
Phylogeography – Session 1

Colonization and speedy speciation of an island invasive

Sofia I. Gabriel¹, Jeremy B. Searle², Maria da Luz Mathias¹

¹Centre for Environmental and Marine Studies (CESAM), Dep. of Animal Biology, Faculty of Sciences University of Lisbon, Lisbon, Portugal, sofiagabriel@gmail.com

²Department of Ecology and Evolutionary Biology, Cornell University, Ithaca, USA

Chromosomal rearrangements may play an important role during the process of speciation. Rearrangements may promote hybrid unfitness leading to reduced gene flow as well as recombination suppression, processes which could lead to differentiation and ultimately reproductive isolation. The western house mouse (*Mus musculus domesticus*) inhabiting the Madeira island is an excellent model to study the potential role of chromosomes in speciation. From an ancestral karyotype consisting of 40 telocentric chromosomes, six distinct chromosomal races have arisen, characterized by different combinations of centromeric (Robertsonian) fusions of the telocentrics, sometimes further modified by whole-arm reciprocal translocations (WARTs). This astonishing level of chromosomal variation seems to have been attained in only ~1,000 years, the estimated time of colonization of the island by the house mouse. The combination of both molecular and paleontological data (radiocarbon dating of bone structures) supports the presence of mice in Madeira one millennium ago, most likely accidentally transported by Viking navigators.

Phylogeography – Session 1

The chromosomal variability of lesser blind mole-rat populations (*Nannospalax*, *Spalacinae*, *Rodentia*) in Greece

Efthimios Assimakopoulos, George P. Mitsainas

Section of Animal Biology, Department of Biology, University of Patras, GR-26504 Patras, Greece, efassimsb@gmail.com

Extreme chromosomal variability is a common trait in several rodent taxa and lesser blind mole-rats (*Nannospalax*, *Spalacinae*) constitute an excellent example, with dozens of chromosomal races described so far. The genus has been extensively studied cytogenetically in its Asian range, but comparatively less in Europe, with virtually no data from differentially stained chromosomes! Regarding Greece, only two karyological studies – more than thirty years old – exist. However, each of the four localities studied in the past revealed a different chromosomal race with $2n=52, 56, 58$ (continental Greece) and $2n=38$ (Lesvos island), respectively, implying a rather remarkable chromosomal diversity for *Nannospalax* in Greece, which this study aspired to unravel. Thus, mole-rats were collected from several continental and one island locality of Greece and the karyological study was conducted on G- and C- banded metaphase spreads. All individuals from continental Greece were verified to belong to the super-species *Nannospalax leucodon*. Interestingly, despite the large distance between most collected populations (ranging from Peloponnese to E. Macedonia), all were characterized by $2n=56/NF=84$ and had an identical autosomal morphology, with the exception of one specimen. In fact, this chromosomal form constitutes a new, rather widespread, chromosomal race for the species, whereas at the same time the existence of the race, previously described as 'Hellenicus', with $2n=58/NF=88$ was not confirmed! Remarkably, the single specimen from Viotia, E. Sterea Ellada with a slightly different karyotype, due to pericentric inversions in two autosomal pairs, resembled the "Epiroticus" race, which, however, lies ca. 250 km to the NW! On the other hand, the population from Limnos island with $2n=38/NF=74$ is formally placed in the super-species *Nannospalax xanthodon* ('Anatolicus' race). Based on the overall study results, the phylogenetic relationships among the Greek chromosomal races of *Nannospalax* and those of neighbouring countries are discussed and the next research steps are proposed.

Phylogeography – Session 1

Adaptive phylogeography of bank voles in Europe – what can the genome tell us?

Michaela Stráznická^{1,2}, Silvia Marková¹, Jeremy B. Searle³, Petr Kotlík^{1,3}

¹Institute of Animal Physiology and Genetics CAS, v. v. i., Liběchov, Czech Republic, straznicka@iapg.cas.cz

²Department of Zoology, Faculty of Science, Charles University, Czech Republic

³Department of Ecology and Evolutionary Biology, Cornell University, Ithaca, NY, USA

Bank vole (*Myodes glareolus*) represents our key model species for studies of adaptive phylogeography in which we examine the possible role of interpopulation variability and selection in postglacial colonization of continental Europe. In Great Britain, the bank vole populations underwent a replacement event in which the first colonizing population was partially replaced by later coming population bearing different haemoglobin (Hb) variant. This variant contains amino acid cysteine (Cys) on the position 52 of beta globin instead of serine (Ser) and as previous studies showed, it gives its bearer's red blood cells significantly higher antioxidative capacity. Since higher levels of oxidative stress may arise under multitude of ecological conditions and the colonizing populations originated in different glacial refugia, we assume that this difference in capacity to resist oxidative stress could represent an adaptation to particular environmental conditions encountered in refugium. Moreover, it could have given the second colonising population selective advantage over the first during the period of significant climatic changes after last glacial maximum. The glacial refugia of both colonists were located in continental Europe, where the discontinuous distribution of some mtDNA clades also points to possible population replacement events. To determine whether the pattern present in mtDNA will be reflected also in the genome, we sequenced more than 800 individuals from over 90 localities throughout Europe by massively parallel genotyping-by-sequencing (GBS). In this talk we will present our newest results of population structure analyses from these data. Both Admixture and Bayesian Analysis of Population Structure programs confirm that particular continental populations underwent a true population replacement event on the level of their genome, not only mtDNA. The Cys Hb distribution in continental Europe and its correlation with environmental variables also points to a possibility that this Hb variant could have played an important role in those events.

Phylogeography – Session 1

Ecological divergence and species response to climate change: niche modelling in the bank vole

Marco A. Escalante¹, Michaela Strážnická¹, Jeremy B. Searle², Petr Kotlík^{1,2}

¹Laboratory of Molecular Ecology, Institute of Animal Physiology and Genetics of the Czech Academy of Sciences, Liběchov, Czech Republic, marko.escalante@gmail.com

²Department of Ecology and Evolutionary Biology, Cornell University, Ithaca, USA

The bank vole (*Myodes glareolus*) is a widespread rodent inhabiting the temperate zone of Eurasia. Its range extends from Ireland and the north of Spain on its westernmost limits to central Siberia in the east. This broad distribution is explained by a postglacial colonization from multiple last glacial maximum (LGM) refugia located primarily in the Carpathian Mountains and on the Mediterranean peninsulas. Previous phylogeographic studies defined at least six distinct genetic lineages for the bank vole across Eurasia, each of which likely originated in a different LGM refugium. Generally, ecological divergence plays an important role driving the origin and maintaining distinct genetic lineages within species and therefore is considered as one of the main mechanism of intraspecific variation. Ecological Niche Modelling (ENM) approaches have been used to assess current and past distribution ranges of species based on the environmental characteristics of locality records, and their integration with phylogenetic information can help us understanding the influence of environmental heterogeneity on the origin and maintenance of intraspecific variation. In this work we apply ENM to assess the environmental variables influencing the current and past distribution of the distinct lineages of the bank vole across Eurasia. We expect the variation in hydroclimatic variables (i.e. temperature and precipitation) to reveal differences in ecological niches among the lineages, and explain their persistence in different glacial refugia during the LGM as well as their relative success during postglacial colonization.

Phylogeography – Session 1

More insights in the evolution of edible dormouse from the old growth Hyrcanian forests

Morteza Naderi

Department of Environmental Sciences, Faculty of Agriculture and Natural Resources, Arak University, Arak, Iran, ghnadery@yahoo.com

The edible dormouse (*Glis glis*), a species from a monotypic genus of family *Gliridae*, which has been frequently used as a model to promote the understanding of patterns of arboreal species regarding glacial oscillations. Ancient Hyrcanian forests, one of the old-growth relicts of the temperate deciduous forests worldwide has been recently documented as an important refugium during the Last Glacial Maximum (LGM). More investigation based on sequencing mitochondrial *Cytb* belonging to the different local populations distributed along the Hyrcanian forests as well as skull and mandible morphological assessments indicated considerable intraspecific evolutionary divergence of the species. The integration of phylogeny, geometric morphometric and environmental niche modeling approaches in this study confirms the presence of multiple cryptic refugia for fat dormice as small forest-dwelling species during paleontological oscillations.