

PHYLOGEOGRAPHY AND INTERSPECIFIC HYBRIDIZATION OF
BANK AND RED VOLES (*CLETHRIONOMYS GLAREOLUS* AND
RUTILUS) IN THE EURASIAN REGION

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Many rodent phylogeographic structures were described in Europe pointing out the impact of climatic changes (e.g. Quaternary glaciations) and the role of the multiple glacial refugia on the genetic diversity of species. This study presents the phylogeography of two Eurasian vole species, the bank vole (*Clethrionomys glareolus*) and the red vole (*Clethrionomys rutilus*) using mitochondrial cytochrome b gene. The bank vole inhabits temperate and boreal forests from Western Europe to Western Siberia and the red vole occurs in forests of Northern Europe spreading eastward across the Eurasian region and the Beringian strait.

The mtDNA phylogeography of bank vole previously described in Europe showed a complex pattern with multiple mediterranean and continental lineages. These results suggested a contraction and expansion of populations from multiple glacial refugia (Iberian, Italian, Balkan, Carpathian). On the other hand, the new sequences from Russian voles reveal a distinct pattern than that in Europe. The phylogenetic reconstructions show a single widespread bank vole lineage in Russia (called 'Eastern lineage'). Concordant with the bank vole pattern, a single lineage is found for the red vole in Northern Europe and in Russia (called 'Western Palaearctic lineage'), while the pattern in the Asian regions is more complex with multiple lineages. The analyses of nucleotide diversity among the eastern lineage of bank vole and the Western Palaearctic lineage of red vole do not support any sampled regions as potential glacial refugia. Two hypotheses may explain these results. (1) Populations in the glacial refugia may be nowadays extinct; alternatively (2), the populations would not have survived in multiple glacial refugia (as it is observed in Europe) but in a single large glacial refugium. This hypothesis is further supported by some paleoenvironmental data that suggest the presence of a forest belt in the south of Russia.

Our study also shows a complex hybridisation event between the two vole species running from Northern Fennoscandia to Southern Urals. The large geographic distribution and connections of these introgressed mtDNA haplotypes suggest both past and recent hybridisation events. In conclusion, the two species display a concordant phylogeographic pattern in Russia that becomes more complex in Europe and in Asia, respectively for bank and red voles. This suggests that both of these forest species may have shared a similar demographic history in Russia with also some hybridisation that may still occurs nowadays.