

Evolution of genetic structures in Metapopulations

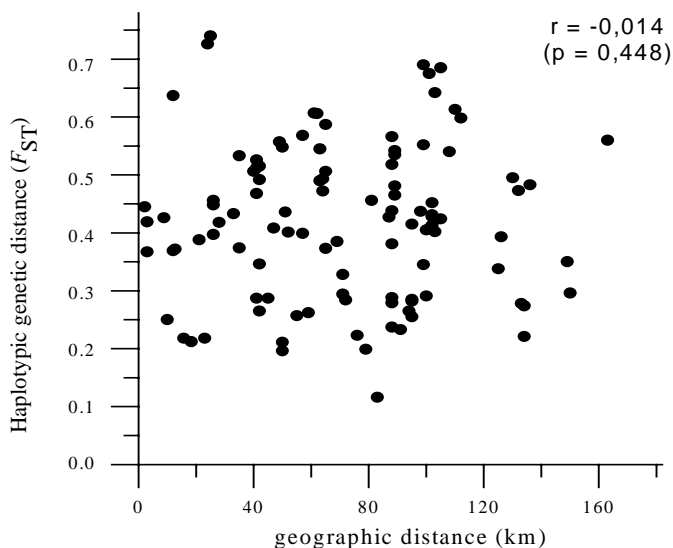
We investigated 21 populations of brown hare ($n=307$), from North-Rhine Westphalia in Western Germany. Research was focused on genetic diversity and population structure. Analyses were performed using 5 microsatellite loci and the mitochondrial control region.

Average pairwise F_{ST} -value among populations was 0.31 ($p>0.001$), indicating a clear matrilinear structure within the hare metapopulation. In terms of microsatellite allele frequencies, no differences were detectable among populations ($F_{ST}=0.054$, non-significant).

While mitochondrial DNA is inherited maternally only, microsatellite DNA is inherited in a mendelian manner. Based on the distribution of haplotypes, female hares are considered to contribute less to the gene flow than males (male-biased gene flow) who cause the admixture of microsatellite alleles among populations. The reasons for these findings may on one hand lie in a highly philopatric behaviour of females, and on the other a higher degree of dispersal or a larger home range of males.

Another main finding of our studies is that the genetic structure of the single populations is predominantly influenced by genetic drift and much less by migration among populations (Fig. 1).

Fig. 1: Genetic *versus* geographic distances among *Lepus europaeus* populations in North-Rhine Westphalia.



Legend:

Pairwise genetic distances (noted as F_{ST} -values) plotted against pairwise geographic distances (in km) among 21 *Lepus europaeus* populations in North-Rhine Westphalia.