Summary

Mitochondrio is a semi-autonomous organelle of the cell, which produces the majority of the cellular energy through the Oxidative Phosphorylation system (OXPHOS). OXPHOS is mediated by 5 multisubunit enzymatic complexes. The subunits of the complexes are encoded by genes mapped in both the cellular genomes, the nuclear and the mitochondrial. The mitochondrial genome possesses some unique features, mentioning the maternal inheritance, the absence of repairing mechanisms, its autonomous replication system, resulting in faster evolutionary rhythms compared to the nuclear genome. So, in order to keep the functionality of the OXPHOS machinery, the nuclear genome has to keep the pace in the evolutionary rhythms of the genes that are cooperating with the mitochondrial genome, by co-adapting the respective nuclear genes.Until the last decade, the mtDNA was considered neutral in terms of natural selection and it was believed that is didn't participate in adaptive mechanisms. However, in nowadays, mtDNA is not considered neutral and natural selection acts on mutations that affect the organisms' fitness. Due to its maternal inheritance, the selection acts solely in the females rather than the males, so mutations that are neutral or beneficial to the females are favored. Though, these beneficial or neutral mutations for the females may have a negative impact in males' fitness, leading to the phenomenon of the "mother's curse". Allopatric populations of the species differentiate genetically through natural selection and the random genetic drift and this divergence can lead to reproductive isolation. The interpopulation hybrids tend to show lower fitness and reproductive ability compared to the parental populations, and these effects are mainly caused by the mitochondrial dysfunction of the hybrids. This model of incompatibility is well-known as the Dobzhansky-Muller model of incompatibility (DMI) and includes many genetic loci. Nowadays, there are numerous studies that detect the cause of the hybrid failure in the mitochondrial dysfuncntion of the hybrids. In this thesis, we studied the selective pressures that act upon the mitochondrial genome in the species of the European brown hare (Lepus europaeus) as well as in closely relative species of the genus and how these pressures are shaping the levels of genetic variability.Also, by using data of transcriptomic analyses, we studied the effect of coadaptation in the genetic differentiation of both genomes, the nuclear and the mitochondrial, by assessing the relative rhythms of the genes encoding for the major energy producing mechanisms of the cells, namely the glycolysis, the Krebs cycle and the OXPHOS. The results, both in interpopulation and interspecies level, are in accordance with the coadaptation patterns of cooperating genes that are mapped in different genomes. Lastly,by studying both nuclear and mitochondrial markers in a hybrid population of the species of the European brown hare, we defined the major factors that affect the lack of gene flow and the introgression between the two lineages of the species.