

Abstract

The hawkweed subgenus *Hieracium* s. str. is notoriously known for its extreme morphological variability and variation in ploidy levels that is associated with differences in modes of reproduction. Extensive past hybridization is supposed for the subgenus, but recent hybridization was evidenced only in few cases. The subgenus attracts the attention of botanists already for more than a century. Therefore the species diversity is largely examined and the taxonomy of the subgenus is well elaborated, although several contradictory taxonomic concepts exist. However the relationships among the species are unknown and haven't been studied yet. The investigation of these relationships from a phylogenetic perspective using molecular approaches was the main aim of the presented thesis. Basic species (both diploid and polyploid), representing morphologically unique taxa, that are supposed to be the basic evolutionary units of the subgenus were studied. The sequences of two intergenic spacers of the cpDNA (*trnT-trnL* and *trnV-ndhC*) and the external transcribed spacer of the nuclear ribosomal DNA (nrDNA ETS) were analyzed. Moreover, three new low-copy nuclear markers with higher variability than nrDNA and cpDNA markers were developed and their suitability for phylogenetic studies in *Hieracium* s. str. was evaluated. One of these, a part of the gene coding for squalene synthase (*sqs*) was included to the study as the second nuclear marker. Based on ETS, two previously unrecognized major evolutionary lineages were found, that correlated well with the geographic origin and distribution of the species. The observed pattern in genome size variation was in high correlation with this phylogenetic pattern. On the other hand, the cpDNA and *sqs* phylogenies were incongruent with the ETS, in respect of these major groups. However, they reflected well the subgroups identified within the major ETS clades. This pattern together with the low interspecific variability of the ETS indicates that *Hieracium* s. str. is a group with rather recent speciation. The level of interspecific hybridization found greatly exceeded the previous expectations: almost half of the studied accessions was evidenced to be of hybrid origin. Moreover, hybrid origin was inferred not only for the polyploids, but it concerned diploids as well. Genetic material representing most probably already extinct parental lineages was identified in some of the hybrid accessions. Hybridization in the subgenus is probably even more abundant as described above, but its detection was obscured by population level (genetic drift, incomplete lineage sorting) or intragenomic (concerted evolution) processes.