In forensic research and practice is used an analysis of nuclear DNA commonly. However, in some cases we can use only mitochondrial DNA. The mtDNA is maternally inherited and it is located in the each cell approximately in 500 copies. Barring mutation in special noncoding segments, the mtDNA sequence of siblings and all maternal relatives is identical. This unique haplotyp can be helpful in forensic cases, such as analyzing the remains of a missing person, where known maternal relatives can provide reference samples for direct comparison to the questioned mtDNA type. MtDNA is also very resistant to the external influences, so in the cases where the amount of extracted DNA is very small or degraded it is more likely that a DNA typing result can be obtained by typing mtDNA than by typing polymorphic markers found in nuclear DNA. If we want to have a certain probability to exclude or confirm the match of two samples, classify suspect or missing person into a population, we need some enough wide comparison by the population databases. Then we can study the frequencies of different haplotypes in particular population. The aim of this thesis is summery of history of DNA analysis, mtDNA sequencing and comparison of data available in published databases in the world and mainly in the Czech Republic. There is also added an analysis of two hypervariable segments (HV1 and HV2) in 138 unrelated individuals. This sequence comparison led to the identification of particular haplogroups and frequencies in the Czech population.