

# HISTORICAL EVENTS, GENETIC AND ENVIRONMENTAL BARRIERS – THEIR IMPACT ON GENE FLOW AND POPULATION STRUCTURE IN ANIMALS

## Summary

In many species genetic distances increase with geographic distances, resulting in the “isolation by distance” (IBD) pattern. However, more complex patterns usually are observed in heterogeneous habitats. Geographic obstacles limit gene flow in a discontinuous way and might confound a simple IBD relationship. Moreover, current population structure is not only determined by present-day evolutionary processes but also shaped by population history. Barriers to gene flow lead to differences in gene pool composition among populations, so that molecular population genetics methods should allow these barriers to be detected. It is also possible to identify cryptic boundaries, which may represent secondary contacts among previously isolated populations. Landscape genetics approach that combines molecular population genetics and landscape ecology aims

to detect such genetic discontinuities and to correlate them with environmental features. In this paper, the effects of genetic and environmental factors that affect population genetic structure and population history, are explored with a focus on the following examples: (1) the common vole populations in heterogeneous habitats of the Biebrza valley in NE Poland; (2) red deer populations in France that experienced isolation and translocations; (3) different chromosome races of the common shrew in Poland forming hybrid zones and (4) two sympatric subspecies of the chequered skipper in the Białowieża Primeval Forest, NE Poland. Implications of such approaches for evolutionary biology, ecology and conservation biology are discussed in the context of most recent achievements in the field.