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## Taxonomy Genetics

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### **Genetic structure and morphological evolution of the house mouse on the Orkney Archipelago**

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The house mouse has colonized numerous islands following human travelers. This has exposed it to a high variety of environments, prone to trigger adaptive evolution. The colonization itself, processing by successive founder events and bottlenecks, may promote evolution. Hence, both adaptive and stochastic processes could contribute to an accelerated evolution on islands. We developed an approach coupling genetic and morphometric approaches on a set of more than 250 mice from eight of the Orkney Islands. A first genetic analysis using mitochondrial D-loop sequences allowed us to determine the relationships between Orkney and western European mice. A second analysis based on 21 microsatellites provided insights into genetic structure within the archipelago, revealing a strong geographic structure at a small spatial scale. Morphometric analyses were performed on the first upper molar. Despite their phylogenetic relatedness, Orkney mice displayed a morphological diversity as high as among Western European populations. This diversification erased the phylogenetic signal in the tooth morphology, and is ascribed to an accelerated morphological evolution on Orkneys. In contrast, within Orkneys, morphological and genetic divergences are largely in agreement. This holds true at the scale of the archipelago, of the main island, and even at the scale of local genetic clusters (<5 km). This suggests that on Orkneys tooth morphology evolved in a rather neutral way in isolated populations, and does not correspond to an adaptive divergence. It further suggests that the strong genetic structure at a small spatial scale was a fuel for the important morphological diversification.

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Jens Jacob, Jana Eccard (Editors)

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



Julius Kühn-Institut  
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