

Reconstructing the origin and spread of yellow-necked mouse *Apodemus flavicollis* (Rodentia, Muridae) in the Balkans

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The reconstruction of the glacial and postglacial history of species has been in a focus of many genetic researches. A comparative analysis of the levels and patterns of genetic variation across a range of Palaearctic animal taxa has revealed the existence of refugia in the Iberian, Italian and the Balkan peninsula. Numerous studies described the Serbia as a meeting point of different recolonization routes of *A. flavicollis*.

Due to the existence of different natural barriers between studied populations, we expected to find different genetic lineages that survived last glaciations in independent local Balkan refugia. The aim of this study is to assess the population divergence and effects of present and past microevolutionary processes on genetic differentiation of populations and reconstruct phylogenetic history of studied populations.

Empirical data set: Total of 166 individuals from four populations from Serbia were analyzed by AFLPs. Using Arlequine v.3.5 software, molecular variance (AMOVA) was analyzed to examine the amount of genetic variability partitioned within and among the studied populations.

Bayesian clustering method implemented in STRUCTURE software v. 2.3 was used to examine the most likely number of distinct genetic clusters (K) in our data set.

Forward time simulation: Simulation was run for 30 000 generations of spatial migration model which was found to be enough for the system to reach stable F_{ST} values (Easypop software).

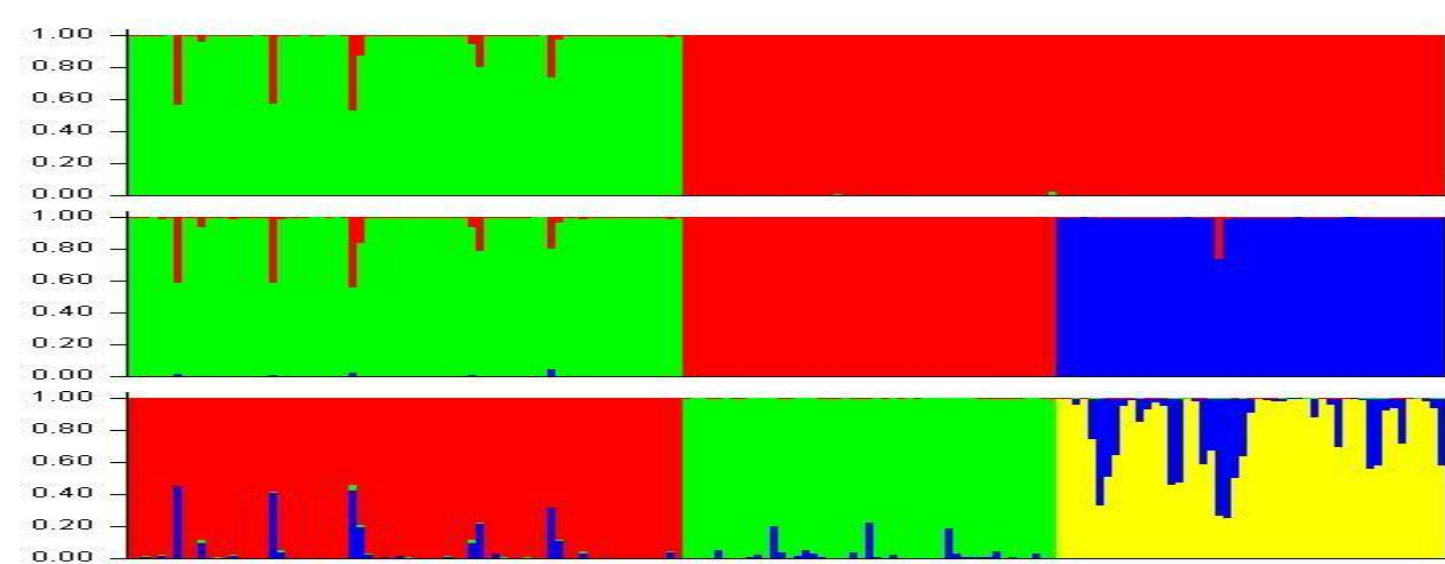
Number of populations was fixed to four virtual sites that corresponded to real sites. Migration rates was set to 0.1, and dispersal rate for females was set to 0.05, and for males to 0.08. Mutation rate was set to be compatible with AFLP loci, i.e. 10^{-4} per generation. A total of 403 loci was simulated and analyzed by Arlequine and Structure software to estimate population structure and detect possible clusters.

Backward time simulation: Using Fastsimcoal 1.1.2 we simulated system consisted of two migration matrices. Scenario assumed 3 ancestral populations with symmetric gene flow. The populations were allowed to diverge to separate populations without gene flow between each other, but with limited gene flow with ancestral population. Scenario simulated 403 loci after 48 000 generations. Simulated data were analyzed by Arlequine and Structure software to estimate population structure and detect possible clusters.

Empirical data set

$F_{ST} = 0.466$

K=2 FG vs TR+BD+ LS
K=3/4 FG vs TR vs DB+LS

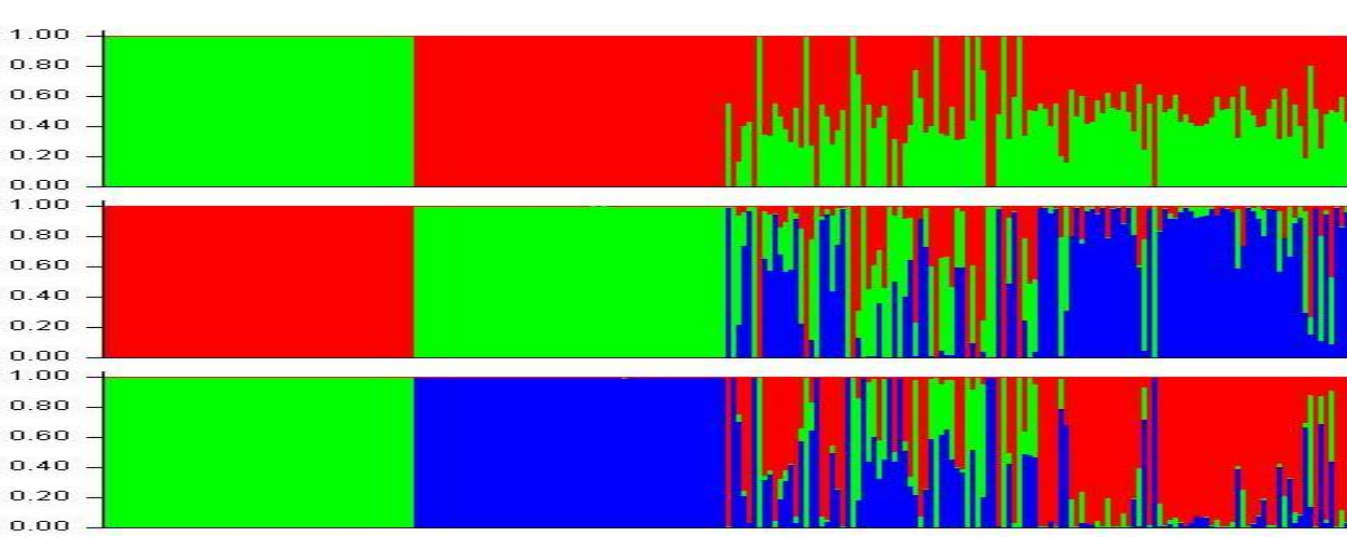


Numerous studies have characterized Balkan Peninsula as source of postglacial colonization of *A. flavicollis*. Studied populations from Serbia seem to have evolved from already isolated populations that correspond to different genetic lineages that survived last glaciations in independent local Balkan refugia.

Forward time simulation

$F_{ST} = 0.534$

K=2 FG vs TR+BD+ LS
K=3/4 FG vs TR vs DB+LS



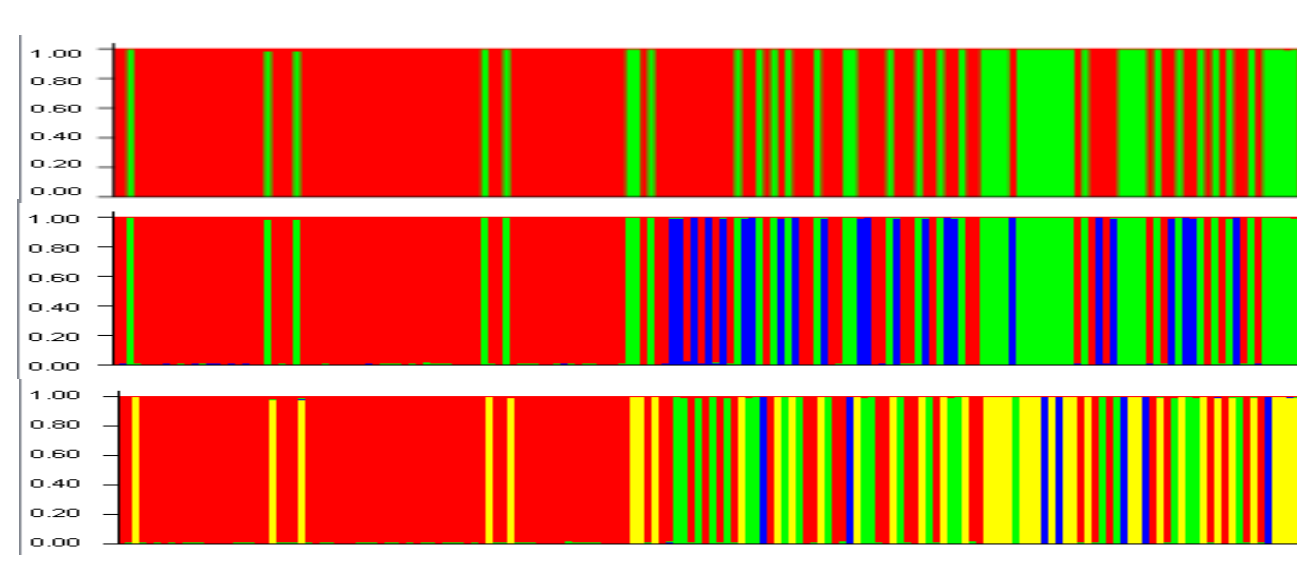
Mantel test
Empirical vs. Backward time data $r=0,4522$ $p=0$

In order to explain the origin and maintenance of the genetic variation we employed computer simulations. Forward and backward simulations were used because they differ in approach, capabilities and computation times, and they are suitable for addressing different questions. The comparison of empirical and simulated data suggests that population divergence in *A. flavicollis* can be best explained through simple migration scheme that includes spatial expansion.

Backward time simulation

$F_{ST}=0.200$

K=2 FG vs TR+BD+ LS
K=3/4 FG vs TR vs DB+LS



Mantel test
Empirical vs. Backward time data $r=0,0695$ $p=0,0136$

The main cause of population structure is history of populations, while we cannot exclude more contemporary causes such as existence of barriers that increase level of genetic differentiation. This study provides new insights into the geographical distribution of the different genetic lineages, and allows better definition of the location of microrefuge.