
Phylogeography – Session 2

Ethiopian rodents - extremely diverse, endemic and endangered

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Ethiopia is an African country with very diverse geomorphology, which is reflected in its amazing biodiversity. For example Ethiopian highlands, harbouring the largest areas of Afromontane ecosystems in Africa and one of the most striking elevational ecological gradients on the Earth, are known as one of the most important centres of endemism in the world. Other ecosystems, e.g. Somali-Maasai and Sudanian savannahs, rain forests or semi-deserts, have been less studied, however, available data suggest they also often host endemic evolutionary lineages of otherwise widespread taxa. In this presentation we summarize both published and unpublished genetic data about Ethiopian rodents, collected in two last decades. Using huge genetic datasets of rodents from Ethiopia as well as other regions of sub-Saharan Africa, we will describe their major evolutionary patterns and biogeographical relations. Not surprisingly, the Ethiopian highlands served as a cradle of diversity for numerous mountain taxa - many of them remained endemic in Ethiopia (and often diversified at elevational gradient or in "local" allopatry), but some others dispersed and speciated in southern parts of Eastern Afromontane biodiversity hot-spot. More surprisingly, we found that even taxa living now in the wide belt of Sudanian savanna started their Plio-Pleistocene diversification in Ethiopia, i.e. in the easternmost part of this ecosystem. Last, but not least, unique and geographically restricted Ethiopian rainforests harbour the so-called "palaeoendemics", i.e. the evolutionary lineages that survived here several millions years, but are now highly endangered because of intense exploitation by humans. The research was funded by the Czech Science Foundation project No. 18-17398S and the Russian Foundation for Basic Research project No. 18-04-00563.

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Biogeography of small mammals in south-western Angola: the first genetic evidence

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Angola represents one of the most understudied African countries with respect to biodiversity at all levels. Furthermore, Angola represents an area which holds particular interest for biogeographers owing to its immense habitat diversity and the confluence of three very different biomes: northern Congo basin lowland forests, eastern Zambezi miombo woodlands and southern Namib Desert. Although recent activities of various research groups brought some interesting results about the diversity and biogeographic affinities of Angolan birds, virtually nothing is known about mammals. Especially small mammals are a very useful model for testing the uniqueness/endemicity/biodiversity value since humans have had a strong impact on mammalian distributions in Angola, particularly on those of large carnivores and ungulates during the civil war (1975-2002), when widespread poaching affected strongly a range of species. A field expedition with the main purpose of collecting small mammals was conducted in July 2017. Altogether, we sampled 318 individuals at 11 different localities in south-western Angola. According to external identification, sampled specimens belong to 18 different genera. This high diversity reflects the habitat diversity of sampled localities as we were trapping in dry, semi-desert and desert habitats (typical for some *Elephantulus*, *Petromyscus* and *Gerbilliscus*) up to moist forest (here we found *Lophuromys*, *Aethomys* and *Mus*). Phylogenetic analyses based on DNA barcoding in the context of our collection of samples from mostly eastern and central Africa have revealed an interesting biogeographic pattern in four genera or species lineages (*Mus minutoides*, *Mus triton*, *Mastomys* and *Dendromus*). All of them were represented by two different species or lineages in south-western Angola, the first one has its relatives in the north (southern Democratic Republic of Congo) whilst the second easterly in Zambia.

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Comparative phylogeography of the Mongolian region based on its mammals

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The periodic oscillations of glacials and interglacials have had an enormous impact on formation and changes of global mammal communities. Particularly, refugia play a significant role in species diversification and modification of their genetic diversity. Refugia were crucial for the survival of some taxa and their subsequent recolonization of particular regions or whole continents during inhospitable conditions (glacial elements during interglacial periods and vice versa). The recognition of refuge from a geographical point of view and fauna compositions in certain (macro)regions helps us to understand earlier conditions and biological processes which have influenced the recent diversity and distribution of particular species. Refugia have been well studied, especially in North America and Europe. In the context of the entire Palaearctic Realm, however, it is worthwhile to focus also on refugia in Asia. There are several proposed refuge areas such as: Beringia, South Ural, Caucasus or southern part of Asia. In the recent studies, the area including Altai, (Western) Sayan and the adjacent areas of Mongolia and China is emerging as a significant refugium, especially for glacial species or so-called mammoth-steppe fauna. The current results indicate the peculiarity of local populations and the refugee character of this region and also the key position of the entire Altay-Sayan-western Mongolian region characterized by the continuous presence of grasslands and deserts until at the present since the Late Pleistocene. Within our research, we analyze basic phylogenetic and population-genetic parameters in selected species in order to find out the degree of diversification for sub-populations and corresponding time spans, links to other populations, and current and past biogeographical influences. This is the first introduction of our results realised for several selected species (e.g. *Apodemus peninsulae*, *Microtus gregalis*, *Allactaga sibirica*, *Eolagurus luteus*, *Dipus sagitta*, *Dryomys nitedula*).

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Genetic structure and origin of remnant red squirrel (*Sciurus vulgaris* L.) populations in the south of England

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The Eurasian red squirrel (*Sciurus vulgaris*) is an emblematic species for conservation and represents a good example of the negative effect the impact of alien introductions. Indeed, red squirrel (*Sciurus vulgaris*) populations in the UK have experienced a dramatic decline over the last 60 years due to habitat loss and the spread of the “red squirrel parapox” virus following the introduction of the grey squirrel (*Sciurus carolinensis*). Currently, red squirrel populations in the UK are highly fragmented and need to be closely monitored in order to assess their viability and the success of conservation efforts. The situation is even more dramatic in the south of England, where it survives only on islands where the grey squirrel is absent, and the Isle of Wight is its main stronghold. Using the D-loop, we investigate the genetic diversity and the putative ancestry of the squirrels on three islands from the South of England (Brownsea Island, Furzey Island and the Isle of Wight) in order to infer their conservation status.

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Collagen fingerprinting of Late Pleistocene rodents

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Microfaunal remains are often used as palaeoenvironmental proxies and underpin studies of phylogeography and climate. They provide physical evidence for the presence of species at particular locations and times, and are used to define faunas related to climate stages or events. Consequently, they provide a context in which to examine genetic data and may be used to validate phylogeographic studies. Rodent remains are abundant in numerous sites of archaeozoological interest, potentially forming an important part of the fauna represented there, but are often difficult to identify. For example, postcranial elements from different species are frequently incomplete and indistinguishable, as are many isolated teeth of arvicoline rodents, and this has led to significant mis-identifications in the past. We demonstrate the application of a relatively recent method, collagen fingerprinting (or Zooarchaeology using Mass Spectroscopy: ZooMS), to rodent remains from a Late Pleistocene cave site in England. The method distinguished the arvicoline rodent genera that were present and a range of extant and extinct *Microtus* vole species. ZooMS is much less time-consuming and expensive to apply than modern morphometric or DNA-based techniques, allowing bulk sampling of thousands of specimens. It can be used on a wider variety of material than the former and is not subject to the chronological limits of DNA preservation. It is also less destructive than sampling for ancient DNA, so material is still available for subsequent studies of morphological variation, preservation and taphonomy. The data provide an accurate and comprehensive record of the species present at the site, Pin Hole Cave in Derbyshire, which has previously been designated as the British type location for the Marine Isotope Stage 3 fauna (ca. 60-30 Kya). It is important that definitive faunal data are available from such sites, to provide the essential background for studies of phylogeography and climate change.