

# The genetic structure of the Lithuanian wolf population

## Research Article

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Received 24 August 2012; Accepted 26 January 2013

**Abstract:** Lithuanian wolves form part of the larger Baltic population, the distribution of which is continuous across the region. In this paper, we evaluate the genetic diversity of the Lithuanian wolf population using mitochondrial DNA analysis and 29 autosomal microsatellite loci. Analysis of the mtDNA control region (647 bp) revealed 5 haplotypes distributed among 29 individuals and high haplotype diversity (0.658). Two haplotypes were distributed across the country, whilst the others were restricted to eastern Lithuania. Analysis of microsatellites revealed high heterozygosity ( $H_e=0.709$ ) and no evidence for a recent bottleneck. Using detection of first generation migrants, four individuals appeared to assign better with populations genetically differentiated from those resident in Lithuania. These immigrants were males carrying rare mitochondrial haplotypes and were encountered in the eastern part of the country, this indicates that Lithuania is subject to immigration from differentiated populations. Additionally, we did not detect any signs of recent hybridisation with dogs.

**Keywords:** *Canis lupus* • Genetic structure • Lithuania • Microsatellites • Mitochondrial DNA

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## 1. Introduction

The Gray wolf *Canis lupus* is widespread throughout Europe, but its distribution is patchy, with semi-isolated populations varying in sizes from less than fifty to several thousand. The conservation status of the species also varies from being strictly protected in some countries to a legitimate game species in others [1,2]. Several studies (reviewed in Randi [3]) have found that wolves, even though capable of dispersing over large distances and across difficult terrain, show genetic differentiation at smaller geographical scales [e.g. 4,5]. This highlights the importance of applying knowledge about genetic diversity and differentiation when preserving species distributed across large geographic areas. Wolf management is largely centred on resolving conflicts between wolves and humans [3], in several cases this is attempted by controlling the distribution and number of wolves. Such management actions might, however, result

in smaller and more distant populations, consequently leading to increased loss of genetic variation, the accumulation of deleterious alleles and higher levels of inbreeding [6]. The conservation of wolves and other large predators may therefore rely on our capabilities to ensure connectivity between these semi-isolated populations. Genetic research on European wolves may therefore provide vital information when defining proper units of conservation and assessing their genetic status with regard to, for example, effective population size, inbreeding and hybridisation level with dogs [7].

The Baltic wolf population has a continuous distribution range extending through Estonia, Latvia, Lithuania, Russia (Kaliningrad and western parts of continental Russia), eastern Poland, northern Ukraine and Belarus, potentially reaching 3600 individuals [2]. Knowledge relating to the genetic structure amongst wolves in this region is, however, sparse and restricted to Latvia, Poland/Belarus (Białowieża National Park),

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