

## Research Project

Génétique des populations et conservation de la coronelle lisse Coronella austriaca (Squamata : Colubridae) en Alsace

## Project funded by own resources

Project title Génétique des populations et conservation de la coronelle lisse Coronella austriaca (Squa-

mata: Colubridae) en Alsace

Principal Investigator(s) Ursenbacher, Sylvain;

Project Members Vacher, Jean-Pierre;

Organisation / Research unit

Departement Umweltwissenschaften / Naturschutzbiologie (Baur)

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Status Completed

Habitat loss and habitat fragmentation are major issues in conservation biology. Both has a negative effect on population sizes and are followed by a decrease of gene flow between populations and of genetic diversity within populations, both of which lead to population decline and eventually extinction. It is thus interesting to study the genetic structure of populations that are supposed at risk (in fragmented habitat for example) in order to assess their conservation status. Reptiles are particularly sensitive to habitat fragmentation, and are therefore good study organisms in conservation biology. Alsace is a region located in North-Eastern France that is highly fragmented with linear infrastructure, urbanization and intensive agriculture. Therefore, it is interesting to focus on the conservation genetics of a snake species in this region in order to assess the effect of fragmentation on its populations. The smooth snake, Coronella austriaca, is widely distributed in the region, and has a fairly low dispersal rate. We studied the population genetics of 12 populations distributed in the whole region at different natural localities (plain, foothills and mountain) in order to detect any effect of habitat fragmentation on their genetic structure. We studied 8 microsatellite loci from nuclear DNA. Results show a lack of genetic structure between populations. This result is rather surprising and unexpected. Even though home range and dispersal rates of the smooth snake are small, the migration rate is high enough to maintain enough gene flow between populations. This could be explained by a high migration rate of young snakes, but this would need to be tested.

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