

Combining citizen science and conservation genomics to reveal the causes of rapid population decline in the Garden Dormouse (*Eliomys quercinus*)

Alina von Thaden^{‡,§}, Sven Büchner[‡], Johannes Lang[‡], Holger U. Meinig[‡], Carsten Nowak^{‡,§}

[‡] Conservation Genetics Group, Senckenberg Research Institute and Natural History Museum Frankfurt, Clamecystraße 12, 63571 Gelnhausen, Germany

[§] LOEWE Centre for Translational Biodiversity Genomics (LOEWE-TBG), Senckenberganlage 25, 60325 Frankfurt am Main, Germany

| Justus-Liebig-University Giessen, Clinic for birds, reptiles, amphibians and fish, Working Group for Wildlife Research, Frankfurter Strasse 114, 35392 Giessen, Germany

Corresponding author: Alina von Thaden (alina.vonthaden@gmail.com)

Abstract

The Garden Dormouse (*Eliomys quercinus*) is a native European rodent species that has suffered extensive range contraction and severe population decline across large parts of its distribution in Central and Eastern Europe and is now considered extinct in several countries. At the same time, contrasting population dynamics are observed in its western distribution, where Garden Dormice are regionally abundant and even occupy habitats in the built environment. Reasons for these opposing range dynamics and drastic declines remain unknown. We therefore started a long-term cooperation project, joining the efforts of different research institutions, conservation NGOs and citizen scientists to investigate the underlying causes. Here, we present the results of a RADseq analysis of 103 samples collected from several parts of the European species range to infer regional phylogeography and delineate different conservation units. Preliminary genomic data show the existence of highly divergent genetic lineages, even on a local scale. Based on these findings, we have developed a reduced SNP panel, which allows for lineage discrimination, assessment of population structure and identification of individuals from non-invasively collected samples. The panel is now routinely applied in Garden Dormouse conservation, e.g., when selecting appropriate locations to release displaced Garden Dormice found accidentally or to identify isolated Garden Dormouse populations in need of improved habitat connectivity.

Keywords

RADseq, reduced SNP panel, non-invasive samples, applied conservation genomics, In Search of the Garden Dormouse

Presenting author

Alina von Thaden

Presented at

Oral presentation at the 11th International Dormice Conference (May 9-13, 2022)

Conflicts of interest