

MtDNA variability in the field vole (*Microtus agrestis* L., 1761, Arvicolinae, Rodentia) in the Urals and adjacent territories

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Motivation: The field vole is a widespread Palearctic species ranging from Western Europe eastwards to Lake Baikal in southeast Siberia [1]. Because of its wide distribution and significant ecological role in ecosystems of different countries, the species often serves as a model for studying spatial patterns of genetic variation. Mitochondrial DNA variation has been relatively well-studied based on *cyt b* [2-6]. However, there are almost no data on the central part of Northern Eurasia (the Urals and adjacent areas). Geographical location of the Ural region determines the diversity of its climatic conditions and the uniqueness of its fauna, comprising both European and Asian elements as well as widespread species of mammal. We hypothesize that biogeographic patterns detectable at the level of species might have been also reflected in intraspecific genetic structure of *M. agrestis*, a native species with well-documented paleontological record in the study area.

The aim is to analyze mtDNA variability in the field vole in the Urals and adjacent territories based on *cyt b* data and to determine phylogeographic status of recent Uralian populations of the species.

Material: Original: 33 samples of *M. agrestis* from 13 localities in the Cis-Urals, the Southern, Middle, Northern Urals, and Western Siberia, 30 haplotypes; GenBank: 350 haplotypes (Fig.1). *M. arvalis*, *M. rossiaemeridionalis*, *M. socialis*, *M. kirgisorum* are used as an out-group.

Methods: Total genomic DNA was isolated by the method of salt extraction. PCR and subsequent sequencing was carried out with primers L7 and H6. Data analysis was carried out in the BioEdit v. 7.2.0 (4.30.2013), MEGA v. 6., Arlequin v. 3.1 and DnaSP v. 5.10 software programs. Construction of phylogenetic trees using Bayesian inference (BI) was carried out in MrBayes v. 3.2.2.

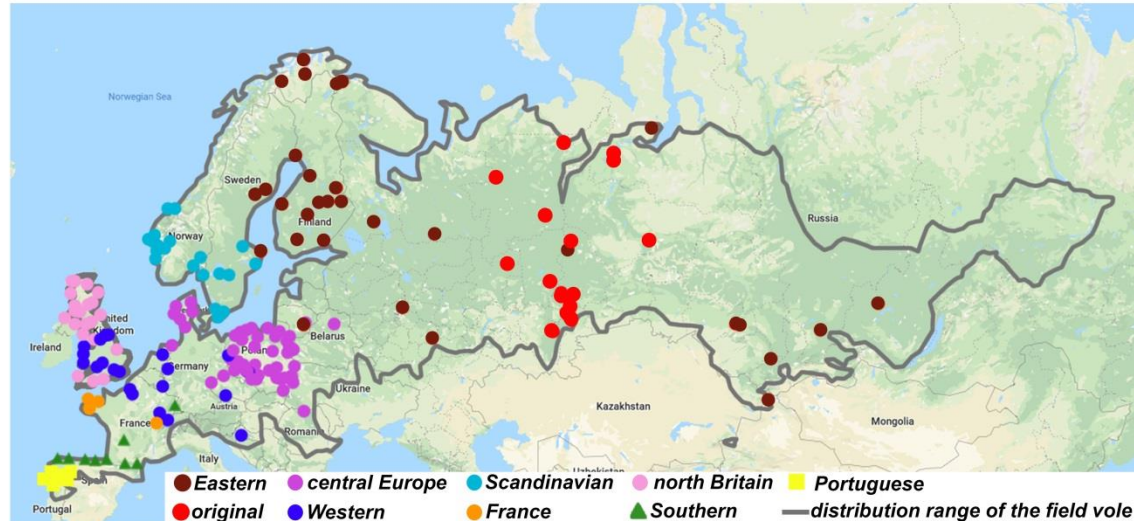


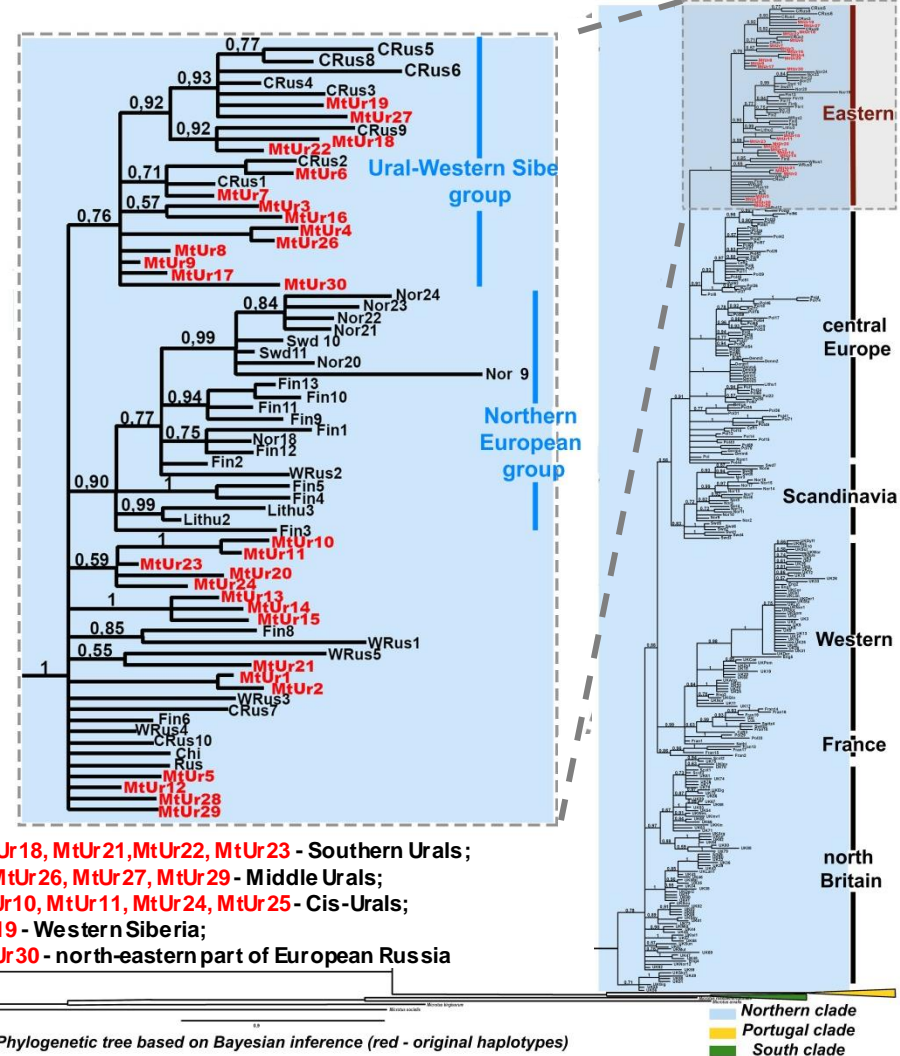
Fig 1. The range of the field vole and the geographic location of the samples

Results

Table. Genetic diversity and values of Tajima's and Fu's tests of six subclades of the Northern clade

| The Northern Clade Haplogroup | N | Nh | $\pi \pm SD, \%$ | D | Fs |
|-------------------------------|-----|----|------------------|-------|-------|
| Eastern | 79 | 66 | 0,800±0,030 | -2,24 | -33,2 |
| Ural-Western Siberia | 35 | 22 | 0,615±0,052 | -1,93 | -18,5 |
| Northern Europe | 44 | 44 | 0,763±0,043 | -2,14 | -33,6 |
| Scandinavia | 32 | 26 | 0,703±0,107 | -1,8 | -14,5 |
| Central Europe | 127 | 88 | 0,902±0,132 | -1,7 | -89,5 |
| France | 6 | 4 | 0,686±0,180 | -0,32 | 1,9 |
| North Britain | 133 | 82 | 0,631±0,115 | -2,0 | -86,4 |
| Western | 109 | 46 | 0,722±0,130 | -2,1 | -67,3 |

N - sample size, Nh - number of haplotypes, π - nucleotide diversity, D - Tajima's neutrality test statistics, Fs - Fu's neutrality test statistics



MtUr1, MtUr2, MtUr3, MtUr4, MtUr12, MtUr17, MtUr18, MtUr21, MtUr22, MtUr23 - Southern Urals;
 MtUr5, MtUr6, MtUr15, MtUr16, MtUr20, MtUr26, MtUr27, MtUr29 - Middle Urals;
 MtUr7, MtUr8, MtUr9 - Northern Urals; MtUr10, MtUr11, MtUr24, MtUr25 - Cis-Urals;
 MtUr13, MtUr14, MtUr19 - Western Siberia;
 MtUr28 - eastern part of European Russia; MtUr30 - north-eastern part of European Russia

Fig2. Phylogenetic tree based on Bayesian inference (red - original haplotypes)

Northern clade
 Portugal clade
 South clade

Conclusions

- **Obtained data on mtDNA variability (complete cyt b gene) in *M. agrestis* in the Cis-Urals, the Southern, Middle, Northern Urals, and Western Siberia expand significantly the geography of investigations of the species genetic diversity.**
- **Analysis of the genetic variability with the inclusion of new data does not contradict present views on the genetic structure of the *M. agrestis* (the Southern, Portugal and Northern clades existence, and the six subclades in Northern clade), but reveals the genetic heterogeneity of populations within the Eastern subclade, which was not previously considered (Fig.2).**
- **Nucleotide diversity and the Tajima's and Fu's values (tests of selective neutrality) of Northern European and Ural-Western Siberian groups are similar to values known for subclades (exclude France) of the Northern clade and indicate their recent expansion (Table).**
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- **To clarify the genetic structure of *M. agrestis* within the wide-ranging Eastern subclade further studies of the species in the central and eastern parts of the Northern Eurasia are necessary.**

References

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