

## ABSTRACT

Crayfish are an important part of European fauna, but since the 19<sup>th</sup> century native crayfish species have been largely influenced by biological invasions, when large number of their populations was dramatically reduced due to the introduction of the pathogen of the crayfish plague (oomycete *Aphanomyces astaci*) to Europe. Several North American crayfish species were then brought to the European continent to substitute lost populations of native crayfish, the most widespread being the spiny-cheek crayfish (*Orconectes limosus*), the signal crayfish (*Pacifastacus leniusculus*) and the red swamp crayfish (*Procambarus clarkii*). However, these crayfish can carry pathogen of the crayfish plague and therefore represent a serious threat to the native species.

My work focused mostly on the spiny-cheek crayfish (*O. limosus*). Available literature data suggest that the species was brought to Europe only once, and all European individuals may be descendants of the founder population. However, other cases of introduction may not have been documented, and cannot be ruled out.

The first aim of my thesis was to evaluate the haplotype variation of the spiny-cheek crayfish populations from Europe and North America. Mitochondrial gene for cytochrome c oxidase subunit 1 (COI) of selected *O. limosus* individuals from several European countries and from a part of its American range (Maine, Pennsylvania) was sequenced to obtain data about haplotype variation of the examined populations and to get more information about the possible origin of the European individuals of the species. Our results showed that the founder population for European spiny-cheek crayfish came most likely from the northern part of its American range. Differences in distributions of haplotypes found in studied populations in America were most likely connected with anthropogenic origin of populations in the northern part of the range or with the location of refugia during the last glaciation and the subsequent recolonisation of the territory.

After assembling detailed data on the distribution of *O. limosus* in the Czech Republic, we analysed genetic variability of selected Czech populations of the species using allozyme electrophoresis in order to test whether enough variability was maintained during the introduction of the species to Europe. Our results show, that although the founding population was relatively small, allozyme variability was not dramatically reduced. No correlation between genetic and geographic distances among populations suggest that the distribution of the species was influenced by translocations of crayfish by people, followed by random drift in allele frequencies.

Last aim of my study was to analyse individuals of another North American crayfish, the virile crayfish (*Orconectes virilis*), which has been discovered several years ago in London (UK). We tried to assess their position within the lineages of the *O. virilis* species complex known from a part its American range by sequencing of the mitochondrial gene for COI. As the analysis shows, London individuals (and also one sample from Iowa, USA) represent new lineages of the *O. virilis* complex.