

## The Influence of Land Cultivation on the Genetic Variability and Genetic Population Structure of *Arion lusitanicus* Mabilie (Gastropoda, Pulmonata)

The aim of this dissertation was to examine the influence of land cultivation on the genetic variability and genetic population structure of the Neozoen *Arion lusitanicus*. *Arion lusitanicus* is a slug, which is spreading quickly in its range. This species has been chosen as it is possible to classify them easily to single plots due to their low mobility and as they are especially exposed to environmental and cultivation influences. Another well known factor in Herl is the age of this quite young population, thus enabling to classify genetic changes to recent working environmental and cultivation influences. To examine small spatial effects on various cultivation systems, ten plots – mostly used for agriculture – have been chosen in the Hunsrück-municipality Herl. Among them were four ecologically and four conventionally cultivated areas with partly varying land development dynamics. Furthermore a waste land of many years and a meadow have been included in the test. Wahlen in Northern Saarland and Belm in South Lower Saxony have been chosen as reference areas. Two fundamentally different PCR-based molecular genetic methods came into operation. The RAPD-analysis (randomly-amplified-polymorphic DNA) and the microsatellite analysis. As microsatellite primer have not been known for *A. lusitanicus* so far, primer of other mollusc species have been successfully tested. Two microsatellite Loci showed results which were easy to analyse. Thus it was possible to analyse five alleles on 360 individuals. In the RAPD-analysis 94 polymorph marker have been analysed. In a comparison of the conventionally and the biologically cultivated plots no significant differences with regard to the analysed parameter (genetic diversity, genetic distances and population structuring) could be found with either of the two molecular genetic methods. The RAPD-analysis in particular showed a population division in the test area that could come into being due to reduced gene flow and gene drift through environmental-stochastic influences. A part of this population structuring can be explained through „isolation by distance“. With „isolation by distance“ the similarity between populations decreases with increasing distance. Although a regression analysis could proof a statistically significant connection between the ground height and the genetic diversity of the single samples ( $p= 0,029$ ), is it difficult to establish functional connections. Nevertheless is it probable that abiotic factors such as temperature, humidity and soil moisture have an influence on mortality and vitality and thus on the genetic structure of slug populations. With regard to the cultivation three slug populations in Herl showed especially low genetic diversities. These were a waste land, a meadow and a plot, which had been uncultivated until the year 2001 („conv1“). The difference between these three plots and the rest of the agriculturally used areas was significant on the basis of data of both microsatellite sites (Ari1: U-Test,  $p=0,033$ ; HA-7:  $p=0,017$ ). In the RAPD-analysis the areas „conv1“ and „meadow“ showed higher diversities, the area „waste land“ lay also on a higher scale with regard to diversity. As 94 Loci have been analysed in the RAPD-analysis, while there were only two sites in the microsatellite analysis, the RAPD-results are more trustworthy. Possibly these results can be interpreted as indication that land cultivation – unaffected by biological or conventional cultivation – is able to have an influence on the genetic diversity of *Arion lusitanicus*.