Potential Barriers to Gene Flow in the Endangered European Wildcat (Felis silvestris)

Researchers
S. Hartmann, K. Steyer and R. Kraus

Principal Investigator
Dr. Carsten Nowak

Project Term
2015 - 2015

Project Areas
Basic Research in Biology and Medicine

Clusters
LOEWE CSC Cluster Frankfurt

Institute
Senckenberg Forschungsinstitut und Naturmuseum Frankfurt / GU, World of Biodiversity

University
Goethe Universität Frankfurt am Main

Introduction

The European wildcat (*Felis silvestris silvestris*) is protected and needs conservation actions in many countries in Europe. The severe population declines in the 19thcentury lead to extinction or at least isolation accompanied by population bottlenecks in most parts of its range. Also in Germany,habitat suitable for wildcats is judged to be highly fragmented. We thus investigated fine-scale genetic structure of wildcat populations in Central Germany across two major potential barriers, the Rhine River with its valley and a major highway, by the analysis of 260 hair and tissue samples collected between 2006 and 2011 in the Taunus and Hunsrück mountain ranges (3,500 km^2 study area). With 14 microsattelite loci we found 188 individuals in our sample, which displayed significant genetic substructure in the study area. Both the Rhine River and the highway were identified as significant barriers to gene flow. The river seems to have a long-term effect with genetic differentiation. Estimates of current gene flow and relatedness across the two barriers indicated a similar or even stronger barrier effect to ongoing wildcat dispersal of the highway. Despite these barrier effects, we found evidence for the presence of recent migration across both the river and the highway.

Methods

The study of migration was particularly aided by making use of a coalescent modeler called migrate-n. This software suite calculates coalescence trees from genetic data of individuals within and between populations. In this way the partitioning of genetic diversity is modelled through time and migration events between populations are inferred. Multi-population models become impossible to solve exactly and Bayesian statistics is used to approximate parameter values in the complex solution space. Arriving at the optimal solution of the coalescence tree requires Monte-Carlo Markov-chain implementations of the Bayesian algorithms. The Markov-chain needs to explore a vast parameter space and approaches the global maximum of posterior likelihood by continuously updating its parameter values. To avoid getting trapped in local maxima and miss the global maximum, it is important to run many independent chains in parallel. The CSC cluster FUCHS has implemented a „message parsing interface“ (mpi) to facilitate the process of computing many coalescence trees in parallel. This offered us the possibility to estimate migration rates with very high precision in a rather short runtime.

Results

The results of our analyses suggest that although wildcats have the capability of dispersal across major anthropogenic and natural landscape barriers, these structures still lead to an effective isolation of populations as reflected by genetic analysis. Our findings show that currently ongoing national strategies of wildcat conservation aiming for large scale habitat connectivity are important and will be successful in connecting even more the currently fragmented wildcat habitat.

Last Update: 2020-11-12 19:01