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The first record of the white-toothed rock shrew from "pergrisea" complex (Mammalia: Soricidae: *Crocidura*) on the territory of Russian Federation

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ABSTRACT. The white-toothed shrew (*Crocidura*) from the species complex "pergrisea" was found in the Dagestan Republic, it is the first registration for the territory of Russian Federation. Information on the morphology of two captured animals, external and cranial features, is provided. The position of white-toothed shrews from the northern slope of Caucasus Mts. in the phylogenetic structure of "pergrisea" complex was studied. The clade that includes *C. serezkyensis* s.str., *C. arispa* and rock shrews from Dagestan was proposed to recognise as a separate species — *Crocidura serezkyensis* Laptev, 1929

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Первая находка скальной белозубки из комплекса видов "pergrisea" (Mammalia: Soricidae: *Crocidura*) на территории Российской Федерации

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РЕЗЮМЕ. Впервые на территории Российской Федерации в Республике Дагестан обнаружена белозубка (*Crocidura*), принадлежащая к комплексу видов "pergrisea". Приводятся сведения по морфологии двух отловленных зверьков: экстерьерные и краниальные признаки. На основе митохондриального гена *cytb* рассмотрено место белозубок с территории северного макросклона Кавказа в филогенетической структуре комплекса "pergrisea". Предложено рассматривать кладу, включающую *C. serezkyensis* s.str., *C. arispa* и белозубок с территории Дагестана, в качестве одного самостоятельного вида — *Crocidura serezkyensis* Laptev, 1929.

КЛЮЧЕВЫЕ СЛОВА: сарезская белозубка, *pergrisea*, цитохром б, Республика Дагестан.

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Introduction

White-toothed shrews (*Crocidura*) from the species complex "pergrisea" are one of the less studied and the most interesting shrews from taxonomic position. They are distinguished by their specific appearance (light fur colour and long tail) and biotopic preferences, inhabiting rocky habitats: talus, rocks, etc. (Stogov & Bondar, 1966; Zaitsev, 1991; Kryštufek & Vohralík, 2001).

Despite the fact that, according to various publications, only about 30 specimens of representatives of this complex are stored in museums around the world, several species and subspecies were described within the complex (Zaitsev, 1991; Hutterer, 1993, 2005; Kryštufek & Vohralík, 2001): *C. pergrisea* Miller, 1913 (Pakistan); *C. portali* Thomas, 1920 (Israel); *C. serezkyensis* Laptev, 1929 (Pamir Mts.); *C. armenica* Gureev, 1963 (Armenia); *C. pergrisea arispa* Spitzenberger, 1971 (Turkey); *C. ramona* Ivanitskaya, Shenbrot et Nevo, 1996 (Israel). Several taxa: *C. tatianae* Ognev, 1921 (Iran); *C. zarudnyi* Ognev, 1928 (Iran; substitute name for *C. tatianae*); *C. pamirensis* Ognev,

1928 (Pamir Mts.); *C. zarudnyi streetorum* Hassinger, 1970 (Afghanistan), were formerly included in the *Crocidura pergrisea* complex, but are currently assigned to the lesser shrews group *C. suaveolens* Pallas, 1811 (Zaitsev, 1991; Hutterer, 1993, 2005). The proximity of *C. zarudnyi* and *C. suaveolens* was demonstrated in the study of karyological and molecular data without comparing the studied specimen with the type specimen (Dubey *et al.*, 2007; Bannikova *et al*., 2023). *Crocidura portali* is considered as a synonym of *C. suaveolens* (Hutterer, 1993), or *C. gmelini* Pallas, 1811 (Hutterer, 2005). B. Kryštufek and V. Vohralík (Kryštufek & Vohralík, 2001), guided by exterior characteristics, admit that *C. portali* may be the senior synonym for *C. ramona*. The status and validity of *C. armenica*, another taxon classified in the "pergrisea" complex, is controversial (Zaitsev *et al*., 2014; Burgin *et al*., 2020).

The aggregation of the taxa into the "pergrisea" complex was carried out on the basis of morphological characters (Zaitsev, 1991). A complete molecular revision of the complex does not exist up to date (Bannikova *et al*., 2023) — taxon *C. pergrisea* s.str. is known by the type series only, the karyotype and molecular data have not been studied. A long period of confusion in the names use led to a false sense of understanding a taxonomic position of *C. pergrisea* s.str. The most northwestern finding of shrews of the group under consideration was made in the Araks River basin (Nakhichevan). Several animals were caught in the vicinity of the city of Julfa there. M.V. Zaitsev (Zaitsev, 1991; Zaitsev *et al*., 2014) identified these animals (due to his interpretation of the species) as *C. pergrisea*, while Hutterer (due to a different interpretation of the species) classified them as *C. serezkyensis* (Hutterer, 2005). Multidimensional morphometric data (Zaitsev, 1991) and karyological material (Grafodatsky *et al*., 1988), published as for *C. pergrisea* s.l., were studied using this sample from Nakhichevan. Araks River is geographically closer to the terra typica of taxon *C. armenica*, which relation to *C. pergrisea* s. str. has also never been studied. Therefore, the belonging of a "flag" species to the complex of its name is rather conditional (Zaitsev *et al*., 2014).

Currently, the following species are allocated to the "pergrisea" complex: *C. pergrisea*, *C. serezkyensis*, *C. arispa* and *C. ramona* (Bannikova *et al*., 2023). The geographical distribution of the species of the complex under consideration is associated with the arid territories of Western and Central Asia, up to the limits of Inner Asia. What about the Caucasus, in a broad sense, shrews from this complex were caught in Nakhichevan, as mentioned above, and in Armenia (the villages of Sisian and Garni). The last specimens were used for the description of *C. armenica*. We caught two shrews from the "pergrisea" group on the northern macroslope of the Greater Caucasus in the Republic of Dagestan in 2023. This is the first record of these shrews on the territory of Russian Federation. Since any information on representatives of the "pergrisea" complex can be valuable for understanding the phylogeny and taxonomy of the complex as a whole, we publish here a brief description of our finding and a description of the phylogenetic position of the collected specimens.

Materials and methods

We caught two animals in the vicinity of the town Gunib (Dagestan, 42.4054° N, 46.9099° E) in April 2023 in a rocky cliff in a shallow grotto, that is used by shepherds to keep sheep from time to time (Fig. 1). Voucher specimens are kept in the Zoological Museum of Lomonosov Moscow State University (S-210050, S-210051).

We used following primers: L14728_Cr, L15136, Cro_481b, H1310_Cr (Bannikova *et al*., 2006, 2011) in order to obtain PCR products and sequence the *cytb* gene. The sequences have been deposited in GenBank (OR995289, OR995290). The selection of the optimal model (on the basis of AICc) with partitioning, construction of a phylogenetic tree using the maximum likelihood (ML) method, bootstrap analysis (1000 replicates) and calculation of patristic distances were carried out in TREEFINDER (Jobb, 2011). Sequences deposited in GenBank were used as comparative material (Table 1).

Results

Two adults, a male and a female, were captured. The latter was pregnant and had five embryos. The animals had a two-color fur, the upper part of the body was light brown with an opalescent grayish tint, the belly was gray, and the boundary separating them was not clearly defined. The paws and tail were white and pubescent. Morphological characteristics of specimens from the vicinity of Gunib in comparison with previously studied shrews from the "pergrisea" group are given in Tables 2–3.

The optimal evolution model for phylogenetic reconstruction was chosen as follows: TN+G for the first codon position, HKY for the second and J2 for

Table 1. Material used in phylogenetic analysis.

GenBank ID	Taxon	Sample location	Authors
OP599553	*C. arispa*	Turkey	Bannikova *et al*., 2023
OP599554, OP599555	*C. serezkyensis*	Tajikistan	Bannikova *et al*., 2023
LR536329, LR536373, LR536374	*C. ramona*	Israel	Shpirer *et al*., 2021
OR995289, OR995290	*C. serezkyensis*	Dagestan, Russia	Our data

the third. The speed ratio for the three codon partitions was: 0.363:0.078:2.559. According to the phylogenetic reconstruction (Fig. 2), based on the results of analysis of the complete *cytb* gene, our shrews fell into the clade *C. serezkyensis–C. arispa*. They occupied an outer position in the group, although the clade with *C. serezkyensis* and *C. arispa* had weak support. The genetic ML distance between Gunib specimens and *C. arispa* was 2.91%. Our specimens were separated from *C. serezkyensis* from Tajikistan by a slightly bigger distance of 4.06% (Table 4). The genetic distance between *C. arispa* from Turkey and *C. serezkyensis* from Tajikistan was 3.98%.

Discussion

White-toothed shrews of the "pergrisea" complex have not previously been recorded on the northern macroslope of the Caucasus Mountains. Our data extends the distribution range of this complex northward across the Main Caucasus Range. Most likely, the distribution of this species in Dagestan is not limited to the vicinity of Gunib only. Considering that "pergrisea" shrews are petrophilic and xerophilic, they should be looked for in appropriate habitats. Two xerophilic refugia are known in Dagestan (Mazanaeva & Tuniev, 2011). The first one is located on the Caspian shore, where habitats biotopes are absent. The second one includes semiarid mid-mountain basins between the Bokovoy and Ska-

Fig. 1. Habitat, where the rock shrews were found.

Table 2. Body measurements of ″pergrisea″ shrews.

Taxon/ID	Locality	Sex	m	L	C	Pl	Au	Data source
C.* cf. *serezkyensis ZMMU S-210050	**Gunib, Dagestan, Russia**	**m**	**5.0**	**50**	**50**	**12.0**	**4.0**	**Our data**
C.* cf. *serezkyensis ZMMU S-210051	**Gunib, Dagestan, Russia**	**f**	**5.5**	**60**	**49**	**12.0**	**5.0**	**Our data**
C. arispa SZE 69/452	Cığlıkara, Turkey	–	–	75	48	12.6	–	Spitzenberger, 1971
C. arispa NMW 13284	Madenköy, Turkey	–	–	70	48	12.5	–	Spitzenberger, 1971
C. pergrisea USNM 175918	Baltistan, Pakistan	f	–	75	54	12.6	–	Miller, 1913
C. pergrisea	Baltistan, Pakistan	f	–	72	53	12.6	–	Miller, 1913
C. pergrisea	Baltistan, Pakistan	f	–	75	53	12.6	–	Miller, 1913
C. pergrisea BMNH 191183	Baluchistan, Pakistan	–	–	60	53	13.0	10.0	Spitzenberger, 1971
C. armenica ZIN 45277	Armenia	m	–	60	45	12.0	–	Gureev, 1979
C. serezkyensis ZIN 77431	Tajikistan, Sarezskoe Lake	–	–	75	45		–	Laptev, 1929 (from Spitzenberger, 1971)
C. serezkyensis	«Central Asia»	–	–	55–70	45–50	11.0–12.0	–	Stogov & Bondar, 1966
C. serezkyensis	Tajikistan, Panj River	–	–	67.3	49.6	12.0	–	Rozanov, 1935 (from Stogov, 1985)

L — body length, C — tail length, Pl — hind foot length, Au — ear length. USNM — Smithsonian Institution, BMNH — British Museum of Natural History, SZE — Sistematik Zooloji Enstitüsü der Ege University, NMW — Naturhistorisches Museum Wien, ZIN — Zoological Institute RAS, ZMMU — Zoological Museum of Lomonosov Moscow State University.

Table 3. Cranial measurements of ″pergrisea″ shrews.

	CID	CBL	Zyg	Iob	Hcra	LF	MLT	LMp	AML	HM	Data source
C.* cf. *serezkyensis ZMMU S-210050	**18.94**	**18.29**	**5.65**	**4.11**	**4.51**	**8.01**	**8.57**	**4.72**	**9.63**	**4.39**	**Our data**
C.* cf. *serezkyensis ZMMU S-210051	**18.88**	**18.24**	**5.79**	**4.16**	**4.64**	**7.95**	**8.26**	**4.59**	**9.73**	**4.41**	**Our data**
C. armenica (holotype) ZIN 45277	17.70±0.00	16.70±0.00	5.20±0.14	4.20±0.00	–	–	–	4.30±0.14	–	–	Zaitsev, 1991
"*C. pergrisea*" (Julfa) ZIN 77972–77976	18.88±0.22	18.22±0.19	5.66±0.11	4.10±0.10	–	–	–	4.72±0.11	–	–	Zaitsev, 1991
C. serezkyensis ZMMU S-11841, S-11842, ZIN 77431, SZMN 418 (Kopetdag)	18.13±0.31	17.23±0.29	5.33±0.17	4.10±0.22	–	–	–	4.48±0.05	–	–	Zaitsev, 1991
C. arispa (Cığlıkara) SZE 69/452	–	18.4	–	–	–	–	–	–	–	–	Kryštufek & Vohralík, 2001
C. arispa (Madenköy) NMW 13284	–	17.9	–	–	–	–	–	–	–	–	Kryštufek & Vohralík, 2001
C. ramona type series (n = 11).	18.05±0.26	–	5.37±0.15	–	–	–	–	–	–	–	Ivanitskaya *et al*., 1996

CID — condyloincisive length, CBL — condylobasal length, Zyg — zygomatic breadth, Iob — interorbital breadth, Hcra — skull height, LF — rostral length, MLT — upper tooth row length, LMp — upper multicuspid tooth row length, AML — angular length of mandible, HM — mandible ascending branch height. SZE — Sistematik Zooloji Enstitüsü der Ege University, NMW — Naturhistorisches Museum Wien, ZIN — Zoological Institute RAS, ZMMU — Zoological Museum of Lomonosov Moscow State University, SZMN — Siberian Zoological Museum, Novosibirsk.

Table 4. Average pairwise maximum likelihood distances for the complete *cytb* gene between samples of "pergrisea" shrews.

	C. serezkyensis (Tajikistan)	*C.* cf. *serezkyensis* (Gunib)	*C. arispa*	*C. ramona*
C. serezkyensis (Tajikistan)				
C. cf. *serezkyensis* (Gunib)	0.0406			
C. arispa	0.0398	0.0291		
C. ramona	0.1540	0.1259	0.1425	

listiy Ranges; some of them are located in Dagestan (Gunibskaya and Botlikhskaya basins), while the rest are in Chechnya, Ingushetia, Northern Ossetia (Alania) and Kabardino-Balkaria (Itumkalinskaya, Targimskaya, Assinskaya, Armkhiyskaya, Sadono-Unalskaya basins etc.).

In terms of exterior characteristics, the caught shrews differ somewhat from the previously described few specimens (Table 2). The differences include the shorter body length, as well as the greater relative length of the tail, which reached 82 and 100% of the body length. The length of the hind foot, although small, was generally comparable with previously studied shrews from the "pergrisea" complex. Thus, our finding somewhat expands the information on variation within the "pergrisea" group. The skull of our specimens, on the contrary, is quite large and, in general, correspond to that previously studied by M.V. Zaitsev (1991) sample of "*C. pergrisea*" from the vicinity of Julfa in Nakhichevan.

A special issue is the name of the discovered shrews. At the moment, the only point of agreement between all taxonomists is the need to collect a new material to clarify the composition of species (Zaitsev, 1991; Pavlinov & Rossolimo, 1998; Kryštufek & Vohralík, 2001; Hutterer, 2005; Zaitsev *et al*., 2014). The "splitting" concept dominates in taxonomy of the complex now, that is, the number of recognized species

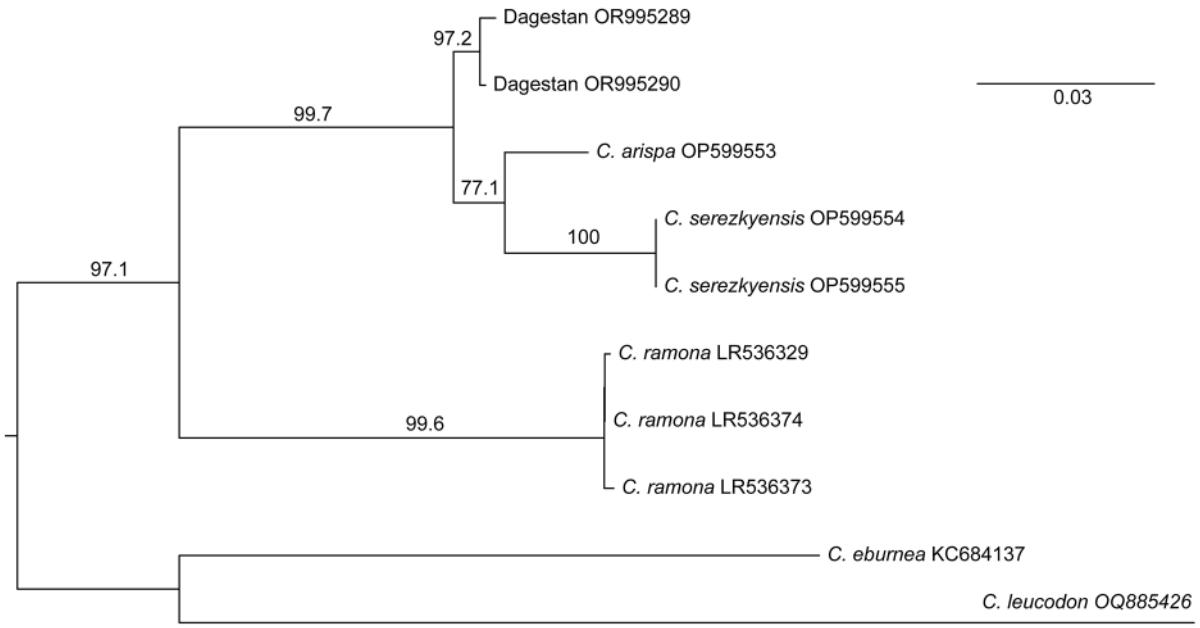

Fig. 2. Maximum likelihood dendrogram of "pergrisea" shrews constructed on the basis of the *cytb* gene.

corresponds to the number of described taxa (Hutterer, 2005; Bannikova *et al*., 2023). As it was already noted by A.A. Bannikova *et al*. (Bannikova *et al*., 2023), the genetic distances between the (not numerous) studied specimens are minimal. The authors of the latter publication suggest that the taxa of the "pergrisea" complex most likely correspond to allospecies within the single superspecies *C. pergrisea*. It is obvious that the volume of genetic material is so small now (4 specimens in Bannikova *et al*., 2023 and 8 specimens in this study) that any conclusions drawn from such analysis are the assumptions only.

Working within the framework of the "splitting" concept, we would have to describe a new taxon (and/or conduct a taxonomic revision of the Transcaucasian specimens to clarify the phylogenetic position of the nominal taxon *C. armenica*), since it is not possible to classify our sample to one of the already described and genetically studied nominal taxa (Fig. 2; Table 4). Taxonomic revision was not a part of our tasks; besides, we do not share the idea of dividing species solely on the basis of genetic distances, especially at the level of 3–4%.

Considering that our study reduces the minimum distance between taxa in the group under discussion from 3.6% (Bannikova *et al*., 2023) to 2.9% (Table 4) and changes the branching character from dichotomous to unresolved trichotomous, it seems logical to consider decreasing of the taxonomic rank of taxa accepted in the previous study (Bannikova *et al*., 2023). We consider possible combining them into one polytypic species together with the discovered Dagestan shrews. It should be noted that accepting the one polytypic species have a practical nomenclatorial use. If taxa will be divided in the future on the basis of genetic distances, this will lead to an inevitable increase in synonymy with appearance of new material.

The senior synonym for the species in such taxonomic composition is *C. serezkyensis* Laptev, 1929. It should be noted that the name *C. serezkyensis* has already been used for Transcaucasian shrews (Hutterer, 1993, 2005). It is clear that the name *C. arispa*, recently used in relation to these shrews (Sheftel, 2014; Burgin *et al*., 2020), cannot be applied to our Dagestan animals, since it is an objective junior synonym for the species in the supposed taxonomic composition.

We also want to note that using the "generalized" name *C. pergrisea* for Caucasian shrews (Zaitsev *et al*., 2014) is not the best taxonomic solution. Today it is known that the "pergrisea" complex contains at least another one good species, *C. ramona* (Bannikova *et al*., 2023; Fig. 2). The genetic distance between *C. ramona* and other taxa of the complex is 12.5–15% (Table 4). The use of the name *C. pergrisea* for Caucasian shrews implicitly implies their phylogenetic proximity to *C. pergrisea* s.str. relative to *C. ramona*. At the same time, discussion on the phylogenetic position of *C. pergrisea* s.str. and its possible conspecificity with *C. serezkyensis* seems premature until the appearance of the new molecular genetic data.

Guided by the logic described above, including the stability of nomenclature, and pending the appearance of new representative material on the group of shrews under discussion, we propose to consider the clade including *C. serezkyensis* s.str., *C. arispa* and North Caucasian shrews as one separate species *C. serezkyensis*.

Thus, we believe that the new specimens belong to *C. serezkyensis*.

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