Abstract

Landscape genetic approaches allow to study effects of landscape to population microevolution. Landscape can influence gene flow even in large carnivores with good dispersal ability. Understanding the influence of landscape to the gene flow between populations is crucial for species conservation, especially in the species with low population densities. Aim of the study was to describe genetic structure of the grey wolf (*Canis lupus*) and snow leopard (*Panthera uncia*) in selected areas and to determine the influence of the landscape features on observed structure.

Non-invasive genetic samples of snow leopard from Nepal were analysed, as well as invasive and non-invasive samples of grey wolf from Central Europe. Population structure was determined *a posteriori* using Bayesian clustering approaches that integrate genetic and geographical data, and compared to landscape connectivity models.

Population structure of snow leopards is mostly influenced by human presence and presence of frequented roads, which represent a substantial dispersal barrier. Habitat suitable for this species is greatly restricted by altitude, however, during dispersal they are able to overcome areas with higher elevation than what is optimal for them.

Pronounced genetic difference was found between central European and Carpathian population despite a lack of direct barrier to gene flow. The barrier role is connected with transition zone of two habitat types (lowland vs. mountain), therefore both populations could be considered as ecotypes separated by proximate mechanisms of natal habitat dispersal. However, lowland population partly spreads to the Carpathians.

keywords: conservation genetics, landscape genetics, connectivity, dispersal, snow leopard, grey wolf