The 13th Rodens et Spatium Conference

Abstracts

Henttonen, H. & Huitu, O. (eds)
Recent advances in molecular biology and biogeography have revolutionized our understanding of biodiversity. These methods have been successfully used in many rodent species, providing new insights into the evolutionary history and biogeography of these species. The use of genetic markers and micromorphologies has allowed for a detailed reconstruction of phylogenetic relationships, revealing the complexity of rodent diversity.

The European population of small rodents and their distribution have been a subject of study due to their ecological importance. This research has provided a better understanding of the historical and contemporary patterns of species distribution, which in turn has implications for conservation and management strategies.

The aim of my presentation will be to present several of the most recent researches developed in the field of rodent molecular phylogeny and biogeography, as well as an overview of the biogeography of small mammals in Europe.
Phylogeny and systematics of the subfamily Arvicolinae (Cricetidae, Rodentia): new insights from molecular markers

Natalia Abramson, Aleksey Kostygov, Tatyana Petrova
Zoological Institute RAS, St. Petersburg, Russia

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 suprageneric 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 widespread 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, Onatrinini, 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. (=Clethrionomyes) and Aliticola 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)

Julie Pires, Marie Pages, Vladmir Lebedev, A. Bannikova, G. Shenbrot, Johan Michaux
1 Lab of Conservation Genetics, Univ. Liege, Liège, Belgium; 2 CBGP (Biological Center for Population Management, INRA), Montpellier-sur-Loz, France; 3 Zoological Museum of Moscow State University, Moscow, Russia; 4 Lomonosov Moscow State University, Moscow, Russia; 5 Mitrani Department of Desert Ecology, Jacob Blaustein Institutes for Desert Research, Ben-Gurion University of the Negev, Midreshet Ben-Gurion, Israel

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, Cardiocricetinae, Dipodinae, Euchoreutinae, Smirniinae, 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 nucleotidal 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

Hana Patzcnahauerský1, Josef Bryja1, Radim Sumbera2
1Institute of Vertebrate Biology AS CR, Brno, Czech Republic, 2Department of Zoology, Faculty of Science, University of South Bohemia, Ceske Budejovice, Czech Republic

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*

Alice Mouton1, Andrea Grill1, Maurizio Sarà1, Boris Krystufek1, Ettore Randi2, Giovanni Amori3, Rovnydas Julikans1, Gaetano Aloise4, Alessio Mortelliti3, Ferhat Matur5, Morten Elmerot1, Helle Vihelmersen1, Goedehe Verheylen1, Fabiana Panchetti1, Johan Michaux1
1Institut de Biologie, biol 22, Université de Liège (Sart Tilman), Liège, Belgium, 2Institut Biodiversiti der Tier, Universität Wien, Wien, Austria, 3Dipartimento Biologia Animale, Laboratorio di Zoogeografia ed Ecologia Animale, Paterno, Italy, 4Science and Research Centre, University of Primorska, Koper, Slovenia, 5ISPRA ex INFS, Ozzano Emilia, Bologna, Italy, 6CNR, Institute of Ecosystem Studies, Rome, Italy, 7Institute of Ecology of Nature Research Centre, Vinnus, Luhuwan, 8Museo di Storia Naturale della Calabria e Orto Botanico Rende (Casentolo), Italy, 9Dipartimento di Biologia Animale e dell’Uomo, Università “La Sapienza”, Roma, Italy, 10Science and Art Faculty, Department of Biology, Zanguldak Karatay University, Zanguldak, Turkey, 11Department of Bioscience - Wildlife Ecology and Biodiversity, Aarhus University, Rende, Denmark, 12Boaakay 13, 5700 Svendborg, Denmark, 13Naturværkets Studie / Mammutløve Group, Mchelen, Belgium, 14Dipartimento di Biologia, Università “Roma Tre”, Roma, Italy, 15CGP (Centre de Biologie des Populations), INRA, Montferrier sur Lez, France/Institut de Botanique, Université de Liège, Belgium

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, Betalidinogen) 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

Leah Baggio 1, Nathalie Chatenay 1, Holger Hermsmeier 2, Gert Otterstatter 1, Martin Galant 1

1 Laboratory of Conservation Genetics, Univ. Uppsala, Sweden. 2 Swedish University of Agricultural Sciences, Umeå, Sweden. Correspondence to: Martin Galant (mgalant@agron.swu.se).

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 two subspecies, M. m. musculus and M. m. domesticus, from Schleswig-Holstein to southern Bavaria. In initial studies, we revealed the presence of two populations along the boundary of the secondary contact zone. However, we found that most of the introgression did not originate from the secondary contact zone, but rather from another area. To test the hypothesis that the presence of introgression along the secondary contact boundary is due to secondary contact, we analyzed molecular markers from the area. Our hypothesis was confirmed by both molecular and phylogeographic analyses. We conclude that the secondary contact boundary is not a barrier to gene flow, but rather a hub for introgression from the two subspecies.