

Genetic assessment of the Forest Dormouse *Dryomys nitedula* (Pallas, 1773) in Latvia

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Abstract

The Latvian population of the Forest Dormouse is small and isolated, situated far from the main distribution range of this species. The population is located in the south-eastern region of Latvia, close to the Belarusian border. Sixty-three nest-boxes were located throughout this distribution area and captured forest dormouse individuals were sampled for genetic analysis. Animal age, sex, and coordinates from place of capture were recorded. DNA was extracted from 120 individuals using the QIAamp DNA Mini Kit (Qiagen, Germany). RAPD-PCR polymorphisms at 65 loci were used to examine the genetic diversity and differentiation of the Forest Dormouse population in Latvia. 89% of loci were polymorphic, average expected heterozygosity over all loci was 0.321, average polymorphism information content (PIC) was 0.246. The program 'Structure' was used to perform Bayesian assignment of individuals to a predefined number of clusters. The deltaK method identified that the most likely number of clusters within the Latvian Forest Dormouse population was three. Assignment of individuals to a particular cluster mostly corresponded with the location where the individual was captured. Analysis of molecular variance (AMOVA) indicated that there was significant genetic differentiation between the three clusters with pairwise F_{st} (a modification of F_{st}) values ranging from 0.118 to 0.180.

Keywords

Forest Dormouse, genetic, clusters

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