

**Post-doc position at the Institute of Vertebrate Biology of the Czech Academy of Sciences**

available from May 2022 to December 2022

**(1) Biogeographic phylogenetic regionalization of the Eastern Afromontane Biodiversity Hotspot, using small mammals as a model animal group**

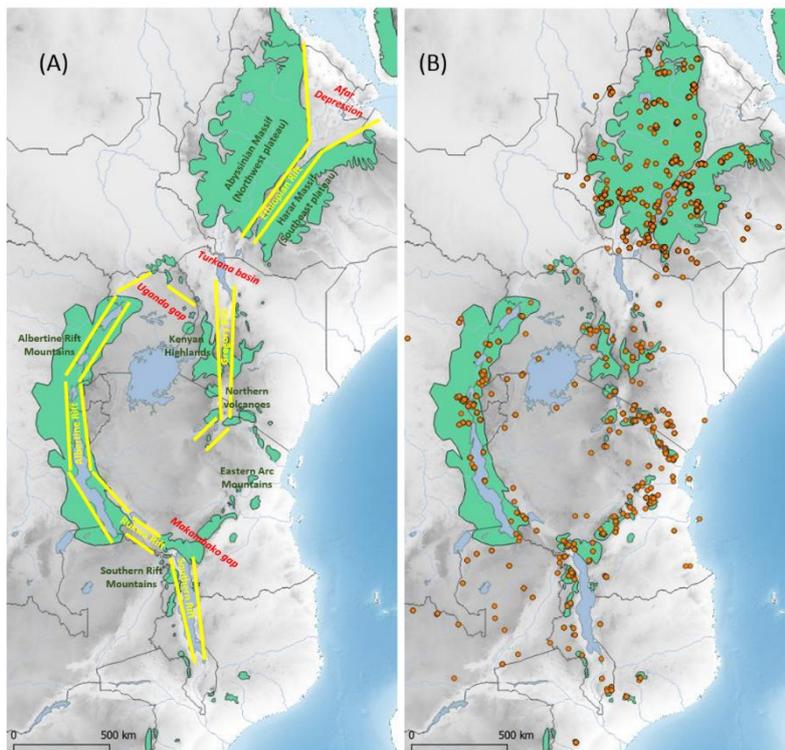
or

**(2) Comparative phylogeography of montane small mammals of Ethiopian highlands**



**Project background:**

The Eastern Afromontane Biodiversity Hotspot (EAMBH; Fig. 1) is one of the biological wonders of the world, with globally significant levels of diversity and with the second highest number of endemic species of higher vertebrates on Earth (after Madagascar). Its ecosystems provide tens of millions of people with freshwater and other ecosystem services that are essential for their survival. Despite its wealth in natural resources, the region is characterized by intense and pervasive poverty. Because most parts of EAMBH are localized in economically poor countries, where human population growth threatens natural ecosystems, **identification of most valuable areas within the large hotspot is necessary for its efficient conservation.** Overall, the hotspot holds nearly 7,600 species of plants, of which more than 2,350 are endemic. The hotspot is also home to nearly 500 mammal species, more than 100 of which are endemic (without taking into account widespread cryptic diversity of small mammals) (BirdLife International 2012). Two parts of EAMBH, the Ethiopian highlands and Albertine Rift Mts., are considered among the most important centres of mammal endemism on Earth. At the same time, they are much endangered and they were included among globally important aggregations of threatened small mammals - they form two of three African IUCN priority Key Regions for conservation (see <https://www.small-mammals.org/conservation-2/key-regions/>).



**The model system:**

**Fig. 1:** (A) Eastern Afromontane Biodiversity Hotspot (EAMBH; in green) as defined by BirdLife International (2012). Yellow lines = East African Rift features, red names = additional expected barriers of the gene flow for Afromontane taxa, green names = major montane complexes. (B) Available material of genetically characterized small mammals. Each dot represent locality, from which we have available genetic data of small rodents. In numerous cases the DNA-barcoded individuals have been already used in our previous studies, so the information on genetic diversity of Afromontane small mammals is already available.

Small terrestrial mammals are used as a principal model animal group. These animals are extremely well suited for comparative studies of microevolutionary processes and for testing alternative hypotheses of biodiversity evolution since late Miocene. They show high level of phylogenetic niche conservatism and low level of dispersal, which is reflected in their **high phylogenetic beta diversity**. Compared to other taxonomic groups, small mammals of Eastern Africa have been recently subjected to intensive phylogeographic research followed by species delimitations, and general patterns of their biodiversity are now emerging.

### **Goal of the project:**

The revolution in phylogenetic systematics has generated unprecedentedly high number of cladograms at very fine spatial scale. They can be used to discover natural "monophyletic" biogeographic areas, which have great explanatory power as they represent natural regions formed by biological and geological evolutionary processes (*sensu* Ebach & Parenti 2015). Recently developed approaches for the so-called phylogenetic regionalization (e.g. Daru et al. 2017) can significantly help to reveal the spatial and evolutionary structure of biodiversity and identify centres of evolutionary radiation, museums of diversity and extinction hotspots.

Ad (1) The post-doc researcher **will use already collected phylogenetic/phylogenomic data for phylogenetic regionalization of the Eastern Afrotropical Biodiversity Hotspot**. He/she will follow widely suggested pipeline, using genomic trees as main input data (see Daru et al. 2017). (i) In the first step they will quantify the phylogenetic beta diversity (PBD) - this can be done by variety of approaches (Leprieur et al. 2012), e.g. PhyloSor, UniFrac or Simpson's phylogenetic index. Especially the latter is commonly used in biogeographic regionalization because it is insensitive to differences in species richness. (ii) The second step includes the selection of a clustering algorithm that best describes the site x site PBD matrix. The performance of particular algorithms will be evaluated e.g. by using cophenetic correlation coefficient or Gower's distance. (iii) The last step is determination of optimal number of clusters (bioregions) - we will use more objective approaches based on transition zones, e.g. the "elbow" method implemented in R package VEGAN.

The phylogenetic regionalization will allow to identify regions that are mutually "replaceable" in terms of evolutionary diversity. At the same time, it will pinpoint the priority areas for conservation, i.e. those containing high level of (cryptic) endemic evolutionary lineages. In the next step, the outputs will be communicated with local conservation agencies, where direct suggestions for future conservation actions will be provided.

Ad (2) Within the recent projects we obtained numerous genomic data (thousands of SNPs by ddRAD sequencing) from multiple genera of Ethiopian rodents and shrews. The aim of this post-doc stay will be to the **deep comparative analysis of geographic patterns in genetic diversity of small mammals and testing phylogenographic hypotheses in the Ethiopian Highlands, one of the most important centres of biodiversity and endemism on Earth**. The possible questions can include: How old is divergence between populations from neighbouring massifs? How strong is reticulation link between them (if there is any) and how old is it (if it takes form of the introgression link)? Which massifs are inhabited by populations of hybrid origin? What is the contrast between relationships of populations found on the same vs. the opposite side of the Rift? And similar questions addressing persistence of migration barriers separating the populations as well as timing and extent of, possibly recurrent, contacts between them.

### **Research conditions:**

The post-doc will work in a small team (<https://www.ivb.cz/en/team/evolutionary-genetics-of-mammals-group/>) at Institute of Vertebrate Biology CAS, at Research Facility Studenec (<https://www.ivb.cz/en/workplace/external-research-facility-studenec/>). The Studenec campus (two hours from Prague) is situated in woods beside a lake in the Czech-Moravian highlands, half an hour from Brno, the second city of the Czech Republic, where the new large biological campus of the Masaryk University was recently built. The region's rolling hills and woods are popular with cyclists.

The research groups in the Studenec facility are heavily biased toward early-career researchers, with a good gender balance at all levels, many young families and shared crèche/childcare services. On campus work discussion is in international English. The position is well suited to candidates who wish to broaden their experience and skills in an area of evolutionary study that will always be in demand, while at the same time maintaining a healthy work/life balance. The personal car can be useful, but not necessary (there is a train station 10 mins walk from the lab). The monthly salary will be about 40,000 CZK (+ social and health insurance), the accommodation in nearby towns (accessible by trains) can be found around 10,000 CZK. The salary is high enough for a comfortable life in the region even with a small family.

**Requirements:**

The successful candidate will have wide interests and a thirst for deep understanding of evolutionary processes. They will be intellectually mature and quick to learn. They will have experience in several of the following: population genetics, speciation, evolution, phylogenetics, biogeography, programming in R environment. The postdoc academic advisors are trained in zoology, population genetics, and evolutionary studies. The candidate's existing and proposed work will be judged on its quality and utility to the scientific community rather than gross number of publications.

Candidates should submit a short CV and letter of interest in a single PDF file to Josef Bryja ([bryja@brno.cas.cz](mailto:bryja@brno.cas.cz)), who is the principal investigator of projects focussing on evolution of African small mammals (<https://www.ivb.cz/en/person/josef-bryja/>). The work will be done in close collaboration with Ondřej Mikula (<https://www.ivb.cz/en/person/ondrej-mikula/>), a specialist for data analysis in speciation genetics/genomics and biogeography. The applications will be read directly by the academic advisors and interviews will be held until a suitable candidate is found.

There is not specific deadline for applications, the contract can start immediately when the suitable candidate is selected.