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## Poster Session 1 – Phylogeography

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### **42 Genetic variation and population structure of the red squirrel (*Sciurus vulgaris*) in Lithuania**

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Red squirrels (*Sciurus vulgaris*) are occurring in many types of coniferous and mixed deciduous forests and are widely distributed throughout Europe and part of Asia, this species is the only one native to Lithuania. Seventy years ago almost 200 individuals of *Sciurus vulgaris exalbidus* were introduced to Lithuania from Altai. The motivation of introductions was to improve fur quality. The data of genetic diversity of red squirrels in Lithuania are scarce. Red squirrels have been investigated only using random amplified polymorphic DNA method. The aim of this study was to investigate the genetic variability of red squirrels using mitochondrial DNA and microsatellites. All specimens of the red squirrel used in this study were found dead on the road or in the forests. A total 39 samples during the 2001 – 2018 period was collected from different areas of Lithuania. DNA was isolated from frozen muscles of each individual. For microsatellite analysis seven different primers were used to obtain genetic diversity of red squirrels. For mitochondrial DNA analysis primers of D-loop sequence were used, average number of nucleotide differences (k) between Lithuanian red squirrels was 10.167, more than 10 haplotypes (h) were determined. The results revealed high-level genetic diversity of red squirrels in Lithuania.

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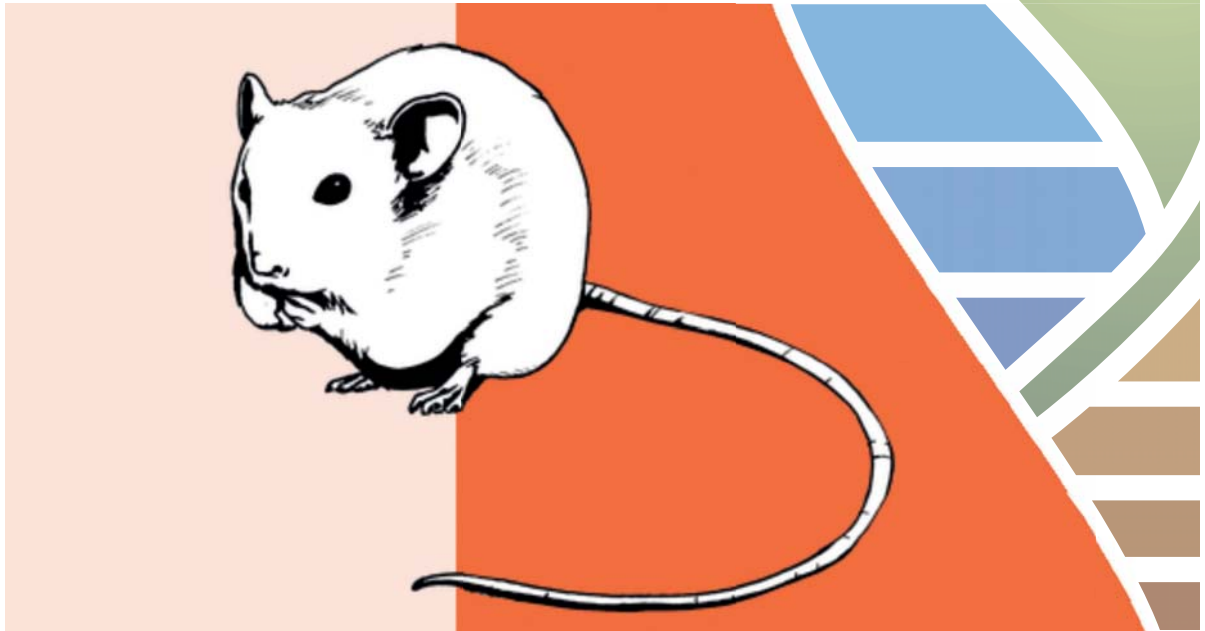
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6<sup>th</sup> International Conference of Rodent  
Biology and Management  
and  
16<sup>th</sup> Rodens et Spatium

Potsdam, Germany, 3-7 September 2018

Book of Abstracts



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