

0.4 English summary

Phylogeographical studies of aquatic plants are relatively rare, although river corridors are amazing study system. There are many questions about dispersal within river catchment and between different river basins.

Using 10 nuclear microsatellite (SSRs) primers, 528 individuals of *Nuphar lutea* from 70 populations (66 from the Czech Republic and one from Belgium, Germany, Slovakia and Lithuania) were analysed. Those analysis allowed reveal kinship of the individuals and obtain information about character of spatial structure of populations of *Nuphar lutea* and about dispersal of *Nuphar lutea*.

Populations seems to consist from many genetically different individuals. There were only 15 clonal individuals found among all samples. Clones are small (biggest sampled clone consisted from 4 ramets — sampled individuals, usual size was 2–3) and common only in specific conditions, when an individual has enough free space for continual growth and frequency of disturbances is low.

Vegetative dispersal is not very important. Among 489 samples from 66 Czech populations, there were detected only 7 clones. The longest distance between clones was about 120 km.

There is not clear tendency for downstream change of genetic diversity. It seems, genetic diversity is more reflecting characteristics of the population: if it is connected with the river (and another populations) or isolated in small water body (pool) separated from the river.

Populations (and especially river catchments) are relatively separated, although there is some communication even between very distant populations. Bayesian clustering did not show any clusters covering more than one population. PCoA shows separation of populations from Odra river and Morava river catchment from populations from Labe river catchment. According to software Structure, populations from Labe (Elbe) river system north-east from Prague together with populations from Berounka river (Central Bohemia, south-west from Prague) are forming strongly separated cluster. But there is some connection with the rest Czech populations.

AMOVA shows high proportion of genetic variability among river catchments and fixation index shows very high separation of river catchments, probably due fixation of very different alleles in populations in different river catchments. It might be result of beginning genetic drift due to the fragmentation of area (because of various human activity like river ship transportation).

There is significant positive autocorrelation among individuals up to more than 100 km of straight distance. It means that repeated seed dispersal on the rate of tens km does regularly occur. *Nuphar lutea* shows clear isolation by distance in the Czech Republic.