

The genetic diversity of migratory Long-eared owl *Asio otus*

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Long-eared owl is a widespread migratory owl species in Europe, of which there is little information on migration ecology. In Northern Europe, Long-eared owl population consists of dozens of thousands of pairs, with large populations in Eastern Europe and Russia (BirdLife International 2004). This species has regular migrations in Baltic and Eastern Europe regions (Michalonek *et al.* 2005). Long-eared owls passage through Latvia starts in the first part of October and lasts until the end of November. One of the most important birds concentration places in Europe during the autumn migration is Pape (Račinskis, Stīpniece 2000).

For genetic analysis 96 blood samples were taken from migratory owls during the autumns of 2011 and 2012 at Pape Ornithological station. Retrotransposon-based molecular marker system (Kalendar *et al.* 2010) was used to detect the genetic diversity of migratory owls. DNA samples were extracted from the blood of the specimens of migratory owls and used for polymerase chain reaction with two primers, which provided higher level of polymorphism – primer 2080 and primer 2271. As a result, 25 loci were revealed by primer 2080 and 21 loci - by primer 2271.

Results revealed low genetic diversity among Long-eared owls during autumn migration. Genetic similarity between all individuals was higher than 90%, and complete polymorphic loci number was 23,91%. The total number of 11 polymorphic loci was detected by the two primers, which composes 24% of all loci. The higher number of polymorphic loci was detected by primer 2080 - eight loci, with only two loci detected by primer 2271. The comparison of samples of seasons 2011 and 2012, treated as two separate populations, revealed genetic similarity of 99%.

References

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