
Poster Session 1 – Phylogeography

38 Effects of rivers on gene flow in small rodent populations

Zbigniew Borowski¹, Anna Tereba¹, Michal J. Dabrowski²

¹Department of Forest Ecology, Forest Research Institute, Braci Lesnej 3, Sezkocin Stary, Raszyn 05-090 Poland, m.dabrowski@ipipan.waw.pl

²Institute of Computer Science, Polish Academy of Sciences, Jana Kazimierza 5, Warsaw, Poland

Understanding the role of dispersal barriers is crucial for predicting population responses to landscape and environmental changes. That is why in this study we assessed the role of a medium size lowland river (Biebrza), which is a natural barrier, on gene flow and connectivity in the root vole (*Microtus oeconomus*) population in Biebrza National Park (Poland). This is a hygrophilous rodent species which settles on the banks of the rivers, lakes and other watercourses and swims very well. We analysed molecular data of 176 voles, based on eleven DNA microsatellite loci. Voles were caught at six sites – three on each river side in autumn in years 2009 and 2015. Contrary to our expectations we found a strong effect of the river on genetic distance between the root vole populations in some locations only, whereas in other locations we did find none. Our results show that for small rodents, a well-visible river barrier does not have to impact the gene flow. Interestingly, it follows that some of the barriers, invisible to a human, such as type and amount of vegetation, presence of small roads or pastures may strongly influence root vole genetic structure.

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39 Aquatic and terrestrial water voles: phylogeography and morphometrics

Pascale Chevret¹, Zeycan Helvacı², Jean-Pierre Quéré³, Sabrina Renaud¹, Johan R. Michaux⁴

¹LBBE, UCBL-Lyon 1, Villeurbanne, France, pascale.chevret@univ-lyon1.fr

²Aksaray Üniversitesi Fen Edebiyat Fakültesi, Aksaray, Turkey

³CBGP, Campus international de Baillarguet, Montferrier-sur-Lez, France

⁴Laboratoire de génétique de la conservation, ULG, Liège, Belgium

Water voles from the genus *Arvicola* display an amazing ecological versatility, with aquatic and terrestrial populations. Their taxonomic status and evolutionary relationships have caused a long-standing dispute. Two aquatic (*Arvicola sapidus*, *Arvicola amphibius*) and one fossorial species (*Arvicola scherman*) are currently described. We used mitochondrial cytochrome b (cytb) gene sequences to reconstruct the phylogenetic relationships among fossorial and aquatic water voles belonging to *Arvicola amphibius* (formerly *terrestris*) collected in various regions of Europe. We combined 147 new sequences collected mostly in France, Germany and Great Britain, with available datasets from the entire range to provide an up-to-date phylogeny of this species. Phylogenetic and network reconstructions retrieved 4 major lineages all containing fossorial and aquatic morphotypes, discarding the view of each ecotype corresponding to a distinct species. Morphometric analyses of skull shape were performed on a set of aquatic and fossorial populations documenting the main lineages. Fossorial and aquatic populations tend to display convergent morphological features related to their ecology, blurring a part of the phylogenetic signal. Different allometric trajectories related to the constraints of the aquatic vs. subterranean habitats may contribute to this morphological convergence.

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40 Local persistence of Mann's soft-haired mouse *Abrothrix manni* (*Cricetidae*, *Sigmodontinae*) during Quaternary glaciations in southern Chile

Guillermo D'Elia, Lourdes Valdez

Guillermo D'Elia, Universidad Austral de Chile, Valdivia, Chile, guille.delia@gmail.com

Here we present results of a phylogeographic study focused on the recently described sigmodontine species *Abrothrix manni* that is distributed in the temperate Valdivian forests in southern Chile and its neighboring areas of Argentina. Analyses were based on the first 801 bp of the mitochondrial gene Cytochrome-b from 49 individuals of *Abrothrix manni* from 10 collection localities, covering most part of the known distribution range of the species. Genealogical and demographic analyses depict for *Abrothrix manni* a history of local divergence and population long-term persistence even when facing Pleistocene climate oscillations. This information adds up to the growing evidence of a lowland coastal refuge, which would also include low altitude Andean sites.

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41 Root vole *Microtus oeconomus* in the post-glacial landscape: how the history of the Pleistocene glaciations and a contemporary distribution of habitats reflects the genetic structure of the population

Elżbieta Jancewicz¹, Ewa Falkowska²

¹Department of Forest Zoology and Game Management, Faculty of Forestry, Warsaw University of Life Sciences – SGGW, Warsaw, Poland, elzbieta.jancewicz@wl.sggw.pl

²Faculty of Geology, University of Warsaw, Warsaw, Poland

The contemporary distribution of habitats in central and north-east Europe is largely the result of the processes occurring during the Pleistocene glaciations. This is due to the fact that the quaternary successive glaciations in the northern hemisphere in Eurasia had a diversified and generally smaller range. We checked, therefore, whether and how the landscape shaped as a result of subsequent glaciations affects the diversity and sustainability of the population, expressed by the genetic diversity of the species. We assumed that in Europe and Asia: (1) different history of glaciation at different latitudes translates into (i) different number and different character (e.g. connectivity) of favorable habitats and also (ii) various time of colonization by species in post-glacial landscape zones; (2) a different number of favorable habitats and a different level of their connectivity/isolation means a various course of in situ evolution; (3) different connectivity of favorable habitats, their different attractiveness and different availability translate into various directions and intensity of modern species migration. We studied root vole *Microtus oeconomus* (*Arvicolinae*, *Cricetidae* *Rodentia*), model species of small mammals preferring humid habitats. The research was carried out in eastern Poland in 33 locations in different landscape zones shaped by subsequent Pleistocene glaciations: Sanian 1, Sanian 2, Odranian, Warthanian, Vistulian and at different distances from the southern boundary of the present occurrence of the species. Samples of tissue were collected from 439 individuals of root vole during live trapping in boggy and meadows habitats. Based on the analysis of 908 bp of cytochrome b (mtDNA) and 12 microsatellite loci, the genetic structure of *Microtus oeconomus* in studied area was determined. The results show the genetic dissimilarity of some populations in zones. The relationship between genetic diversity and zonal variability of the post-glacial landscape and the distribution of optimal habitats in these zones was found.

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42 Genetic variation and population structure of the red squirrel (*Sciurus vulgaris*) in Lithuania

Irma Ražanskė, Indrė Lipatova, Lukas Budginas, Algimantas Paulauskas

Magnus University, Kaunas, Lithuania, indre.lipatova@vdu.lt

Red squirrels (*Sciurus vulgaris*) are occurring in many types of coniferous and mixed deciduous forests and are widely distributed throughout Europe and part of Asia, this species is the only one native to Lithuania. Seventy years ago almost 200 individuals of *Sciurus vulgaris exalbidus* were introduced to Lithuania from Altai. The motivation of introductions was to improve fur quality. The data of genetic diversity of red squirrels in Lithuania are scarce. Red squirrels have been investigated only using random amplified polymorphic DNA method. The aim of this study was to investigate the genetic variability of red squirrels using mitochondrial DNA and microsatellites. All specimens of the red squirrel used in this study were found dead on the road or in the forests. A total 39 samples during the 2001 – 2018 period was collected from different areas of Lithuania. DNA was isolated from frozen muscles of each individual. For microsatellite analysis seven different primers were used to obtain genetic diversity of red squirrels. For mitochondrial DNA analysis primers of D-loop sequence were used, average number of nucleotide differences (k) between Lithuanian red squirrels was 10.167, more than 10 haplotypes (h) were determined. The results revealed high-level genetic diversity of red squirrels in Lithuania.

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43 Phylogeography of the striped field mouse (*Apodemus agrarius*, Pallas 1771): new data from the western part of the disjunctive range

Lidia E. Yalkovskaya, Petr Sibiryakov, Alexander V. Borodin

Institute of Plant and Animal Ecology Ural Division of the RAS, Ekaterinburg, Russia, lida@ipae.uran.ru

The striped field mouse (*Apodemus agrarius*, Pallas 1771) is a typical species of mesic open habitats. It is widely distributed in the temperate zone of the palearctic and oriental regions. The range of *Apodemus agrarius* is represented by two main parts: western part (Europe, Siberia, Kazakhstan) and eastern part (Far East, China) separated by arid and mountainous regions of inner Asia. Due to the wide distribution and presence of numerous local specific populations, the striped field mouse is an excellent model for studying genetic variability and phylogeography. Numerous studies are devoted to the intraspecific genetic variability in *Apodemus agrarius* in the context of phylogeny and phylogeography of the genus *Apodemus*. However, there are almost no data from the central part of northern Eurasia. Thereupon, complete cyt b (1140 bp) and D-loop (865 bp) sequences of 133 specimens of *Apodemus agrarius* from 35 localities in the Urals, western Siberia and Altai were analyzed. The data from the territories studied for the first time expand significantly the geography of the investigations of the species genetic variability. Results of the analysis clarify the phylogeographic structure of the species and allow us to verify the previous hypotheses concerning historical roots and phylogenetic relationships of *Apodemus agrarius* in the western part of the range. The study was supported by RFBR №16-04-01625.