Title: Conservation genetics of the common dormouse: Phylogeography and mitochondrial DNA (mtDNA) diversity of the common dormouse *M.avellanarius* in the UK, *PhD Thesis, University of Liverpool, 2010*

Author: D.Md. Naim

Country: UK and Lithuania

Background to study

Evolutionary Significant Units (ESUs) describes distinctive populations of the same species that have evolved in reproductive isolation of each other and as such may hold different adaptive traits which should be conserved to promote the continued evolution of the species. This information can be obtained through phylogenetic studies and provides a valuable insight into the historical distribution and expansion of a species and identifies management units for species conservation. This information is particularly important for the common dormouse whose conservation involves relocation and reintroduction programmes.

Method

- DNA samples from buccal swabs and hair were obtained from 161 dormice of 15 localities from across the UK and from 7 dormice from Lithuania. Two regions of mitochondrial DNA were targeted across all samples and were used to investigate phylogenetic differences between regions (ESUs) and genetic diversity within each identified ESU. The time since populations diverged was also investigated.

Key results

- Dormouse populations in the UK are characterised by strong geographical subdivision with at least three distinct phylogenetic lineages: 1) North western; 2) Central and 3) Southern lineage.
- Genetic diversity was highest in the Southern UK lineage, suggesting larger population sizes compared with the central and north western dormice whose genetic diversity reduced with latitude.
- The level of genetic diversity of dormice was as high as or higher than other mammal species in the UK which is unexpected given their declining population size.
- It is possible that the genetic divergence between the UK lineages occurred glacial age, however further investigation is needed.
- There is a strong divergence between the UK dormice population and dormice from Central Europe (Lithuania) that probably occurred during the Pleistocene age (0.7-1.5 Mya)

Key messages to landowners and managers derived from these results

- Future reintroductions should take into account the three identified Evolutionary Significant Units and translocations between these may compromise the fitness of populations and the genetic integrity of dormice within regions.
- Further investigation into the effects on the fitness of populations resulting from previous admixing between regions is recommended.

Key words/phrases

Dormice; *Muscardinus avellanarius;* mitochondrial DNA; genetic diversity; Evolutionary Significant Units; phylogenetics