

Abstract

Aquatic plants are a heterogeneous assemblage of species that, although surviving in similar habitats, have evolved from very different genetic and ecological backgrounds. However, many aquatics share a number of anatomical, morphological, metabolic and reproductive adaptations, which have arisen independently in remarkable similarities (through convergence and parallelisms) in many unrelated groups. Despite their evolutionary uniqueness, aquatic plants are markedly underrepresented in contemporary biosystematic studies. Moreover, the taxonomic evaluation of numerous aquatic plant groups is intricate due to the strong morphological reduction and a high degree of phenotypic plasticity. This thesis focuses on two notoriously challenging aquatic plant groups, *Callitriche* and *Ranunculus* sect. *Batrachium*. The combination of several approaches (genome size estimation, chromosome counting, sequencing of nrDNA ITS and plastid *trnT-trnL* regions, examination of herbarium collections) was applied in order to improve our knowledge on principal evolutionary processes such as hybridization, polyploidization and cryptic variation and demonstrate their role on the shaping of overall aquatic plant diversity. The distribution of particular species in the Czech Republic was mapped for the first time. For both groups, cytometric genome size estimation proved to be an effective method for distinguishing taxa, even homoploid ones and most hybrids. In the studied range (a large part of Europe for *Callitriche*, central Europe for *Batrachium*), both model groups include five ploidy levels. Intraspecific ploidy level variation was revealed in *Ranunculus fluitans* ($2x + 3x$), *R. penicillatus* ($4x + 6x$), *R. peltatus* ($4x$ and rarely $5x$, $6x$) and *Callitriche stagnalis* ($2x$ and rarely $3x$). The phylogenetic relationships of *Callitriche* taxa were reconstructed with particular emphasis on the origin of polyploids *C. platycarpa* and *C. hamulata*. Flow cytometric and molecular analyses also helped to detect multiple cryptic taxa, particularly within *C. stagnalis*, *C. truncata*, *C. heterophylla*, *R. trichophyllus* and *R. penicillatus*. The frequency and manifestations of hybridization differ significantly among both model systems. Four different hybrid combinations were detected in *Callitriche*, two of which were newly described and validated as *C. ×nyrensis* and *C. brutia* nothosubsp. *neglecta*. However, hybridization is generally rare in the genus, mainly as a result of the different pollination biology of particular taxa and high proportion of selfing. In contrast, hybridization is a frequent phenomenon in *Ranunculus* sect. *Batrachium*. In total, 16 cytotypes of hybrid origin were revealed in this group, which accounted for ca 15% of the individuals studied. Introgressive hybridization takes place particularly between *R. peltatus* and *R. trichophyllus*. The gene flow tends to be biased towards the big-flowered *R. peltatus*, which is probably more often a pollen donor than the small-flowered *R. trichophyllus*. In the *R. penicillatus* group, the occurrence of a large hybrid swarm was documented, occupying a 150 km long stretch of the Ohře river. Due to the prolific clonal growth, *Callitriche* and *Ranunculus* hybrids often persist in nature without their parental species. The mineral richness of the substrate is the key factor influencing the distribution of *Batrachium* taxa in the Czech Republic, while distribution ranges of *Callitriche* species correlate with the climatic oceanicity and continentality.