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Mitochondrial genome introgression from the northern red-backed vole *Clethrionomys rutilus* into the bank vole *Clethrionomys glareolus* (Rodentia: Arvicolinae): new data from the zone of sympatry in the Southern Urals

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ABSTRACT. New data on the introgression of northern red-backed vole mitochondrial genome in bank vole populations in the zone of sympatry in the Southern Urals have been obtained. Specimens from three previously unstudied localities were genotyped using real-time PCR with hydrolyzing fluorescent DNA-probes. It was shown that all studied animals with the nuclear marker (gene *LCAT*) of *Clethrionomys glareolus* (Schreber, 1780) had the mitochondrial marker (gene *COI*) of *Clethrionomys rutilus* (Pallas, 1779). According to the morphological analysis, those specimens corresponded to the bank vole in all diagnostic characteristics. Sequenced fragments of introgressed mtDNA (gene *MT-CYB*) clustered into the Western clade, which also included *C. rutilus* from Northern Europe, Urals, western Siberia and western Mongolia. Taking previously published data into account, the most likely hypothesis explaining the observed high frequency of mitochondrial introgression in bank vole populations in the Southern Urals is the continuous process of hybridization of the two species in the zone of their sympatry, which might have begun from the moment of this zone's formation.

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Интрогрессия митохондриального генома красной полёвки *Clethrionomys rutilus* в геном европейской рыжей полёвки *Clethrionomys rutilus* (Rodentia: Arvicolinae): новые данные из зоны симпатрии на Южном Урале

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РЕЗЮМЕ. Получены новые данные об интрогрессии митохондриального генома красной полёвки *Clethrionomys rutilus* (Pallas, 1779) в популяциях рыжей полевки *Clethrionomys glareolus* (Schreber, 1780) в зоне симпатрии обоих видов на Южном Урале. Образцы из трех ранее не изученных местонахождений были генотипированы с помощью системы ПЦР в реальном времени с использованием гидролизующих флуоресцентных ДНК-зондов. Было показано, что все изученные животные с ядерным маркером (ген *LCAT*) *C. glareolus* имели митохондриальный маркер (ген *MT-COI*) *C. rutilus*. По результатам морфологического анализа эти особи соответствовали рыжей полёвке по всем диа-

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гностическим признакам. Секвенированные фрагменты интрогрессированной мтДНК (ген *MT-CYB*) сгруппировались в западную кладу, включающую также *C. rutilus* из Северной Европы, Урала, Западной Сибири и Западной Монголии. С учётом ранее опубликованных данных, наиболее вероятной гипотезой, объясняющей наблюдаемую высокую частоту митохондриальной интрогрессии в популяциях рыжей полёвки на Южном Урале, представляется продолжающийся процесс гибридизации двух видов в зоне симпатрии, который мог начаться с момента образования этой зоны.

КЛЮЧЕВЫЕ СЛОВА: митохондриальная интрогрессия, одонтологические признаки, real-time PCR-генотипирование, *Clethrionomys*, Южный Урал.

Introduction

Interspecific hybridization is a source of new genetic variants which can demonstrate high adaptive value (Hedrick, 2013). On the other hand, some populations may be damaged by intercrossing with closely related species to the extent of elimination of genetic variants or even extinction of rare species (Todesco *et al.*, 2016). The possible consequences of hybridization must be considered carefully while planning nature conservation projects.

One of the hybridization consequences is introgression — the transfer of genetic material from one species into the gene pool of another by repeated backcrossing. Numerous cases of introgression have been described in plants and animals (Toews & Brelsford, 2012; Burgarella *et al*., 2019), and at present introgression is considered to be an important aspect of reticulate evolution (Mallet *et al*., 2016). This phenomenon has been found in species of the genus *Clethrionomys* (Tilesius, 1850), the European bank vole *Clethrionomys glareolus* (Schreber, 1780) and the northern red-backed vole *Clethrionomys rutilus* (Pallas, 1779) (Tegelström, 1987; Deffontaine *et al*., 2005). Both species are widespread in the Northern Hemisphere with a vast zone of sympatry in the central part of Northern Eurasia. Introgression of the mitochondrial genome of the red-backed vole into the gene pool of the bank vole was revealed in the zone of sympatry in an area spanning from the northern part of Fennoscandia, the Arkhangelsk Region and the Komi Republic to the Southern Urals, as well as in some localities in Western Siberia, and the frequency of specimens with introgression in those populations varied significantly and could reach up to 100% (Abramson *et al*., 2009a, b; Melnikova *et al*., 2012; Zhigileva & Gorbacheva, 2017). Mitogenome transfer from *C. glareolus* to *C. rutilus* has not been reported yet. Nuclear gene transfer is ambiguous: some Ural red-backed vole specimens demonstrated allozyme forms conspecific to bank vole (Modorov, 2014). Several hypotheses have been proposed to explain both the fact of the introgression in two *Clethrionomys* species and its high frequency in some populations, from ancient hybridization in refugia to crossbreeding during the formation of the modern sympatric zone (Potapov *et al*., 2007; Melnikova *et al*., 2012), but there is not enough data at present to confirm any of the hypotheses.

Three natural hybrids were identified in the sympatry zone of *C. glareolus* and *C. rutilus* in the Urals. Two hybrids had red-backed vole mitogenome, one had bank vole mitogenome, and all three specimens had heterospecific alleles of the nuclear locus (Abramson *et al*., 2009b; Sibiryakov *et al*., 2021). Morphological analysis of the hybrids revealed the mixing of the species-specific features of molars (Borodin *et al*., 2011; Sibiryakov *et al*., 2021). Laboratory originated hybrids demonstrated coloration, tail length and structure of the stomach epithelium which were intermediate between the two species (Naumova *et al*., 2013). The study of the *Clethrionomys* voles' molar morphology revealed that the bank voles with red-backed vole mitogenome introgression demonstrated typical dental characteristics of *C. glareolus* (Deffontaine *et al*., 2005; Ledevin *et al*., 2010). But not all specimens studied were genotyped, and the data on age-related molar variability, which is crucial to the dental analysis of *Clethrionomys* voles, were absent.

In their zone of sympatry in the Southern Urals, full substitution of the native bank vole mitogenome by the red-backed vole one was recorded in *C. glareolus* populations (Melnikova *et al*., 2012). However, the distance between the studied localities exceeded 350 km, and the distribution area and variability of the introgression frequency in the region remained unclear. Furthermore, the new data from the Southern Urals territory is of particular interest in relation to the putative Southern Ural Last Glacial Maximum refugium (Markova *et al*., 2008), from which some modern genetic lineages of *Clethrionomys* were suggested to have originated (Deffontaine *et al*., 2005; Melnikova *et al*., 2012; Kohli *et al*., 2015), and which is important both for studying the phenomenon of introgression, and for reconstructing the evolutionary history of *Clethrionomys* species.

This study presents the results of genetic and morphological analyses of *Clethrionomys* voles from the territory of the Southern Urals, obtained with the aim of clarifying the distribution area of the *C. rutilus* mitogenome introgression into the gene pool of *C. glareolus* in the southern part of the zone of sympatry, and assessing the frequency of occurrence and morphological features of individuals with introgression. Taking the new data into account, the hypotheses about the origin and history of the formation of the modern area of distribution of mitochondrial introgression in the genus *Clethrionomys* have been discussed.

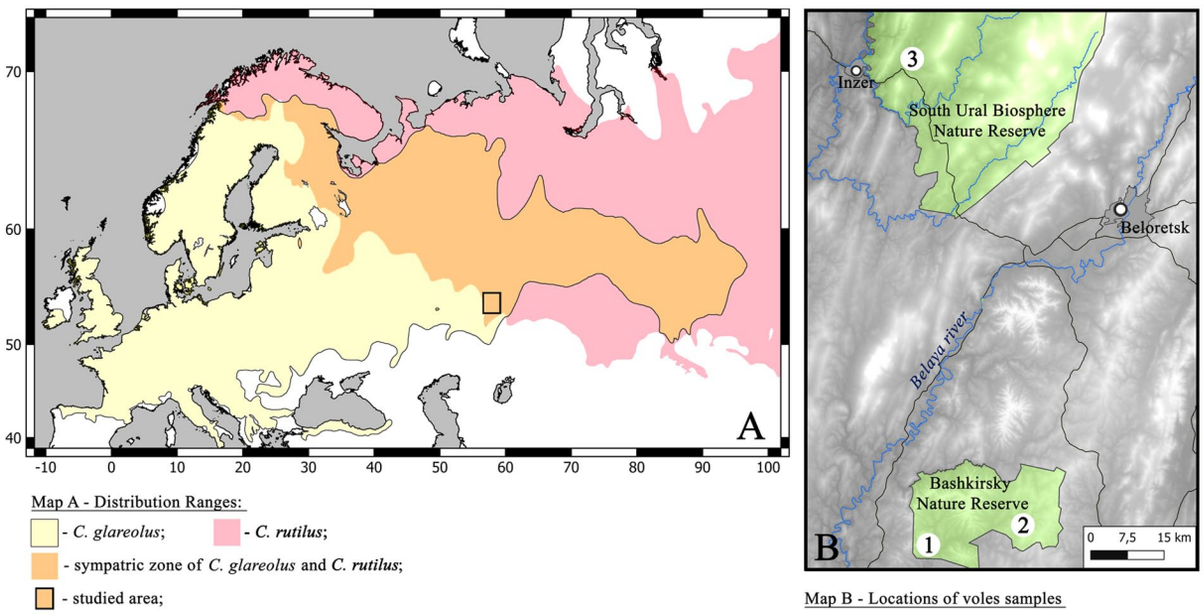

Fig. 1. Bank vole *C. glareolus* (Hutterer *et al*., 2021) and red-baked vole *C. rutilus* (Linzey *et al*., 2020) distribution ranges and their sympatric zone (map A). Locations of studied samples (map B): 1 — the Sargaya Village, Republic of Bashkortostan, 53.34°N, 57.78°E (n = 6); 2 — "Ural-Tau", the mountainous part of the Bashkirsky Nature Reserve, 53.40°N, 58.07°E (n = 2); 3 — "8-th branch" checkpoint of the South Ural Biosphere Nature Reserve, 54.23°N, 57.72°E (n = 21). n — sample size.

Material and methods

Clethrionomys specimens captured in 2022 from three localities near the southern border of the sympatry zone of *C. glareolus* and *C. rutilus* in the Southern Urals (Fig. 1) were studied with molecular genetics and morphology methods. Among 29 animals studied, 23 specimens were identified as bank voles and six specimens as red-backed voles using their exterior characteristics.

In the morphological studies, general metric and morphotypic dental characteristics (Fig. 2), which have been used for *Clethrionomys* species determination (Borodin, 2009; Fominykh, 2011), and the crown complexity ranks of the diagnostic molars (Markova, 2014) were analyzed. Dental ontogenetic stages, determined based on formation and wear degrees of the chewing surface and the root development, were considered, as age-related variability can significantly affect dental variation in *Clethrionomys* voles (Fominykh *et al*., 2010; Fominykh, 2011). Thus, three age groups among the specimens were formed: young animals with 4th stage molars, definitive ones with 5th –7th stage molars and old ones with 9th–10th stage molars (Fig. 2).

DNA was extracted from the muscle tissue pieces preserved in ethanol 96% using the "DNK-Extran-2" kit (Syntol, cat. № EX-511) according to the manufacturer's protocol. Interspecies hybridization and introgression detection was performed with the real-time multiplex qPCR method (Sibiryakov *et al*., 2021), which can determine nuclear (*LCAT*) and mitochondrial

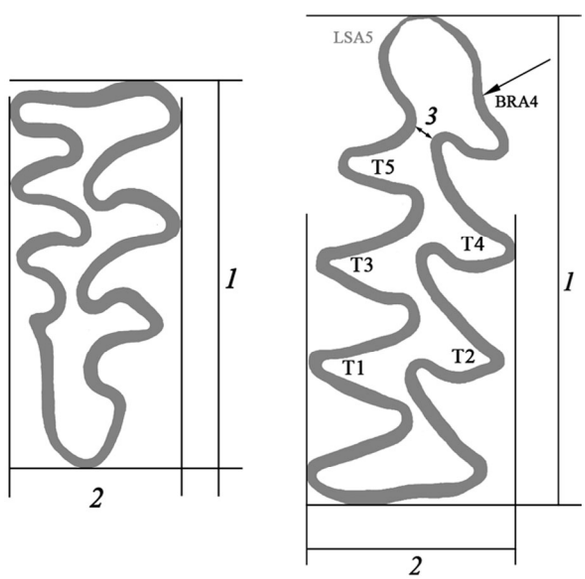

Fig. 2. Contour of the M3 and m1 based on example of *C. glareolus* with the general molar dimensions: 1 — molar length; 2 — molar width; 3 — width of confluence at the base of the anteroconid, and some elements of the occlusal surface of molars: BRA4 — buccal reentrant angle on the anteroconid m1; LSA5 — lingual salient angle on the anteroconid m1; T1–T5 — triangles.

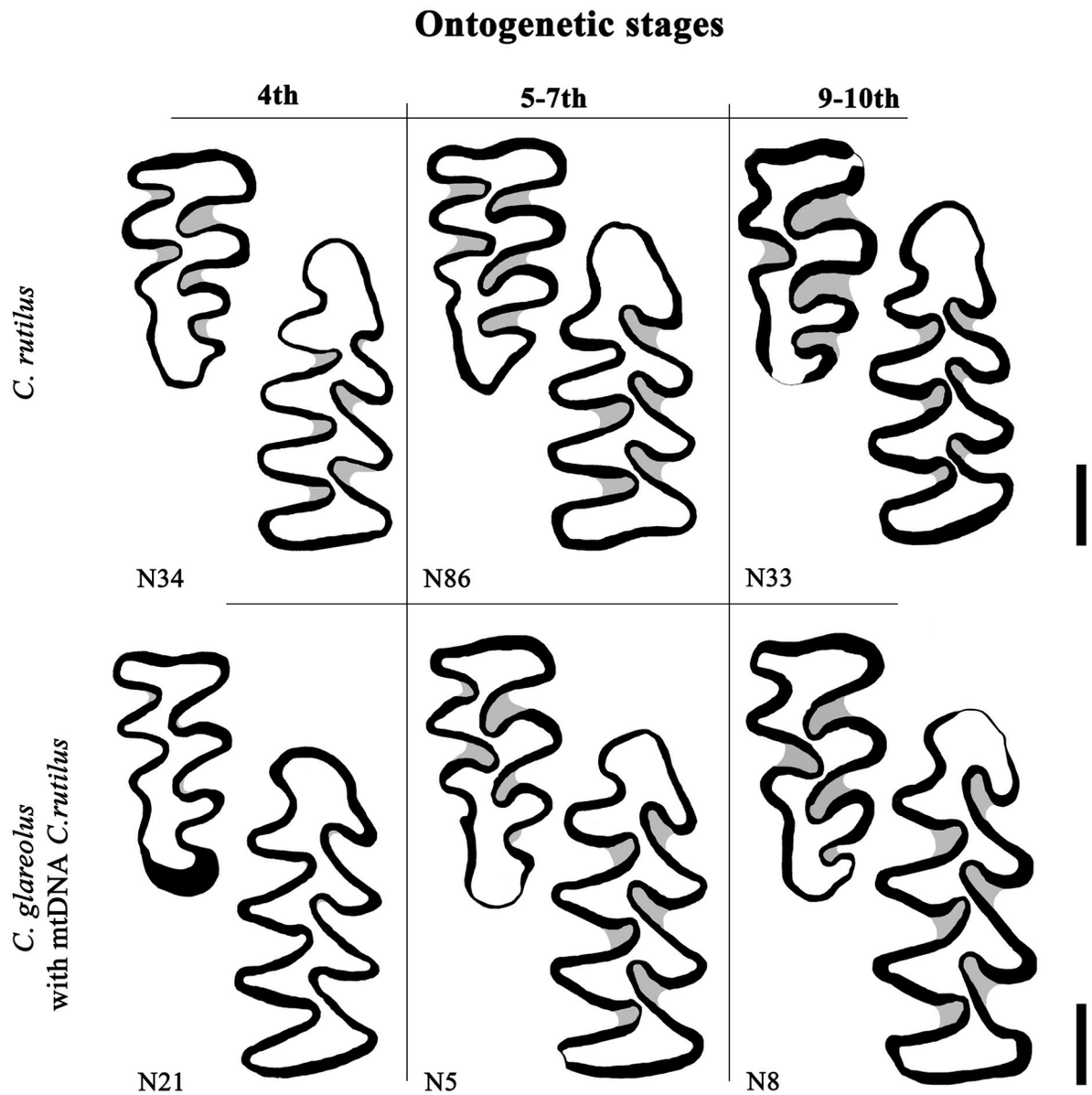

Fig. 3. Configuration of the molars in genotyped *C. rutilus* and *C. glareolus* with mtDNA *C. rutilus* from the Southern Urals (№ — specimen number) on 4th (young), 5th–7th (definitive) and 9th–10th (old animals) ontogenetic stages. Scale bar 0.5 mm.

(*MT-COI*) loci species affiliation simultaneously in one tube. PCR products are 100–130 bp in length, thus making it possible to genotype a wide sample spectrum, including museum material with poor DNA preservation. The following oligonucleotides were used: for *LCAT* nuclear marker — qLCAT_Fw2 (5' CTATGACTGGCGTTTGGAACC 3') and qLCAT_Rw2 (5' TCTTGCTGGCCTGGAGATG 3') as primers, LCAT_Glar (VIC-5' TAGCAGGGAATGGGTTGGGGG 3'-BHQ1) and LCAT_Rut (FAM-5' TTGCGGGGGATGGGTTGGG 3'-BHQ1) as probes; for *MT-COI* mitochondrial marker — qCOI_Fw2 (5' GCACACGCAGGAGCATC 3') and qCOI_Rw2 (5' GGTTTGATATTGTGTTATGGCTGG 3') as primers, COI_probe_G2 (Cy5-5' AGCAGGTGTCTCATCAATCTTAG 3'-BHQ2) and COI_probe_R2 (ROX-5' AGCAGGAGTTTCATCAATTTTAG 3'-BHQ2) as probes. Primers are universal for both species and probes are sensitive to interspecific *C. glareolus*/*rutilus* substitutions: *LCAT* probes recognize the 1457–1477 site (genomic coordinates on NW_025965159.1:581906-585083) with 1458(A/T), 1461(A/G), 1465(A/G) substitutions; *MT-COI* probes recognize the 456–478 site (genomic coordinates by KF918859.1:5309-6853) with 462(T/A), 465(C/T),

474(C/T) substitutions. The reaction mix was made as follows: 15 µl H_2O; 2.5 µl 10xPCR-buffer-B for Taq DNA polymerase (Syntol, cat. No. B-009); 1 µl dNTP for PCR 10mM each (SibEnzyme, art. N025); 3 µl $MgCl_2$ 25 mM (Syntol, cat. № B–005); 1 µl oligonucleotides mix 5 pmol/µl each; 0.5 µl SynTaq DNA polymerase 5 u/µl (Syntol, cat. No. E-039-10000); 2 µl genomic DNA solution 20 ng/µl. Reaction conditions were as follows: 95°C — 5:00 min denaturation phase, then 40x(95°C — 0:15, 60°C — 0:15, 72°C — 0:15, fluorescence registration). The reaction was carried out in Touch Real-Time PCR Detection System (Bio-Rad). Bio-Rad CFX Manager 3.1. program was used for fluorescence curve analysis.

Complete sequences of *MT-CYB* (1140bp) were amplified using two primer pairs (L7 (5' ACCAATGACATGAAAAATCATCGTT 3') and H2 (5′ TAGTTGTCTGGGTCTCC 3′); L8 (5′ CTGCCATGAGGACAAATATCATT 3′) and H6 (5' TCTCCATTTCTGGTTTACAAGAC 3') in the 25 µl reaction mix made as follows: dNTP's (SibEnzyme) 2.5 mM each, 10x ASBuffer (SibEnzyme), 50 mM $MgCl_2$ (Fermentas), 2.5 pM of each primer, 5U Taq DNA Polymerase (SibEnzyme), 50–100 ng DNA matrix); reaction conditions were as follows: 94°C — 3:00 min, 35x(94°C — 00:20, 58°C — 00:15, 72°C — 01:20), 72°C — 10:00) using amplifiers MyCycler (BioRad) and T100 (BioRad). The PCR product was purified with the "QIAquick® Gel Extraction Kit" (Qiagen, Germany). Sequencing was performed with the "BrilliantDye® Terminator Cycle Sequencing Kit V3.1" (NimaGen, Netherlands) in two directions with the same primers used for PCR, using the "NANOFOR-05" (Syntol, Russia) genetic analyzer at the Center for Collective Use of IPAE UB RAS. The sequence readings were checked for errors and corrected manually (BioEdit v. 7.2.0 (4.30.2013) (Hall, 1999)). The same procedure was performed for sequencing the *LCAT* gene fragment, and the primers were the same as for qPCR.

The produced sequences were aligned with the GenBank ones (*MT-CYB*: Appendices 1, 3; *LCAT*: Appendices 2, 4) using the MUSCLE algorithm (Edgar, 2004) integrated into Unipro UGENE (Okonechnikov *et al*., 2012). The Bayesian phylogeny of *MT-CYB* gene was inferred using MrBayes 3.2.7a x86_64, parallel version (Ronquist *et al*., 2012). 30 000 000 generations were performed with default parameters and the Bayesian model selection using rjMCMC model selection procedure (Huelsenbeck, 2004). The final dataset encompassed 196 unique nucleotide sequences with 1140 base pairs, partitioned by codon positions. The *LCAT* sequences were phased in DnaSP v6 (Rozas *et al*., 2017), and the haplotype network was constructed using the TCS algorithm in PopART v1.7 (Clement, 2002).

Results

Dental morphology data were consistent with the data on species determination based on exterior characteristics. Six specimens had typical *C. rutilus* characteristics: the anteroposteriorally compressed crown shape of the molars, wide confluence at the base of the simple configuration of m1 anteroconid without additional reentrant and salient angles (mean values of m1 complexity: M±SD (4th–5th stages) = 1.62±0.25, M±SD (6th–7th stages) = 1.75±0.42) and alteration of wide and narrow dentin fields confluences (Fig. 3). Molar size was consistent with the *C. rutilus* typical scope (Borodin, 2009). The general dimensions of the diagnostic molars (Fig. 2) were consistent with the range of variability of dimensional measurements described in *C. rutilus* (Borodin, 2009).

The dental characteristics of the other 23 specimens corresponded to those described previously in *C. glareolus* from the Ural populations (Fominykh, 2011). These specimens had a more complex anteroconid of m1 with buccal reentrant BRA4 and lingual salient LSA5 angles (mean values of m1 complexity: M±SD (4th–5th stages) = 2.04±0.26, M±SD (6th–7th stages) = 2.07±0.51), and T1–T5 triangles with less wide confluences, including those at the base of the anteroconid (Fig. 3). The dimensional parameters of the molars corresponded to those in *C. glareolus* (Borodin, 2009).

Genotyping of the studied *Clethrionomys* voles revealed that 23 of the 29 analyzed specimens bore homozygous *C. glareolus LCAT* allele and six animals bore homozygous *C. rutilus LCAT* allele, and all the

Table 1. Results of PCR typing and dental morphology analysis of *Clethrionomys* voles from the zone of sympatry in the Southern Urals.

Locality №	Morphology-based species identification			Genetic marker-based species identification		
	Metric characteristics	Morphotypical characteristics	Number of specimens	*LCAT*	*COI*	Number of specimens
1	G	G	6	GG	R	6
2	G	G	2	GG	R	2
3	G	G	15	GG	R	15
	R	R	6	RR	R	6

Notes: Locality № correspond to Fig. 1, *COI* — mitochondrial marker, *LCAT* — nuclear marker, G — *C. glareolus* marker variant, R — *C. rutilus* marker variant.

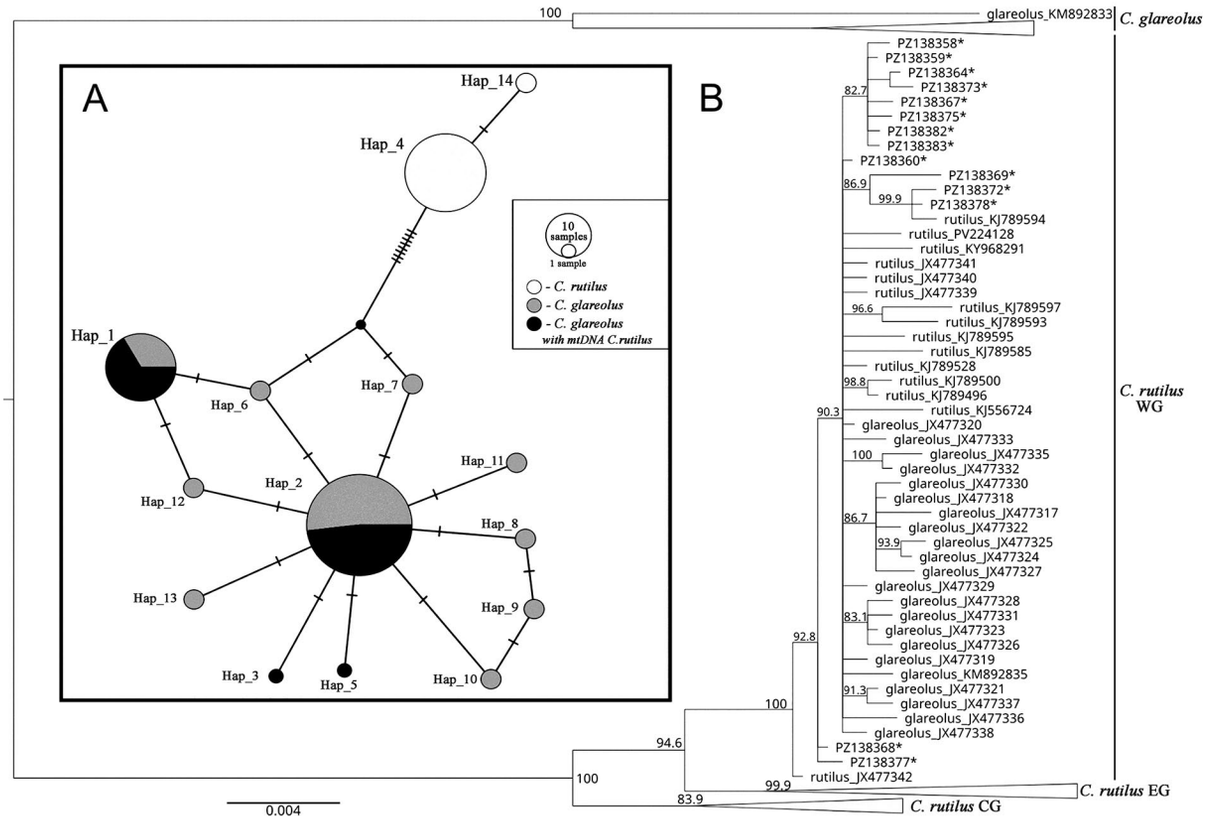

Fig. 4. Phylogenetic reconstructions based on *MT-CYB* and *LCAT* genes. A — TCS haplotype network of *LCAT* gene. Hatch marks represent substitutions; circles sizes are proportional to haplotype numbers. *C. rutilus* haplotypes denoted with white, *C. glareolus* with gray, and *C. glareolus* with *C. rutilus* mtDNA introgression — with black colors. B — Bayesian tree of *MT-CYB* with posterior probabilities (%) of nodes. *C. rutilus* mitochondrial clades: Western group (WG), Eastern (EG) and Central (CG). *C. glareolus*, Central and Eastern clades are collapsed since they don't contain any taxonomically discordant sequences. Haplotypes sequenced in this study are marked with asterisk. Species affiliation of sequences according to GenBank accessions indicated with "rutilus" or "glareolus" before accession number.

genotyped animals had *C. rutilus* mitochondrial marker *MT-COI* (Table 1). Individuals heterozygous for the nuclear *LCAT* gene, as well as individuals carrying bank vole mtDNA, were not detected.

Comparison of the species identification data using genetical and morphological methods revealed that 23 individuals diagnosed as *C. glareolus* based on their dental characteristics correspond to animals carrying a variant of the nuclear *LCAT* gene of the bank vole and a variant of the mitochondrial *MT-COI* gene of the red-backed vole (Table 1). Six individuals carrying variants of the *LCAT* and *MT-COI* genes of *C. rutilus* exhibit a set of dental characteristics typical for this species.

Cytochrome *b* phylogenetic reconstruction revealed that *C. glareolus* mitotypes, introgressed from *C. rutilus*, are clustered into Western *C. rutilus* mtDNA clade (Fig. 4B), which includes *C. rutilus* populations from northern Europe, western Siberia to Yenisei River, and western Mongolia. This clade was hypothesized to originate from the putative refugium in the vicinity of the Southern Ural (Kohli *et al*., 2015). The *LCAT* haplotype network revealed no shared haplotypes between *C. glareolus* and *C. rutilus*, with clear distinction between the haplotypes of the two species (8 substitutions) (Fig. 4A). Nuclear and mitochondrial genes sequencing confirmed PCR-based species affiliation of genetic markers.

Discussion

The study of *Clethrionomys* vole populations from the zone of *C. glareolus* and *C. rutilus* sympatry in the Southern Urals has shown that, although the dental morphology of the studied animals did not demonstrate a mixture of the species-specific characteristics of the two species, molecular genetic typing recorded a combination of species genetic markers in some specimens. 23 specimens, identified by morphological characteristics as bank voles, had a nuclear marker of this species and a mitochondrial marker of the red-backed vole. The homozygosity of the nuclear gene indicated that these specimens were not first-generation hybrids. Conse-

quently, the observed discrepancy between the species affiliation by the nuclear marker and morphological characteristics and the species affiliation by the mitochondrial marker was the result of *C. rutilus* introgression into the *C. glareolus* gene pool, the frequency of which in the studied samples was 100%.

Genetic data observed in the study testified to the existence of a vast continuous zone of mitochondrial introgression from *C. rutilus* to *C. glareolus* in the Southern Urals, as previous studies had suggested (Melnikova *et al*., 2012). The existence of this zone and its peculiarities such as pronounced asymmetry (mtDNA introgressed from *C. rutilus* to *C. glareolus*, but not in reverse), full substitution of species-specific mtDNA in some populations (as in the studied populations), geographic localization, and the extreme rarity of first-generation hybrids need an explanation. Genetic processes in natural populations are subjects of complex system of factors, causes and effects. For this pair of species, hybridization experiments in laboratory conditions established that heterospecific mating occurs only in the absence of conspecifics, and *C. rutilus* females hybridize better than *C. glareolus* ones (Osipova & Soktin, 2006, 2008), so mating asymmetry may play substantial role in determination of gene flow direction. Some studies suggest adaptive effects of mitochondrial introgression in voles (Boratyński *et al*., 2011; Boratyński *et al*., 2014; Boratyński *et al*., 2016), but there is not enough data for definitive conclusions about influence of mitonuclear interactions on current mitochondrial introgression distribution.

Demographic history is another factor relevant to the geographical distribution of mitochondrial introgression. Gene flow modeling between invasive and native populations revealed that its main direction is from native to invasive species (Currat *et al*., 2008), although symmetric gene flow can be shown if some model parameters are tweaked (Zhang, 2014). In (Melnikova *et al*., 2012) hybridization in the Southern Ural LGM refugium and the consequent dispersal were suggested as the primal mechanism of the modern zone of *C. rutilus* mtDNA introgression into the *C. glareolus* gene pool. Other works also place the *C. rutilus* refugium in the Southern Ural, from which Western *C. rutilus* mt DNA clade is supposed to originate (Kohli *et al*., 2015). Introgressed *C. rutilus* mtDNA from this study and the others are clustered in this clade (Fig. 4B). *C. glareolus* phylogeography studies put eastern bank vole mtDNA clade in the same putative Southern Urals refugium (Deffontain *et al*., 2005, Wojcik *et al*., 2010). But in a later work, the mtDNA introgression in Fennoscandia was suggested to take place in the process of postglacial colonization of this region, thus making it independent from the possible hybridization in the Southern Ural refugium (Marková *et al*., 2020). Refugial introgression hypothesis has its strengths but also meets challenges. If the eastern and introgressed mtDNA clads of *C. glareolus* originated from the same Southern Ural refugium, then one can expect a more uniform distribution of introgressed mitotypes in the Eastern clade range of expansion (from Eastern Europe to Western Siberia), not the observed strict association between introgression and sympatry. Observed distribution requires spatial differentiation of introgressed and non-introgressed populations within refugium, or different closely placed refugia in the vicinity of the Southern Ural for the introgressed and eastern *C. glareolus* clades.

Species composition analysis of rodents from the Quaternary paleontological sites (Borodin, 1988, 1992; Fominykh & Zykov, 2012; Borodin *et al*., 2013; Fominykh & Borodin, 2015) suggests that *C. rutilus* and *C. glareolus* have been sympatrically inhabiting the Middle and Southern Ural at least from the Late Pleistocene. Moreover, the territory of the Middle Ural did not belong to LGM glaciation zone (Svendsen *et al*., 2004).

Among all introgression scenarios, considering our data, the hypothesis of introgression as a result of hybridization between *C. glareolus* and *C. rutilus* during post-LGM recolonization (Potapov *et al*., 2007), seems to be most probable. The following facts support it: 1 — mitochondrial introgression is closely associated with modern sympatry, since all specimens with introgression were captured in the sympatry zone or its vicinity (Deffontaine *et al*., 2005; Abramson *et al*., 2009a, b; Melnikova *et al*., 2012; Sibiryakov *et al*., 2021); 2 — Fennoscandian *C. glareolus* populations with introgression were formed in the process of postglacial recolonization of this territory and are independent from the Southern Ural introgression zone (Marková *et al*., 2020); 3 — hybrids of both mating schemes (female *C. rutilus* × male *C. glareolus* and vice versa) occur in natural populations (Abramson *et al*., 2009a; Sibiryakov *et al*., 2021); 4 — there are common mitotypes introgressed into *C. glareolus* and native to *C. rutilus*, 5 — in the western *C. rutilus* phylogroup, introgressed mitotypes do not form a distinct cluster but are distributed among *C. rutilus* native mitotypes (Melnikova *et al*., 2012).

Conclusion

The detection of *C. rutilus* mtDNA introgression in the *C. glareolus* gene pool in the Bashkirsky Nature Reserve and the South Ural Biosphere Nature Reserve is in accordance with existence of a vast continuous introgression zone in the Southern Ural suggested in previous studies. Hybridization between *C. glareolus* and *C. rutilus* during post-LGM recolonization can be the leading process in contemporary sympatry zone formation, affected by mitonuclear interaction, reinforcement of reproductive barriers and demographic history peculiarities of both species. Ancient and historical hybridization did not leave any trace in dental morphology of *C. glareolus* populations from the Southern Ural.

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Appendix 1. Cytochrome *b* sequences, retrieved from GenBank.

Accession	Species	mtDNA clade	Location	Reference
PV105503	*C. rutilus*	Central	Russia, Yakutia Republic, Tomponskiy Ulus	Tang *et al.*, 2018
KY968291	*C. rutilus*	Western	China, Xinjiang, Habahe County, Baihaba Village	Tang *et al.*, 2018
KY968289	*C. rutilus*	Central	China, Liangshui National Nature Reserve, Dailing District, Heilongjiang	Tang *et al.*, 2018
KY968288	*C. rutilus*	Central	China, Liangshui National Nature Reserve, Dailing District, Heilongjiang	Tang *et al.*, 2018
KY968287	*C. rutilus*	Central	China, Mohe County, Heilongjiang	Tang *et al.*, 2018
AF119274	*C. rutilus*	Eastern	–	Conroy & Cook, 1999
AY309427	*C. rutilus*	Eastern	USA, Alaska, Yakutat	Cook *et al.* 2004
AY309426	*C. rutilus*	Eastern	USA, Alaska, Cordova	Cook *et al.* 2004
AY309425	*C. rutilus*	Central	Russia, Stokovo	Cook *et al.* 2004
AY309424	*C. rutilus*	Central	Russia, Stokovo	Cook *et al.* 2004
JX477291	*C. glareolus*	*C. glareolus*	Finland, Kannus	Boratyński *et al.,* 2014
JX477278	*C. glareolus*	*C. glareolus*	Finland, Kannus	Boratyński *et al.,* 2014
JX477342	*C. rutilus*	Western	Finland, Savukoski	Boratyński *et al.,* 2014
JX477341	*C. rutilus*	Western	Finland, Sotkamo	Boratyński *et al.,* 2014
JX477340	*C. rutilus*	Western	Finland	Boratyński *et al.,* 2014
JX477339	*C. rutilus*	Western	Finland, Sotkamo	Boratyński *et al.,* 2014
JX477320	*C. rutilus*	Western	Finland, Sotkamo	Boratyński *et al.,* 2014
JX477333	*C. glareolus*	Western	Finland, Sotkamo	Boratyński *et al.,* 2014
JX477335	*C. glareolus*	Western	Finland, Savukoski	Boratyński *et al.,* 2014
JX477332	*C. glareolus*	Western	Finland, Sotkamo	Boratyński *et al.,* 2014
JX477330	*C. glareolus*	Western	Finland, Kolari	Boratyński *et al.,* 2014
JX477318	*C. glareolus*	Western	Finland, Kolari	Boratyński *et al.,* 2014
JX477329	*C. glareolus*	Western	Finland, Kolari	Boratyński *et al.,* 2014
JX477317	*C. glareolus*	Western	Finland, Kolari	Boratyński *et al.,* 2014
JX477328	*C. glareolus*	Western	Finland, Kolari	Boratyński *et al.,* 2014
JX477319	*C. glareolus*	Western	Finland, Kolari	Boratyński *et al.,* 2014
JX477321	*C. glareolus*	Western	Finland, Kolari	Boratyński *et al.,* 2014
JX477331	*C. glareolus*	Western	Finland, Kolari	Boratyński *et al.,* 2014
JX477323	*C. glareolus*	Western	Finland, Kolari	Boratyński *et al.,* 2014
JX477322	*C. glareolus*	Western	Finland, Kolari	Boratyński *et al.,* 2014
JX477325	*C. glareolus*	Western	Finland, Kolari	Boratyński *et al.,* 2014
JX477336	*C. glareolus*	Western	Finland, Savukoski	Boratyński *et al.,* 2014
JX477324	*C. glareolus*	Western	Finland, Kolari	Boratyński *et al.,* 2014
JX477327	*C. glareolus*	Western	Finland, Kolari	Boratyński *et al.,* 2014
JX477338	*C. glareolus*	Western	Finland, Savukoski	Boratyński *et al.,* 2014
JX477326	*C. glareolus*	Western	Finland, Kolari	Boratyński *et al.,* 2014

Accession	Species	mtDNA clade	Location	Reference
JX477337	*C. glareolus*	Western	Finland, Savukoski	Boratyński *et al.,* 2014
KJ789597	*C. rutilus*	Western	Russia	Kohli *et al.,* 2015
KJ789595	*C. rutilus*	Western	Russia	Kohli *et al.,* 2015
KJ789594	*C. rutilus*	Western	Russia	Kohli *et al.,* 2015
KJ789593	*C. rutilus*	Western	Russia	Kohli *et al.,* 2015
KJ789585	*C. rutilus*	Western	Russia	Kohli *et al.,* 2015
KJ789580	*C. rutilus*	Eastern	Russia	Kohli *et al.,* 2015
KJ789579	*C. rutilus*	Eastern	Russia	Kohli *et al.,* 2015
KJ789576	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789574	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789572	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789571	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789569	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789568	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789567	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789564	*C. rutilus*	Central	Russia	Kohli *et al.,* 2015
KJ789562	*C. rutilus*	Central	Russia	Kohli *et al.,* 2015
KJ789560	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789555	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789554	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789548	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789547	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789538	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789537	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789535	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789534	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789532	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789531	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789528	*C. rutilus*	Western	Finland	Kohli *et al.,* 2015
KJ789525	*C. rutilus*	Eastern	Canada	Kohli *et al.,* 2015
KJ789524	*C. rutilus*	Eastern	Canada	Kohli *et al.,* 2015
KJ789520	*C. rutilus*	Eastern	Canada	Kohli *et al.,* 2015
KJ789518	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789517	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789516	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789515	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789514	*C. rutilus*	Eastern	Japan	Kohli *et al.,* 2015
KJ789513	*C. rutilus*	Eastern	Japan	Kohli *et al.,* 2015
KJ789512	*C. rutilus*	Eastern	Japan	Kohli *et al.,* 2015
KJ789511	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789509	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015

Accession	Species	mtDNA clade	Location	Reference
KJ789507	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789505	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789504	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789503	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789500	*C. rutilus*	Western	Mongolia	Kohli *et al.,* 2015
KJ789496	*C. rutilus*	Western	Mongolia	Kohli *et al.,* 2015
KJ789490	*C. rutilus*	Eastern	Canada	Kohli *et al.,* 2015
KJ789488	*C. rutilus*	Eastern	Mongolia	Kohli *et al.,* 2015
KJ789487	*C. rutilus*	Eastern	Canada	Kohli *et al.,* 2015
KJ789486	*C. rutilus*	Eastern	Canada	Kohli *et al.,* 2015
KJ789485	*C. rutilus*	Eastern	Canada	Kohli *et al.,* 2015
KJ789484	*C. rutilus*	Eastern	Canada	Kohli *et al.,* 2015
KJ789483	*C. rutilus*	Eastern	Canada	Kohli *et al.,* 2015
KJ789482	*C. rutilus*	Eastern	Canada	Kohli *et al.,* 2015
KJ789481	*C. rutilus*	Central	Russia	Kohli *et al.,* 2015
KJ789480	*C. rutilus*	Central	Russia	Kohli *et al.,* 2015
KJ789479	*C. rutilus*	Central	Russia	Kohli *et al.,* 2015
KJ789478	*C. rutilus*	Central	Russia	Kohli *et al.,* 2015
KJ789477	*C. rutilus*	Central	Russia	Kohli *et al.,* 2015
KJ789476	*C. rutilus*	Central	Russia	Kohli *et al.,* 2015
KJ789473	*C. rutilus*	Eastern	Russia	Kohli *et al.,* 2015
KJ789466	*C. rutilus*	Central	Russia	Kohli *et al.,* 2015
KJ789465	*C. rutilus*	Central	Russia	Kohli *et al.,* 2015
KJ789464	*C. rutilus*	Central	Russia	Kohli *et al.,* 2015
KJ789463	*C. rutilus*	Eastern	Canada	Kohli *et al.,* 2015
KJ789459	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789457	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789456	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789451	*C. rutilus*	Central	Russia	Kohli *et al.,* 2015
KJ789450	*C. rutilus*	Eastern	Canada	Kohli *et al.,* 2015
KJ789449	*C. rutilus*	Central	Russia	Kohli *et al.,* 2015
KJ789446	*C. rutilus*	Central	Russia	Kohli *et al.,* 2015
KJ789445	*C. rutilus*	Central	Russia	Kohli *et al.,* 2015
KJ789443	*C. rutilus*	Central	Russia	Kohli *et al.,* 2015
KJ789439	*C. rutilus*	Eastern	Canada	Kohli *et al.,* 2015
KJ789436	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789434	*C. rutilus*	Eastern	Canada	Kohli *et al.,* 2015
KJ789431	*C. rutilus*	Eastern	Canada	Kohli *et al.,* 2015
KJ789429	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789428	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789427	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015

Accession	Species	mtDNA clade	Location	Reference
KJ789426	*C. rutilus*	Central	Russia	Kohli *et al.,* 2015
KJ789425	*C. rutilus*	Central	Russia	Kohli *et al.,* 2015
KJ789424	*C. rutilus*	Central	Russia	Kohli *et al.,* 2015
KJ789420	*C. rutilus*	Central	Russia	Kohli *et al.,* 2015
KJ789419	*C. rutilus*	Eastern	USA	Kohli *et al.,* 2015
KJ789418	*C. rutilus*	Central	Mongolia	Kohli *et al.,* 2015
KJ789417	*C. rutilus*	Central	Mongolia	Kohli *et al.,* 2015
KJ789410	*C. rutilus*	Central	Russia	Kohli *et al.,* 2015
KJ789409	*C. rutilus*	Central	Russia	Kohli *et al.,* 2015
KJ789408	*C. rutilus*	Central	Russia	Kohli *et al.,* 2015
KJ789407	*C. rutilus*	Central	Russia	Kohli *et al.,* 2015
KJ789406	*C. rutilus*	Central	Russia	Kohli *et al.,* 2015
KJ789405	*C. rutilus*	Central	Russia	Kohli *et al.,* 2015
KJ556724	*C. rutilus*	Western	Russia	Kohli *et al.,* 2015
KJ556636	*C. rutilus*	Central	Russia	Kohli *et al.,* 2015
KJ556622	*C. rutilus*	Eastern	Canada	Kohli *et al.,* 2015
JQ182089	*C. rutilus*	Eastern	USA, Alaska	Hope *et al.,* 2013
JQ182088	*C. rutilus*	Eastern	Canada, Yukon, Rock River	Hope *et al.,* 2013
JQ182087	*C. rutilus*	Eastern	USA, Alaska	Hope *et al.,* 2013
JQ182086	*C. rutilus*	Eastern	USA, Alaska	Hope *et al.,* 2013
JQ182085	*C. rutilus*	Eastern	Canada, Yukon, Rock River	Hope *et al.,* 2013
JQ182084	*C. rutilus*	Eastern	USA, Alaska	Hope *et al.,* 2013
JQ182083	*C. rutilus*	Eastern	USA, Alaska	Hope *et al.,* 2013
JQ182082	*C. rutilus*	Eastern	USA, Alaska	Hope *et al.,* 2013
JQ182081	*C. rutilus*	Eastern	Canada, Yukon, Rock River	Hope *et al.,* 2013
JQ182080	*C. rutilus*	Eastern	USA, Alaska	Hope *et al.,* 2013
JQ182079	*C. rutilus*	Eastern	Canada, Yukon, Rock River	Hope *et al.,* 2013
JQ182078	*C. rutilus*	Eastern	USA, Alaska	Hope *et al.,* 2013
JQ182077	*C. rutilus*	Eastern	USA, Alaska	Hope *et al.,* 2013
JQ182076	*C. rutilus*	Eastern	USA, Alaska	Hope *et al.,* 2013
JQ182075	*C. rutilus*	Eastern	USA, Alaska	Hope *et al.,* 2013
JQ182073	*C. rutilus*	Eastern	USA, Alaska	Hope *et al.,* 2013
JQ182072	*C. rutilus*	Eastern	USA, Alaska	Hope *et al.,* 2013
JQ182069	*C. rutilus*	Central	Russia, Sakha, Kenkeme River	Hope *et al.,* 2013
JQ182068	*C. rutilus*	Central	Russia, Sakha, Yakutsk	Hope *et al.,* 2013
JQ182067	*C. rutilus*	Central	Russia, Sakha, Indigirka River Basin	Hope *et al.,* 2013
JQ182066	*C. rutilus*	Central	Russia Chelmodzha	Hope *et al.,* 2013
JQ182065	*C. rutilus*	Central	Russia, Magadan, Byunda	Hope *et al.,* 2013
JQ182063	*C. rutilus*	Central	Russia, Magadan, Byunda	Hope *et al.,* 2013
JQ182061	*C. rutilus*	Central	Russia, Sakha, Lena River Basin	Hope *et al.,* 2013

Accession	Species	mtDNA clade	Location	Reference
JQ182060	*C. rutilus*	Central	Russia, Sakha, Kenkeme River	Hope *et al.,* 2013
JQ182059	*C. rutilus*	Central	Russia, Sakha, Kenkeme River	Hope *et al.,* 2013
JQ182058	*C. rutilus*	Central	Russia, Sakha, Amga River Basin	Hope *et al.,* 2013
JQ182057	*C. rutilus*	Central	Russia, Sakha, Amga River Basin	Hope *et al.,* 2013
JQ182056	*C. rutilus*	Central	Russia, Sakha, Amga River Basin	Hope *et al.,* 2013
JQ182054	*C. rutilus*	Eastern	USA, Alaska	Hope *et al.,* 2013
JQ182053	*C. rutilus*	Eastern	USA, Alaska	Hope *et al.,* 2013
JQ182052	*C. rutilus*	Eastern	USA, Alaska	Hope *et al.,* 2013
JQ231219	*C. rutilus*	Central	Russia, Sakha, Stokovo Station	Hope *et al.,* 2013
AF272632	*C. rutilus*	Eastern	USA	Cook *et al.,* 2001
AF272631	*C. rutilus*	Eastern	USA	Cook *et al.,* 2001
MK482363	*C. rutilus*	Central	China	Zhi-Min *et al.,* 2019
FJ881431	*C. glareolus*	*C. glareolus*	Poland, Lesno	Wójcik *et al.,* 2010
FJ881473	*C. glareolus*	*C. glareolus*	Poland, Bialowieza	Wójcik *et al.,* 2010
MN103073	*C. glareolus*	*C. glareolus*	Sweden	Marková *et al.,* 2020
MN103104	*C. glareolus*	*C. glareolus*	Finland, Vammala	Marková *et al.,* 2020
MN103101	*C. glareolus*	*C. glareolus*	Finland, Tohmajärvi	Marková *et al.,* 2020
KM892810	*C. glareolus*	*C. glareolus*	Czech Republic, Uherský Brod	Filipi *et al.,* 2015
KM892813	*C. glareolus*	*C. glareolus*	Croatia, Jastrebarsko	Filipi *et al.,* 2015
KM892833	*C. glareolus*	*C. glareolus*	Italy, Calabria	Filipi *et al.,* 2015
KM892835	*C. rutilus*	Western	Norway, Rana	Filipi *et al.,* 2015
PV224128	*C. rutilus*	Western	Russia, Krasnoyarsk Krai, Turukhanskiy District	–
KU859998	*C. rutilus*	Central	–	–
MN487102	*C. rutilus*	Central	China?	–

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Appendix 2. *LCAT* sequences retrieved from GenBank.

Accession	Haplotype (phased	LCAT species affiliation	Location	Reference
GQ267506	Hap_2	glareolus	–	Abramson *et al.,* 2009
JF807925	Hap_2	glareolus	Russia, Tomsk Region	Melnikova *et al.,* 2012
JF807926	Hap_2	glareolus	Russia, Sverdlovsk Region	Melnikova *et al.,* 2012
JF807927	Hap_2	glareolus	Russia, Sverdlovsk Region	Melnikova *et al.,* 2012
JF807928	Hap_6	glareolus	Russia, Sverdlovsk Region	Melnikova *et al.,* 2012
JF807929	Hap_2	glareolus	Russia, Komi Republic	Melnikova *et al.,* 2012
JF807930	Hap_2	glareolus	Russia, Karelia Republic	Melnikova *et al.,* 2012
JF807931	Hap_2	glareolus	Russia, Sverdlovsk Region	Melnikova *et al.,* 2012
JF807932	Hap_2	glareolus	Russia, Sverdlovsk Region	Melnikova *et al.,* 2012
JF807933	Hap_7	glareolus	Russia, Sverdlovsk Region	Melnikova *et al.,* 2012
JF807934	Hap_2	glareolus	Russia, Sverdlovsk Region	Melnikova *et al.,* 2012
JF807936	Hap_1	glareolus	Russia, Karelia Republic	Melnikova *et al.,* 2012
JF807937	Hap_1	glareolus	Russia, Karelia Republic	Melnikova *et al.,* 2012
JF807938	Hap_1, Hap_2	glareolus	Russia, Karelia Republic	Melnikova *et al.,* 2012
JF807939	Hap_2	glareolus	Russia, Karelia Republic	Melnikova *et al.,* 2012
JF807940	Hap_2	glareolus	Russia, Tomsk Region	Melnikova *et al.,* 2012
JF807941	Hap_1, Hap_2	glareolus	Russia, Chelyabinsk Region	Melnikova *et al.,* 2012
JF807942	Hap_2	glareolus	Russia, Sverdlovsk Region	Melnikova *et al.,* 2012
JF930082	Hap_8	glareolus	Finland	Boratyński *et al.,* 2011
JF930083	Hap_9	glareolus	Finland	Boratyński *et al.,* 2011
JF930084	Hap_2	glareolus	Finland	Boratyński *et al.,* 2011
JF930085	Hap_10	glareolus	Finland	Boratyński *et al.,* 2011
JF930086	Hap_11	glareolus	Finland	Boratyński *et al.,* 2011
JF930087	Hap_12	glareolus	Finland	Boratyński *et al.,* 2011
JF930088	Hap_1	glareolus	Finland	Boratyński *et al.,* 2011
JF930089	Hap_13	glareolus	Finland	Boratyński *et al.,* 2011
JF807915	Hap_4	rutilus	Russia, Sverdlovsk Region	Melnikova *et al.,* 2012
JF807916	Hap_4	rutilus	Russia, Komi Republic	Melnikova *et al.,* 2012
JF807917	Hap_4	rutilus	Russia, Sverdlovsk Region	Melnikova *et al.,* 2012
JF807918	Hap_4	rutilus	Russia, Sverdlovsk Region	Melnikova *et al.,* 2012
JF807919	Hap_4	rutilus	Russia, Chelyabinsk Region	Melnikova *et al.,* 2012
JF807920	Hap_4	rutilus	Russia, Arkhangelsk Region	Melnikova *et al.,* 2012
JF807921	Hap_4	rutilus	Russia, Sverdlovsk Region	Melnikova *et al.,* 2012
JF807922	Hap_4	rutilus	Russia, Karelia Republic	Melnikova *et al.,* 2012
JF807923	Hap_4	rutilus	Russia, Chelyabinsk Region	Melnikova *et al.,* 2012
JF807924	Hap_14	rutilus	Russia, Sakhalin Island	Melnikova *et al.,* 2012
JF930090	Hap_4	rutilus	Finland	Boratyński *et al.,* 2011
KC962327	Hap_4	rutilus	Russia, Chelyabinsk Region	Bodrov *et al.,* 2016

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Appendix 3. Cytochrome *b* sequences derived from collected material.

Accession	Collection ID	Species	Location
PZ138358	Cl5	*Clethrionomys glareolus*	Sargaya
PZ138359	Cl6	*Clethrionomys glareolus*	Sargaya
PZ138360	Cl7	*Clethrionomys glareolus*	Sargaya
PZ138361	Cl8	*Clethrionomys glareolus*	Sargaya
PZ138362	Cl9	*Clethrionomys glareolus*	Sargaya
PZ138363	Cl10	*Clethrionomys glareolus*	Sargaya
PZ138364	Cl21	*Clethrionomys glareolus*	Ural-Tau
PZ138365	Cl25	*Clethrionomys glareolus*	8-th branch
PZ138366	Cl26	*Clethrionomys glareolus*	8-th branch
PZ138367	Cl28	*Clethrionomys glareolus*	8-th branch
PZ138368	Cl33	*Clethrionomys rutilus*	8-th branch
PZ138369	Cl34	*Clethrionomys rutilus*	8-th branch
PZ138370	Cl49	*Clethrionomys glareolus*	8-th branch
PZ138371	Cl50	*Clethrionomys glareolus*	8-th branch
PZ138372	Cl51	*Clethrionomys rutilus*	8-th branch
PZ138373	Cl52	*Clethrionomys glareolus*	8-th branch
PZ138374	Cl53	*Clethrionomys glareolus*	8-th branch
PZ138375	Cl55	*Clethrionomys glareolus*	8-th branch
PZ138376	Cl60	*Clethrionomys glareolus*	8-th branch
PZ138377	Cl82	*Clethrionomys rutilus*	8-th branch
PZ138378	Cl86	*Clethrionomys rutilus*	8-th branch
PZ138379	Cl87	*Clethrionomys rutilus*	8-th branch
PZ138380	Cl96	*Clethrionomys glareolus*	8-th branch
PZ138381	Cl97	*Clethrionomys glareolus*	8-th branch
PZ138382	Cl98	*Clethrionomys glareolus*	8-th branch
PZ138383	Cl102	*Clethrionomys glareolus*	8-th branch

Note: “Sargaya” — the Sargaya Village, Republic of Bashkortostan, 53.34°N, 57.78°E; “Ural-Tau” — the mountainous part of the Bashkirsky Nature Reserve, 53.40°N, 58.07°E; “8-th branch” — “8-th branch” checkpoint of the South Ural Biosphere Nature Reserve, 54.23°N, 57.72°E. Groups of the shared haplotypes: PZ138359, PZ138361, PZ138362, PZ138363, PZ138365, PZ138366, PZ138371, PZ138376, PZ138380, PZ138381; PZ138364, PZ138370; PZ138369, PZ138379; PZ138373, PZ138374.

Appendix 4. *LCAT* sequences derived from collected material.

Accession	Collection ID	Species	Haplotype (phased)	Location
PZ196501	Cl5	*Clethrionomys glareolus*	Hap_1	Sargaya
PZ196502	Cl6	*Clethrionomys glareolus*	Hap_2	Sargaya
PZ196503	Cl7	*Clethrionomys glareolus*	Hap_1, Hap_2	Sargaya
PZ196504	Cl8	*Clethrionomys glareolus*	Hap_1	Sargaya
PZ196505	Cl9	*Clethrionomys glareolus*	Hap_1, Hap_2	Sargaya
PZ196506	Cl10	*Clethrionomys glareolus*	Hap_1, Hap_2	Sargaya
PZ196507	Cl16	*Clethrionomys glareolus*	Hap_2	Ural-Tau
PZ196508	Cl21	*Clethrionomys glareolus*	Hap_1, Hap_2	Ural-Tau
PZ196509	Cl25	*Clethrionomys glareolus*	Hap_2	8-th branch
PZ196510	Cl26	*Clethrionomys glareolus*	Hap_2, Hap_3	8-th branch
PZ196511	Cl27	*Clethrionomys glareolus*	Hap_1, Hap_2	8-th branch
PZ196512	Cl28	*Clethrionomys glareolus*	Hap_1, Hap_2	8-th branch
PZ196513	Cl33	*Clethrionomys rutilus*	Hap_4	8-th branch
PZ196514	Cl49	*Clethrionomys glareolus*	Hap_2	8-th branch
PZ196515	Cl50	*Clethrionomys glareolus*	Hap_1, Hap_2	8-th branch
PZ196516	Cl51	*Clethrionomys rutilus*	Hap_4	8-th branch
PZ196517	Cl52	*Clethrionomys glareolus*	Hap_2	8-th branch
PZ196518	Cl53	*Clethrionomys glareolus*	Hap_2	8-th branch
PZ196519	Cl54	*Clethrionomys glareolus*	Hap_2	8-th branch
PZ196520	Cl55	*Clethrionomys glareolus*	Hap_1	8-th branch
PZ196521	Cl60	*Clethrionomys glareolus*	Hap_2	8-th branch
PZ196522	Cl82	*Clethrionomys rutilus*	Hap_4	8-th branch
PZ196523	Cl86	*Clethrionomys rutilus*	Hap_4	8-th branch
PZ196524	Cl87	*Clethrionomys rutilus*	Hap_4	8-th branch
PZ196525	Cl97	*Clethrionomys glareolus*	Hap_1, Hap_2	8-th branch
PZ196526	Cl98	*Clethrionomys glareolus*	Hap_1, Hap_5	8-th branch
PZ196527	Cl102	*Clethrionomys glareolus*	Hap_1, Hap_2	8-th branch

Note: “Sargaya” — the Sargaya Village, Republic of Bashkortostan, 53.34°N, 57.78°E; “Ural-Tau” — the mountainous part of the Bashkirsky Nature Reserve, 53.40°N, 58.07°E; “8-th branch” — “8-th branch” checkpoint of the South Ural Biosphere Nature Reserve, 54.23°N, 57.72°E.