

Title: Conservation genetics of the common dormouse: Patterns of genetic divergence among populations of the common dormouse *Muscardinus avellanarius*, PhD Thesis, University of Liverpool, 2010

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Background to study

Specialist species such as the common dormouse are thought to be vulnerable to habitat fragmentation as their dispersal ability is likely to be dependent on arboreal routeways between suitable woodland patches. Fragmented populations may experience greater frequencies of bottlenecks and lower population size, resulting in increased rates of genetic erosion which can lead to inbreeding effects and reduced fitness. Patterns in spatial genetic structure of populations can provide an insight into the influence of fragmentation and is important for dormouse conservation.

Method

- Dormice samples were obtained from Afonwen and Bontuchel regions (separated by 15 km and a major road). Suitable woodland patches separated by 0.3-0.5 km occur in both regions and a continuous habitat patch in Bontuchel wood was used for comparison. 578 nestboxes, spaced 20-40 m apart were located across all habitat patches and Bontuchel wood. Nestboxes were checked in June and September in patchy habitats and in May/June and September/October in Bontuchel wood between 2007 and 2009.
- Dormice were weighed, sexed, aged, their breeding status determined and hair and buccal swab samples were obtained. Dormice in Bontuchel wood only were microchipped.
- A total of 50 and 232 samples were successfully genotyped using ten microsatellites from Afonwen and Bontuchel regions respectively. Analysis included the identification of migrants, recent bottlenecks and the spatial genetic structure of populations and how these are influenced by distance between individuals and populations.

Key results

- Genetic diversity was higher in the Bontuchel region than Afonwen, a potential artefact of smaller population inhabiting Afonwen but no substantial erosion of genetic diversity caused by recent bottlenecks was detected.
- Populations were genetically distinct between regions indicating low levels/no gene flow.
- There was limited gene flow between habitat patches separated by c. >1 km but rare inter patch movement (>600 m) was detected for 2% of the population sampled.
- Dormice inhabiting Bontuchel wood and habitat patches connected by interconnecting tree lines and/or hedgerows exhibited shared ancestry indicating gene flow between these patches.
- There was only a slight difference in the spatial genetic structure of dormice living in continuous and patchy habitats suggesting movement within continuous habitats does not exceed movement within patchy habitats resulting in similar levels of genetic structuring.

Key messages to landowners and managers derived from these results

- Creating larger woodland patches will help to promote larger dormouse populations that may act as sources to surrounding woodland patches, promoting higher genetic diversity of populations within the landscape. More research however is advised.
- Arboreal routeways (hedgerows or interconnected tree lines) should be created and/or maintained to promote dispersal of dormice between woodland patches.
- Proposed developments or changes in woodland management need to be considered in view of the wider landscape. Fragmenting dormouse populations by c. 15 km will cause genetic

distinctness and as such is not advised. Conversely when considering landscape connectivity, populations fragmented by open habitat of c. 15 km are likely to be genetically distinct and as such, reconnecting them may be detrimental to the fitness of populations.

Key words/phrases

Dormice; *Muscardinus avellanarius*; microsatellites; genetic structure; patchy habitats: continuous woodland; dispersal