

Summary

Subtribe *Hieraciinae* includes taxonomically intricate polyploid and mostly apomictic genera *Pilosella* and *Hieracium* as well as diploid sexual genus *Andryala*. It offers a unique possibility to compare evolutionary trends and processes in closely related genera with contrasting frequency of polyploids, modes of reproduction, and geographical distribution. The thesis is focused on *Hieracium* s.str. and *Andryala*; the genus *Pilosella* was studied by another authors.

Genome size of so called ‘basic’ species of *Hieracium* s. str. (*Hieracium* subgen. *Hieracium*) was estimated and correlated with results of phylogenetic analysis based on nuclear DNA marker ETS, ploidy level, breeding system and ecogeographical features. Inter- and intraspecific variability in genome size was also analyzed. Genome size variation corresponded with results of molecular phylogeny that separated three main clades reflecting geographical distribution in Europe (‘western’, ‘eastern’ and hybridogenous). The monoploid genome size in the ‘western’ species was significantly lower than in the ‘eastern’ ones. Intraspecific variability was generally low. Genome size downsizing was confirmed in monoploid C values comparison among diploid and polyploid cytotypes. Correlation of genome size with longitude was apparent for the whole data, correlations with latitude and altitude were not significant.

Evolutionary history and genome size pattern and evolution were explored in *Andryala*, a medium-size genus distributed mainly in the Mediterranean Basin and Macaronesia. To reconstruct the relationships within the genus we used three nuclear markers (ETS, ITS and single-copy gene *sqs*) and two chloroplast markers (*trnT-trnL* and *trnV-ndhC*). While cpDNA analysis confirmed a previously inferred chloroplast capture event with the sister genus *Pilosella*, nuclear markers supported the monophyletic origin of *Andryala*. None of phylogenetic analyses resulted in sufficient resolution, due to very low levels of nucleotide divergence of two nuclear and two chloroplast markers and a high degree of homoplasy and incomplete lineage sorting in the variable *sqs* marker. Only two well-supported basal lineages corresponding to relict species *A. laevitomentosa* and *A. agardhii* were separated. The rest of *Andryala* species collapsed to well-supported large group named here ‘Major Radiation Group’. Relationships inside this group are largely unresolved. Regarding the genome size, highest C values were detected in basal relict species (*A. laevitomentosa*, *A. agardhii*) and in two populations of *A. ragusina*. Another two populations of *A. ragusina* have distinctly lower C values. Higher intraspecific variation of genome size in a few species might be explained by allopatric differentiation including island populations.

In addition, special attention was also paid to phylogeography and cytotype structure of *Hieracium intybaceum*, the sister member of all *Hieraciinae* genera forming transitional lineage among the four *Hieraciinae* genera. 43 populations collected across the distribution range in the Alps and the Vosges Mts were explored using flow cytometry and AFLP molecular markers. We detected two ploidy levels, diploid and tetraploid with contrasting modes of reproduction (sexuality in diploids, apomixis in tetraploids). Diploids were found all across the Alps, while tetraploids only in the westernmost Alps and the Vosges Mts. Genetic variation was very low. Bayesian clustering identified four clusters/genetic groups, which are partly congruent with the ploidy pattern and geographical distribution. We suppose that diploids colonized the deglaciated areas from source populations most likely located in the southern part of the recent distribution range and in the western Alps.