Poster Session 1 – Phylogeography

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

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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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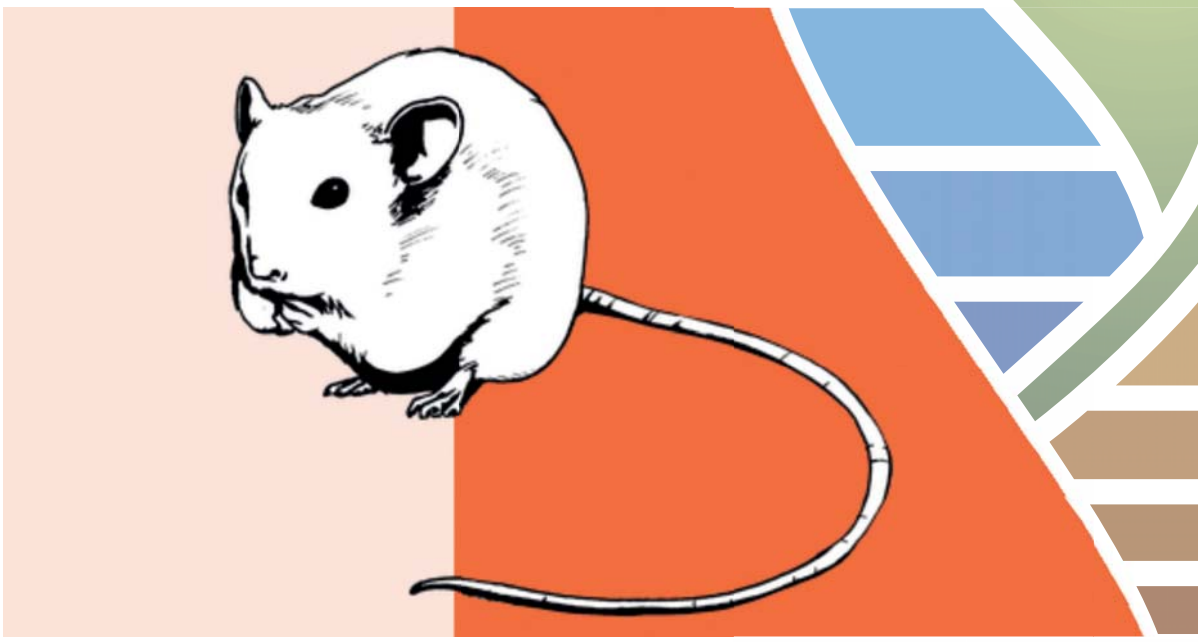

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Bibliografische Information der Deutschen Nationalbibliothek
Die Deutsche Nationalbibliothek verzeichnet diese Publikation
In der Deutschen Nationalbibliografie: detaillierte bibliografische
Daten sind im Internet über http://dnb.d-nb.de abrufbar.

ISSN 1868-9892
ISBN 978-3-95547-059-3
DOI 10.5073/jka.2018.459.000

Printed in Germany by Arno Brynda GmbH, Berlin.