latitudinal gradient. The smallest measured European specimen came from the Moscow region (close to the north of the species distribution range), the largest measured individuals came from the middle Volga region; of the two individuals from the Volgograd Region, one was larger and the other smaller than was the average value. The few measured Crimean samples (four in total) in terms of most skull measurements lied between the European and Caucasian samples; the average values of the two measurements (AD and C) were slightly larger than in both of them.

Molecular genetics

On the tree based on *cytb* gene sequences, specimens from the Caucasus, Crimea, and the GenBank sequence from northeastern Turkey formed a well-supported clade (Fig. 2). The position of this clade was within the genetic diversity of *P. auritus*, in a sister position to the Eastern European clade, which also included a specimen from the European part of Russia. The most basal position was occupied by the clade of *P. a. begognae* from the Iberian Peninsula, which some authors tend to consider as a full species (Mayer *et al.*, 2007; Santos *et al.*, 2014). Nevertheless, the distances between individual clades within *P. auritus* (as accepted here) were quite significant. These distances between the Caucasian clade and the other clades of *P. auritus* were 4.94, 5.62 and 8.28% (Table). The first two were less than the usual interspecific distances described in the genus *Plecotus*, but greater than e.g. distances for the same gene between the two morphologically discrete Asian species *P. ognevi* and *P. kozlovi*.

Discussion

Our data on the *cytb* gene are in good agreement with the idea of phylogeographic splits within *P. auritus* (Kruskop *et al.*, 2012). The isolated position of the Caucasian common long-eared bats according to other mitochondrial genes was indicated by Shpak *et al.* (2020). Çoraman *et al.* (2013), analyzing two mitochondrial genes, including *cytb*, distinguished four lineages within *P. auritus* (not counting the Iberian *P. a. begognae*). One of these lineages occurs, accord-



Fig. 2. Phylogenetic relationships between *Plecotus* species and position of the Caucasian specimens based on sequences (1140 bp) of the mitochondrial *cytochrome b* gene. Bootstrap values resulting from ML analysis with 10000 iterations near appropriate nods; only supports over 70% are shown.

	Group	1	2	3	4	5	6	7	8	9	10	11	12
1	<i>P. auritus</i> (Central and East Europe)												
2	<i>P. auritus</i> (Caucasus, NE Turkey)	0.049											
3	P. auritus (West Europe)	0.033	0.056										
4	P. auritus begognae	0.071	0.083	0.065									
5	P. austriacus	0.163	0.162	0.152	0.152								
6	P. balensis	0.176	0.172	0.160	0.146	0.137							
7	P. teneriffae / P. kolombatovici / P. gaisleri	0.181	0.182	0.180	0.159	0.126	0.140						
8	P. homochrous	0.150	0.145	0.145	0.129	0.157	0.154	0.163					
9	P. kozlovi	0.134	0.140	0.131	0.118	0.161	0.166	0.167	0.152				
10	P. macrobullaris	0.137	0.137	0.127	0.128	0.172	0.158	0.182	0.140	0.138			
11	P. ognevi	0.131	0.144	0.133	0.124	0.157	0.161	0.167	0.146	0.036	0.133		
12	P. sacrimontis	0.145	0.136	0.146	0.134	0.177	0.169	0.165	0.152	0.083	0.129	0.096	
13	P. turkmenicus	0.136	0.128	0.129	0.126	0.167	0.149	0.180	0.143	0.126	0.126	0.134	0.135

Table. Uncorrected *cytb p*-distances among species and lineages of *Plecotus*.

ing to these authors, in the northeast of Turkey and, presumably, in the Caucasus (Clade 3). Genotyping of animals from the Russian part of the Caucasus suggested a justification of such an assumption. At the same time, in the listed works there was no attempt at morphological comparison of animals belonging to different genetic lineages, once again besides *P. a. begognae*, identified as a distinct subspecies back in the era before common use of the molecular genetic approach (Paz, 1994).

Although the morphological differences between the Caucasian population of the common long-eared bats and the European population samples are not discrete, there are differences between them that allow morphometric methods to classify the vast majority of individuals to a particular sample set. The combination of this trend with the presence of a special mitochondrial haplogroup allows us to assign the Caucasian population of *P. auritus* to a separate subspecies, here named as:

Plecotus auritus ponticus subspecies nov.

Holotype: ZMMU S-202311, adult male in alcohol, with skull extracted and cleaned. Collected near Malyj Utrish settlement, Anapa District, Krasnodar Territory, Russia, on 3 June 2018. Collected by I.V. Artyushin.

Paratype: ZMMU S-203310, adult female in alcohol, with skull extracted and cleaned. Collected 1 km W of Afonka farmstead, Anapa District, Krasnodar Territory, Russia, on 31 May 2018. Collected by I.V. Artyushin. Other referred material: ZMMU S-7784 Krasnodar Territory, m; ZMMU S-7785 North Ossetia, m; ZMMU S-169764 Krasnodar Territory, m; ZMMU S-182655 Krasnodar Territory, m; ZMMU S-186991 Kabardino-Balkarian Republic, m; ZMMU S-186992 Krasnodar Territory, m; ZMMU S-186993 Krasnodar Territory, f; ZMMU S-186996 Krasnodar Territory, m; ZMMU S-186997 Krasnodar Territory, m; ZIN 64361 Krasnodar Territory, sex unknown; ZIN 72330 Krasnodar Territory, m; ZIN 80862 Karachay-Cherkessia, f; ZIN 96768 Kabardino-Balkarian Republic, f.

Diagnosis: The long-eared bat (*Plecotus* Geoffroy, 1818) of medium size (FA ca. 39.3 mm), with a typical appearance of the *P. auritus* species complex; it differs from *P. auritus* from the East and Central Europe in being small-sized on the average in both cranial and external measurements, and also in ca. 4–5% of *p*-distance in mitochondrial *cytb* gene. From *P. macrobullaris* from the Caucasus region, *P. a. ponticus* **ssp. nov.** differs in smaller skull size (CBL in *P. macrobullaris* 15.84–16.09 mm) and by the angular process of mandible widened at its tip (not widened, but slightly pointed in *P. macrobullaris*).

Measurements of the holotype (in mm): FA 39.1, A 34.7, Tr 16.2, CCL 13.92, CBL 14.60, RL 3.43, RW 4.22, CM3 5.24, P4M3 3.98, C 0.92, MDL 10.36.

Description: A small Old World long-eared bat, similar in appearance to the typical *P. auritus auritus* (Clade 2 sensu Çoraman *et al.*, 2013). The forearm length 38.2-40.6 mm (*n*=7). Ears are large, poorly pigmented, typi-

cally with 21 folds on the posterior edge. No incomplete folds (shorter than neighbouring) were seen in studied specimens, while such shortened folds are common in P. auritus from the European part of Russia. Ear length on the average is about 90% of the forearm length and tragus length is about 49% of the ear length, compared to ca. 88 and 47% in *P. auritus auritus*, respectively. The thumb length is rather large, ca. 7.5 mm, and the thumb claw is narrow, pointed and curved, ca. 2.7 mm in length. The fur on both aspects of the body is about 9-10 mm long (the guard hairs could be up to 13 mm long). The hair bases are dark, greyish-brown, about 3-4 mm long. On the belly, the pale parts of hairs are fawn-whitish, on the back they are pale fawn. The boundary between pale and dark parts of the hair appears sharper than in European P. auritus, but this may be an artifact of the seasonal or individual variation.

The skull (Fig. 3) is similar in proportions to that of *P. auritus auritus*, but is on average smaller in 13 of the 27 measurements taken (see above). The lower molars are myotodont, with a closed trigonid basin and a quite small hypoconulid located relatively close to the entoconid. The angular process of the mandible, as in other *P. auritus* populations, is relatively long, with a thickened distal portion. Upper molars are with an open trigone basin and an unpronounced hypocone. The canine is practically no different in size and shape from that of *P. auritus auritus*. The large upper premolar (P4) is with a straight or slightly concave mesial edge of the cingulum. The height of the small upper premolar (P2) is usually only twice as high as the mesial edge of the cingulum of P4 (in P. auritus auritus it is often higher). The inner upper incisor (I2) is distinctly bicuspidate. The outer upper incisor (I3) has one large cusp (still noticeably not reaching the second cusp of the inner incisor) and a small additional cusp at the base of the crown. The axis passing through the cusp tips of the inner incisor in P. auritus auritus usually passes through this additional cusp. At the same time, in P. a. ponticus ssp. nov. it usually runs between the main cusp and the additional one (i.e., the outer incisor is slightly shifted inward). All features, both quantitative and qualitative, do not demonstrate discreteness and represent more or less pronounced trends.

Comments: There is no particular doubt that the common long-eared bats of the Caucasus all belong to the subspecies described here. Based on data of Çoraman *et al.* (2013), the long-eared bats from north-eastern Turkey also belong to the same subspecies/form. The common long-eared bats of Crimea belong to the same genetic lineage. This is supported by the results of multivariate analysis, although in terms of skull size and dental characteristics, Crimean individuals occupy an intermediate position between the Caucasian and



Fig. 3. *Plecotus auritus ponticus* subsp. nov. Skull of the holotype, ZMMU S-202311, in upper, lower and lateral views. Scale bar 5 mm.

European ones. We did not have genetic material for animals from the Rostov region, but judging the craniometry, they also most likely belong to *P. a. ponticus* **ssp. nov**. At the same time, the specimens from the Volgograd region, according to morphometric data, belong to the nominotypical subspecies, which is supported by DNA barcoding data (Kruskop, in litt.). Thus, given that *P. auritus* is considered a predominantly forest species, it probably first independently inhabited the forested areas of the European part and the Caucasus, and then penetrated into the steppe regions in between from both the north and the south.

Our data confirmed the heterogeneity of the widespread long-eared bat species and its probable polytypic nature. Including *P. a. ponticus* **ssp. nov**., *P. a. begognae*, and the nominotypical form, the common long-eared bat in the modern understanding already includes three subspecies. Based on its distributional structure / fragmentation and known genetic diversity, it can be assumed that separate lineages of subspecies rank could be identified in Corsica, Sardinia, and possibly the Italian Peninsula. It would be logical to assume that each of these forms has its own specific environmental preferences, knowledge of which is important both for population conservation and for understanding the circulation of parasites and possible pathogens.

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Appendix

List of GenBank sequences used in the analysis:

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Corynorhinus rafinesquii: JN209841.1, NC 016872.1;
Plecotus auritus: AF513756.1, AF513757.1, AF513758.1,
AF513759.1, AF513760.1, AF513761.1, AF513762.1, AF513764.1, AF513765.1, AF513767.1, AF513768.1,
AF513769.1, AJ431650.1, AY306211.1, KF218404.1,
KF218405.1, MN122881.1, MT410875.1, OQ939709.1, OQ939736.1, OQ939741.1, OQ939759.1; P. austriacus:
AF513770.1, AF513778.1, AF513787.1, AJ431649.1, EU360707.1, KF358491.1; P. balensis: AF513798.1,
MW166401.1, MW166411.1, MW166419.1, MW166427.1,
MW166433.1; P. gaisleri: MN045573.1, MN045584.1; P.
homochrous: MN160086.1, MN160088.1, MN160089.1,
OP425735.1, OP425737.1; P. kolombatovici: EU086528.1,
AF513783.1; P. kozlovi: MT583349.1, MT583352.1,
MT583355.1, MT583360.1, MT583363.1, MT583389.1;
P. macrobullaris: AF513802.1, AF513806.1, AY306213.1,
KF218406.1, KR134388.1, KR134409.1; P. ognevi: MF285136.1; MF285153.1, MK410318.1, MT583350.1,
MT583372.1, MT583383.1; P. sacrimontis: LC036637.1,
LC036638.1, LC036639.1, LC036640.1, LC036641.1;
P. teneriffae: AF513810.1, EU360705.1; P. turkmenicus:
MT583353.1, MT583357.1, MT583358.1, MT583367.1,
MT583373.1, MT583376.1.
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List of specimens used for morphological comparison: *Plecotus auritus* (except for Caucasian specimens listed in the main text): Czechia: ZMMU S-74645; Bosnia and

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Herzegovina: ZIN 48068; Moldova: ZIN 62420, ZIN 62421; Belarus: ZMMU S-84114; Crimea: ZMMU S-200480, ZIN 82990, ZIN 82991, ZIN 82992; Bryansk Region: ZMMU S-180204, ZMMU S-180205; Chuvash Republic: ZMMU S-178818, ZMMU S-178826, ZMMU S-204040; Kaluga Region: ZMMU S-206837, ZMMU S-206838; Leningrad Region: ZMMU S-84117; Moscow Region: ZMMU S-105481, ZMMU S-105482, ZMMU S-157987, ZMMU S-105481, ZMMU S-105482, ZMMU S-157987, ZMMU S-105481, ZMMU S-196983, ZMMU S-204894, ZMMU S-205596, ZMMU S-29193, ZMMU S-29402, ZMMU S-84116; Penza Region: ZIN 96705, ZIN 96735; Rostov Region: ZIN 85696, ZIN 88844; Tver Region: ZMMU S-29404; Volgograd Region: ZMMU S-167242, ZIN 72305; Voronezh Region: ZMMU S-186994, ZMMU S-186995.

P. macrobullaris: North Ossetia: ZIN 72328, ZIN 87933, ZIN 87934.

P. ognevi: Amur River: ZIN 49846; Khabarovsk Region: ZMMU S-165793, ZMMU S-165794; North-east China: ZIN 8821; Mongolia: ZMMU S-194110, ZMMU S-194111, ZMMU S-194112, ZMMU S-194114, ZMMU S-194115, ZMMU S-194116, ZMMU S-197038, ZMMU S-198769, ZMMU S-198770, ZMMU S-198771, ZMMU S-198773, ZMMU S-198775; Primorsky Territory: ZMMU S-198773, ZMMU S-173266, ZMMU S-176145, ZMMU S-150218, ZMMU S-173266, ZMMU S-176145, ZMMU S-176146, ZIN 8696, ZIN 9294, ZIN 9306, ZIN 10848, ZIN 56360; Sakhalin: NMSN 7643, NMSN 7644, ZIN 61749; Tyva: ZMMU S-168629; Transbaikalia: ZMMU S-167565, ZMMU S-167567, ZMMU S-175372, ZMMU S-175373, ZMMU S-175375, ZMMU S-175942, ZMMU S-175943.