Central Europe north of the Alps was colonized by one of the Balkan haplotype lineage of stone crayfish *Austropotamobius torrentium* after the end of the last ice age. Stone crayfish is considered a native species in the basins of the Danube and the Rhine. The origin of populations from the Elbe basin is still debated. Most of recent European studies dealing with the crayfish distribution indicate the stone crayfish in Elbe basin as non-indigenous species.

The main aim of my work was to evaluate the question of the origin of stone crayfish in the Elbe catchment by describing the distribution of genetic variability, which has not been yet studied in the Elbe river basin for this species. I have used 617 base pairs long section of mitochondrial gene for small subunit I of cytochrome c oxidase (COI). The variability of this marker is reduced in area on the north of Alps, which agrees with assumption of rapid colonization after the end of last ice age. Observed haplotype diversity is nevertheless sufficient to suggest the most likely scenario. Among 22 populations from Elbe basin, one dominant and three rare haplotypes were found. Individuals from the isolated Luční creek close to the Krkonoše (Giant Mountains) region have a haplotype that has so far been found only in central Slovenia, and this population has most likely been introduced by humans. Of the two rare haplotypes, one occurs also in southern Germany and the other is unique for the Elbe basin. Number and distribution of rare haplotypes in the Elbe basin is very similar as in parts of the Danube and Rhine north of Alps, which supports the assumption of the natural origin of most stone crayfish populations in the Elbe basin. The most likely scenario of colonization of Elbe basin is overcoming the water divide of the Elbe and Danube in the northen part of the Bohemian Forrest, and subsequent colonization of the Elbe basin by the same colonization wave that colonized the whole area north of the Alps.

In the second part of my thesis, I attempted to increase resolution of the dataset, while retaining a direct comparability with previous data. Therefore, I tried to optimize a protocol that would allow amplification and sequencing of a substantially extended section of the COI gene. Primers that have been used in other studies in case of stone crayfish apparently anneal to the sequence of different gene, which is the reason why I obtained only COI-like sequences. They are most likely nuclear pseudogenes of the mitochondrial COI gene and they are thus unusable for my study. Future studies of stone crayfish genetic diversity in the north of Alps should use more variable markers, such as microsatellites.