101 Searching for signatures of genetic adaptation to climate in bank voles

Remco Folkertsma, Jana A. Eccard, Michael Hofreiter

University of Potsdam, Potsdam, Germany, rfolkert@uni-potsdam.de

Temperature and patterns of precipitation are changing on a global scale. This has strong effects on many existing species, influencing the physiology, behavior and range of many populations. In contrast to these ecological effects of climate change, evolutionary responses to climate change are less well studied. With ongoing climate change, adaptation has recently become the focus of much ecological genomic research. Differences in climatic variables between environments influence the spatial distribution of phenotypic and genetic variation across a meta-population which can lead to local genetic adaptation. Thus, the detection of climate-mediated evolutionary responses can potentially shed light on the genetic basis of adaptation to climate change. Bank voles (Myodes glareolus) have a widespread distribution from western Europe into Scandinavia and western Russia, where they encounter a wide range of different climatic conditions. It is an important mammal species used to study the phylogeographic response of European fauna to climate change following the Last Glacial Maximum, but still little research has been done regarding adaptation to local climatic conditions in the bank vole. Therefore, the aim of our study is to uncover signatures of genetic adaptations to local climatic conditions among populations of bank voles. For this, we used a ddRAD sequencing approach and scanned the genome for signatures of genetic adaptations. Using this data, we report on population differentiation and the populations genetic structure of 14 bank vole populations distributed across Europe. By using a variety of tests we identify loci that are under putative selection showing a correlation between allele frequencies and climatic variation across the European continent.

102 Association of rodents with man-made infrastructures and food waste in urban Singapore

Mahathir Humaidi, Ang Kai Yang, Lee Ching Ng, Grace Yap

Environmental Health Institute, National Environment Agency, Singapore 138667, Mahathir_Humaidi@nea.gov.sg

A previous rodent-trapping study at 16 high rise residential estates in Singapore demonstrated high levels of *Rattus norvegicus* activities in waste bin chambers that hold household waste discarded from the apartments. Situated on the ground level of apartment blocks, each chamber serves two columns of apartment blocks and is equipped with a floor trap which is connected to a network of sanitary lines that drains any waste water from the bin chambers. The rodents were observed to access bin chambers via damaged floor trap covers. Here we report a subsequent study on the activity and movement of rodents among the bin chambers and sanitary drain-lines. Passive infra-red hunting cameras were placed in bin chambers with rodent activities and adjacent inspection chambers to capture rodent activities. A capture-mark and release study was then conducted to track the movement of rodents in the sanitary-drain lines that serve the entire block of flats. During the 3 days of observations, the rodents were generally active from afternoon till early mornings, with spikes of activity recorded after lunch and dinner times of local residents. Our cameras did not detect movement of marked rodents to other infested bin chutes connected by the sanitary drain-line network. They were observed to move only between the bin chamber where they were caught and two closest inspection chambers, 2.5 m away. Further investigation with an industrial endoscope revealed that rodents were living in underground cavities below bin chambers with breached floor trap pipe. The study showed how rodents use man-made infrastructures to harbour and access food waste; and the importance of infrastructure design and maintenance in controlling the population of urban population of rodents.

103 Personality dependent corridor use in a grassland species

Gabriele Joanna Kowalski¹, Antje Herde^{1,2}, Jana A. Eccard¹

¹University of Potsdam, Potsdam, Germany, gabriele.kowalski@uni-potsdam.de ²University Bielefeld, Bielefeld, Germany

The effectivity of corridors connecting isolated patches has been investigated for more than three decades with animals of different species. It is already known that the presence and the properties of corridors are crucial for the species' dispersal and mobility in a landscape. But corridor use may also depend on the behavioural traits of its users. Animal personality, i.e. consistent among-individual differences in behaviour, might affect the space use in general, but also the usage of corridors. We investigated whether the width of grass stripes and the personality of the individual are important for the corridor use of common voles (Microtus arvalis). If so, corridors may allow passage only for a proportion of individuals in a population and may thus affect individual mobility and population gene flow. We studied movement behaviour of male common voles in experimental grassland corridors of different width (1 m and 3 m). Voles were tested with established behavioural tests to parametrise boldness and activity. Automated and hand VHF telemetry was used to observe the individual movement of the tested animals (N=34) and to determine whether the animal perceives the structure as a corridor. Results on movement will be discussed in relation to animal personality and corridor width to allow predictions of dispersal abilities of personality types in habitats with different degrees of fragmentation.

104 Diet shift by livestock grazing shape the gut microbiota composition and co-occurrence networks in a local rodent species

Guoliang Li¹, Jing Li², Kevin D. Kohl³, Baofa Yin⁴, Wanhong Wei⁴, Xinrong Wan¹, Baoli Zhu², Zhibin Zhang¹

¹State Key Laboratory of Integrated Pest Management, Institute of Zoology, Chinese Academy of Sciences, Beijing 100101, China, ligl@ioz.ac.cn

²Key Laboratory of Pathogenic Microbiology and Immunology, Institute of Microbiology, Chinese Academy of Sciences, Beijing 100101, China

³Department of Biological Sciences, University of Pittsburgh, 4249 Fifth Ave, Pittsburgh, PA 15260, USA ⁴Colleges of Bioscience and Biotechnology, Yangzhou University, Yangzhou 225009, China

Gut microbes play key roles in maintaining physiological functions and health of their hosts. However, most studies on gut microbes are conducted in model systems under laboratory conditions. The response of gut microbiota to diet changes under field conditions has rarely been investigated. In this study, we utilize field and laboratory studies to test whether sheep grazing induces a diet shift and thus alters the gut microbiota of a small rodent species living in grassland. First, using a field enclosure experiment, we found that enclosures subjected to grazing were mostly dominated by Cleistogenes squarrosa (an unfavorable plant species for both sheep and voles), and that voles in grazing enclosures harbored gut communities with distinct microbial taxonomic composition and cooccurrence networks compared to those in control enclosures. Specifically, voles in grazing enclosures exhibited significantly lower abundances of Firmicutes, increased abundance of Bacteroidetes, and significant lower measurements of alpha diversity. PICRUSt analysis suggests a low mineral absorption capacity of the gut microbiome of voles from grazed enclosures. The microbiota from voles in the grazing enclosures had a smaller but more complex network with more positive interactions. We verified our findings using laboratory experiments where voles were exclusively fed either Cleistogenes squarrosa, Stipa krylovii or Leymus chinensis. We observed similar changes in the gut microbiome, confirming that the effects of sheep grazing on the gut microbiota of Brandt's voles were related to grazing-induced diet shifts. Our results provided evidence for a contribution of grazing-induced diet shift in changes of gut microbiota in Brandt's vole, which in turn may explain the negative interaction between large domestic herbivore and small rodents in the field.

105 Small mammal richness and diversity in the changing landscape of central Italy

Chiara Paniccia¹, Duccio Rocchini², Ludovico Frate¹, Mirko Di Febbraro¹, Steffen Mumme³, Anna Loy ¹

¹Environmetrix Lab, Department of Biosciences and Territory, University of, Contrada Fonte Lappone, I86090 Pesche, Italy, c.paniccia@studenti.unimol.it

²Center Agriculture Food Environment, University of Trento, Via E. Mach 1, 38010 S. Michele all'Adige (TN), Italy

³Department of Biology and Biotechnologies, Sapienza Università di Roma, Rome, Italy

Most research on small mammal decline has focused on limited spatial and temporal scales, especially for the Mediterranean region. To better understand this process, its causes and contexts, a broader spatio-temporal scale approach is needed. In our study we hypothesized that: I) small mammal assemblages are changed through time and that the primary cause is land use and climate change; II) the biodiversity indices of small mammals are related to landscape predictors, especially to a mosaic of natural and anthropogenically influenced habitats. We used a recent extensive dataset about distribution, abundance and traits of small mammals derived by common barn-owl (Tyto alba) pellets, covering a 30year time spam. Through a framework of linear models we assessed the relationship between small mammal diversity (richness, Shannon index and functional diversity) and landscape variables (land use and landscape metrics) for 21 small mammal species (10 Rodentia and 11 Euliphlotypla) occurring in a 10,000 km² area in central Italy. We also explored the variation trough time (1980 - 2017) of nine guilds (i.e. herbivore arboreal forager diurnal, herbivore ground forager diurnal, herbivore ground forager nocturnal, insectivore fossorial, insectivore ground forager diurnal, insectivore ground forager nocturnal, omnivore arboreal forager nocturnal, omnivore ground forager nocturnal, and omnivore ground forager diurnal) selected by a FMDA (factor analysis of mixed data) from 18 qualitative and quantitative functional traits. On a temporal scale, we found a significant decrease in richness and diversity for carnivore species, while omnivores increased significantly and herbivores did not show a trend throughout time. On a spatial scale, richness, diversity and functional diversity of small mammals were higher and positively related to heterogeneous landscape, especially in combination with land use coverage and spatial arrangement of patches affecting each diversity in different ways. Our study provided insights into the complexities of small mammal responses, with an emphasis on community-level changes and can serve as a foundation to predict shifts and trends for future scenarios.

106 Multiple paternity in common hamster (*Cricetus cricetus*) from urban and suburban population

Ekaterina V. Potashnikova, Aleksandra S. Saian

A.N. Severtsov Institute of Ecology and Evolution RAS, Moscow, Russia, potasnikova.k@gmail.com

The common hamster (Cricetus cricetus) over the past fifty years dramaically decline in wild. Along with this, it began actively to settle in the cities. Urban areas are characterized by special environmental conditions. Animals that inhabit the city demonstrate a variety of adaptations, leaded to breeding strategy changes. In this connection, it is interesting to compare their reproductive strategy in the city and in the wild. During three years, we studied the structure of the urban population of the common hamster in the Gagarin park (Simferopol, Russia) on the plot of 2.2 hectares. In April 2016, during the peak of breeding activity, we observed 5 mating groups simultaneously. Each one has included one female and up to five males. Chasing and mating of males with females occurred several times during 2–3 hours. These observations allowed us to suppose a multiple paternity possibility. In the spring, 2017 in the city Park we found a dead female at the last stage of pregnancy. Another dead pregnant female was found in Chisten'koe village (10 km apart Simferopol – agrophytocenosis habitat). Estimation of the population density by active burrows calculating has shown that in urban populationd of the common hamster the density is about 50 animals/ha that is at least 3 times higher as in Chisten'koe village ones. Samples of fifteen embryos and the mother from Gagarin park and of the female with eleven embryos from Chisten'koe were used for molecular-genetic analysis. Allelic composition of 10 microsatellite loci of nDNA, has shown that in the urban population we assumed at least 3 fathers of the litter and at least 2 fathers in the suburban habitat. Thus, for the first time, we have evidence for multiple paternity in Cricetus cricetus in the urban and as well as in wild habitats. The study was supported by RFBR grant 17-04-01061.