

Title: Conservation and ecology of the hazel dormouse, *Muscardinus avellanarius*: Dormice on the edge: population genetics of hazel dormice on the southwest peninsular of England. *PhD Thesis, University of Exeter, 2012*

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Background to study

Conservation genetics helps to identify populations with high levels of extinction risk, informs reintroduction and captive breeding programmes, describes gene flow patterns that can enlighten habitat management and define genetically distinct conservation units. As such this information is valuable for determining future conservation measures for the dormice in the UK.

Method

- Dormouse hair plucks were obtained from 27 populations across Cornwall, Devon and Somerset during routine monitoring of nest boxes. Sample date, site, sex, weight, age and reproductive condition were recorded and accompanied each sample. DNA was also obtained from dead dormice whose location could be determined.
- DNA was extracted from samples using standard protocols and each sample was genotyped using 28 microsatellite markers. Samples which failed to amplify at >3 microsatellite loci were not used in the analysis. Related individuals (parent-offspring and full sibs) and repeat samples were removed to reduce bias in genetic structure analyses.
- A total of 13 populations were used in the analyses to determine genetic diversity, isolation by distance, structure, differentiation between populations and recent bottlenecks.

Key results

- Three genetically distinct regions of dormice were identified; mid Cornwall, east Cornwall and Devon/Somerset and results indicate little admixing of dormice between these regions.
- Dormice were found to be clustered into 3 groups within both mid and east Cornwall regions and into 7 groups within Devon/Somerset.
- There was evidence that dormice in Okehampton were sub-divided into two clusters. A large railway track may contribute to reduced gene flow between these two groups.
- A high level of genetic differentiation was identified between populations suggesting low levels of gene flow. The highest genetic differentiation between populations was identified in mid Cornwall suggesting these populations are unlikely to be interacting with each other.
- There was significant evidence that genetic differentiation increased with increasing distance between populations and this effect was highest in Cornwall.
- East and mid Cornwall dormice populations had a significantly lower genetic diversity than those in Devon/Somerset and may be due to the River Tamar acting as a significant dispersal barrier.
- There was strong evidence for a decline in genetic diversity from the core to the periphery of the dormouse range sampled along the southwest England peninsular.
- Eight dormouse populations showed lower than expected genetic diversity.
- Recent bottlenecks were identified in two populations from Darley and Roadford, however when compared across all populations, none had experienced a bottleneck.

Key messages to landowners and managers derived from these results

- It is not advised to promote mixing of the Devon and Cornwall populations by landscape connectivity measures or by translocations as this may compromise their genetic integrity and potentially reduce the overall fitness of the two discrete populations.

- Railway tracks may cause fragmentation of dormouse populations. Developing strategies to maintain connectivity across railway tracks that bisect woodland patches is advised.
- Conservation measures should focus on increasing connectivity between the Cornish populations whilst maintaining populations in Devon and Somerset. Woodland management to encourage suitable dormouse habitat should be implemented at sites adjacent or close to existing populations in Cornwall to encourage population growth. Hedgerows should be managed or planted to accommodate dormouse dispersal between extant Cornish populations to facilitate dispersal and increase gene flow and population viability.

Key words/phrases

Dormice; *Muscardinus avellanarius*; microsatellites; genetic structure; bottlenecks; genetic diversity; Cornwall; Devon; Somerset; genetic integrity