



The 13<sup>th</sup> Rodens et Spatium Conference

# Abstracts

Henttonen, H. & Huitu, O. (eds)



## New advances on the phylogeography and molecular systematics of the Eurasian rodents

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Recent advances in molecular biology have revolutionized our knowledge of biodiversity. These methods were successfully used in many rodent species spread throughout the Palearctic and South East Asian regions. They helped to revise deeply the taxonomy of some rodent groups, evidencing the complementarities of genetics with other methodologies such as morphology and eco-ethology, to better estimate the taxonomic status of rodent species. The use of genetic markers with high evolutionary rates (e.g. mitochondrial sequences, microsatellites) also allowed to develop a new field of research, phylogeography. This new approach became a powerful field of research revealing the principles and processes determining the geographic distribution of genealogical lineages, within and among closely related species. The number of phylogeographic studies on mammals highly increased during recent years and started providing a good picture regarding the historical and/or ecological events at the origin of their present intraspecific genetic structures, the refuges where they survived during the Quaternary ice ages or their way of recolonisation after the last cold period. Phylogeographic approaches were also particularly efficient to propose the best conservation measures for several threatened species or to better understand the impact of some evolutionary processes such as hybridization as a factor for species diversification. The aim of my presentation will be to present several of the most recent researches developed in the field of rodent molecular phylogeny and taxonomy as well as phylogeography.



## Population dynamics and ecology

Oral presentations

Session chairs: Xavier Lambin and Jens Jacob

## Phylogeny and systematics of the subfamily Arvicolinae (Cricetidae, Rodentia): new insights from molecular markers

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The subfamily Arvicolinae (voles and lemmings) is one of the most complicated groups of rodents with respect to its taxonomy. Its diversity has been studied thoroughly during more than 200 years and all methods of research have been applied. In addition it has a very rich fossil record. In result a number of well defined supra-generic groups of the tribal rank are recognized in most checklists (Gromov, Polyakov, 1977; Pavlinov, 2003; Musser, Carleton, 2005). A new stage in the study of the subfamily involves wide application of molecular methods, and though phylogenetic relationships within subfamily are still not completely resolved some amendments should be made in taxonomy in correspondence with reliably established phylogenetic inference, especially evidence from the study of nuclear genes. Three successive waves of radiation could be defined within the subfamily. The first one includes the tribes Prometheomyini, Ondatrini, Lemmini, Dicrostonychini (including likely N American Phenocomys), the second one includes the only tribe Myodini, and the last wave includes genus *Dinaromys* from the Balkans which should be separated in its own tribe, and tribes Ellobiusini, Lagurini, Arvicolini. The monotypic Prometheomyini occupies the most basal and separate position. Phylogenetic relationships within each radiation are not completely resolved. The content of the tribe Myodini=(Clethrionomyini) remains conventional, except the exclusion of *Dinaromys*. Major amendments here related to elevation of subgenus *Craseomys* to full generic rank, the sister relationships of genera *Myodes* sensu str.(=Clethrionomys) and *Alticola* should be taxonomically designated. The greatest taxonomic revision need to be made within the central tribe Arvicolini.

## Systematic and molecular phylogeny of the Dipodoidea superfamily (Rodentia, Mammalia)

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Although the molecular phylogeny of the most speciose rodent superfamily, the Muroidea is by now well-resolved, the phylogeny and systematic of its sister clade, the Dipodoidea (Rodentia, Mammalia), are still being questioned. The Dipodoidea, encompassing the famous jerboa rodents, comprise 1 single family (the Dipodidae) and contains 51 species in 16 genera and 6 subfamilies (Allactaginae, Cardiocraniinae, Dipodinae, Euchoreutinae, Sminthinae and Zapodinae). A robust tree was reconstructed using DNA sequence data from 1 mitochondrial (cytochrome b) and 4 nuclear-coding genes (IRBP, GHR, BRCA1, RAG1). Bayesian inference and maximum likelihood analyses were both conducted on the combined dataset. Using a relaxed Bayesian molecular clock, this phylogeny was placed in an historical and geographical context to gain insight into the origin and maintenance of the Dipodidae diversity. The results confirmed with strong support the monophyly of Dipodidae and of each subfamily. Relationships among genera and species of Dipodidae have also been resolved. We found rare genomic changes in our nucleotidic alignments that reinforced the topology previously obtained. We established a link between our topology and the evolution of bipedalism from a hindlimb specialisation too. The acquisition seems to have appeared progressively from quadrupedal (among basal subfamily of Sicistinae) to bipedal (among most derived subfamily: Euchoreutinae, Allactaginae and Dipodinae). Finally, the estimated timing of diversification within Dipodoidea superfamily suggests that Sicistinae and Zapodinae lineages branched off in Paleogene. Subsequent diversification and dispersal of bipedal dipodoids was promoted by global cooling and concomitant aridization that progressed since Late Miocene.

## The phylogeography and systematics of the silvery mole-rat, *Heliophobius argenteocinereus*, inferred from mitochondrial and nuclear markers

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The silvery mole-rat, *Heliophobius argenteocinereus*, is a solitary subterranean rodent, inhabiting one of the largest areas among African mole-rats. Recent results based on cytochrome b sequences suggested that it is probably a complex of six to eight cryptic taxa with the basal lineage originating in DRC. In our analysis, we extended the sampling area and combined the cytochrome b from GenBank (74 specimens, 26 localities) with sequences of the same gene obtained from the *Heliophobius* collected by us between 2000–2011 (88 specimens, 30 localities) in Malawi, Kenya, Zambia, Tanzania and Mozambique. We also employed eight nuclear microsatellites (in 187 specimens from 29 localities) in order to complement mtDNA analysis. In concordance with previous results (without the specimens from DRC known only from old museum samples), the phylogenetic results showed three major mtDNA clades: 1) clade A, including the populations from Kenya, north-eastern, central and south-western Tanzania, 2) clade B, encompassing populations from central and southern Tanzania, Mozambique and south-eastern Malawi and 3) clade C, comprising of populations from Zambia and Malawi. We identified two areas of secondary contact between lineages; first in Eastern Arc in Tanzania and second between Malawi and Mozambique. However, based on microsatellite data, there is neither distinct genetic structure nor any sign of reproductive barrier between the populations from different mtDNA clades. We therefore conclude that although the silvery mole-rat exhibits profound phylogeographical structure on mtDNA, nuclear data suggest that populations from Kenya, Tanzania, Malawi, Zambia and Mozambique belong to only one biological species.

## Molecular phylogeography of the common dormouse, *Muscardinus avellanarius*

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The aim of the present study was to reconstruct the phylogeography of the common dormouse, *Muscardinus avellanarius*. We analysed 189 common dormice across the species' range, using sequence data from the mitochondrial cytochrome b gene, two nuclear genes (Apob, Betafibrinogene) and 10 microsatellite loci. The obtained dataset was analyzed using different phylogenetic reconstruction as well as other methods adapted to phylogeography. A complex phylogeographic pattern with the presence of two highly divergent lineages has been retrieved from the mitochondrial DNA gene. These two lineages are subdivided into five sublineages which should be regarded as independent conservation units. We observed low genetic diversity within the lineages in contrast to an important level of genetic differentiation between them. The concatenation of the two nuclear genes tends to show the same results as the cytochrome b analysis. The forthcoming microsatellite gave more precise information about the evolutionary history of the common dormouse in Europe. These results will help to propose the best management measures for dormouse conservation.

## Hybrid zone between house mice in Central Europe: from geography to genomic introgression patterns

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Despite long-term study of the house mouse hybrid zone in Europe, its course in some areas is still known rather vaguely. Comparisons of different portions of the zone showed some common patterns. However, several discordances were also revealed, the most remarkable being introgression of the Y chromosome. We studied mouse populations along a presumable course of the secondary contact zone between two subspecies, *Mus musculus musculus* and *M. m. domesticus*, from Schleswig-Holstein to southern Bavaria, to localize more precisely its position. A second aim was to reveal whether introgression shows some general rules obscured until now by studies of individual, geographically separated, parts of the zone. We employed maternally (mtDNA), paternally (Y), and biparentally inherited markers and related their introgression patterns to the hybrid index (HI) based on five X-linked loci. While transition of autosomal loci across the zone was congruent with changes in HI, mtDNA showed bidirectional introgression with alien alleles occurring far behind the zone. Finally, the Y chromosome displayed asymmetric unidirectional introgression of the musculus type into domesticus background. We discuss evolutionary forces shaping these patterns.

## Genetic structure of the bank vole, *Myodes glareolus*, in Fennoscandia: the contact zones between distinct lineages

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Contact zones provide a unique framework for examining evolutionary endogenous and/or exogenous barriers to gene flow. In this context, we study the genetic structure of the bank vole, *Myodes glareolus*, in Fennoscandia to better understand the hybridization process between distinct lineages. Previous studies have already underlined the presence of 3 mitochondrial phylogroups in Fennoscandia that meet in 2 contact zones – the first one situated in central Sweden, the second one in central Finland. While the Swedish contact zone seems to be a barrier to mitochondrial and nuclear gene flow, a preliminary study based on 14 microsatellites showed that the 2 mitochondrial lineages situated on both sides of the Finnish contact zone seem to share the same nuclear pattern. The goals of this study are 1) to refine the phylogeographic patterns of the Fennoscandinavian lineages of *M. glareolus* by studying a mitochondrial gene (cytochrome b) and 19 microsatellites and 2) to identify the microevolutionary forces that explain why the nuclear loci have differentially introgressed across the Fennoscandian contact zones. Here, we present the first results obtained from the analysis of the cyt b and the 19 microsatellites along these two contact zones. We test the hypotheses that differences in the 1) age of the contact zones, 2) the level of divergence between lineages implicated in the secondary contact, 3) the presence of genetic incompatibilities or exogenous selection pressure, trigger this difference in nuclear locus introgression.