Karyotype evolution in the genus *Crepis*

Crepis (Asteraceae) comprises about 200 annual and perennial species distributed mainly throughout the northern hemisphere and Africa. Most of the species are diploids with relatively small number of rather large and well differentiated chromosomes. For this genus several basic chromosome numbers and quite big differences in genome size were reported. All these features make *Crepis* a suitable model system to investigate the karyotype evolution. A karyotype is the characteristic chromosome complement of a eukaryote species. The number and morphology of chromosomes is a distinctive feature of species. The comparative analyses of karyotype structure among species from one genus could provide a lot of important data on phylogenetic relationships among species and allow insights into the directions of chromosome evolution which accompanying the speciation and diversification of *Crepis* species.

The first most comprehensive hypothesis on phylogeny and karyotype evolution in *Crepis* are those published by Babcock more than 50 years ago. This sectional delimitation included a priori assumptions about character evolution pointed to a reduction in chromosome number which accompanied the evolution of the genus. Babcock's interpretation of karyotype evolution is of special importance, since it tended to be cited as exemplar, however recent data on molecular phylogenetics contradict Babcock's hypothesis on karyotype evolution in the genus. In the present proposal we aim to explore the dynamics and directions of chromosomal changes accompanying diversification and speciation in *Crepis*. The phylogenetic relationships among studied *Crepis* species will be tested using noncoding chloroplast regions and nuclear markers. The obtained phylogenetic trees will be used to infer the patterns of evolution of various cytogenetic characters such as: chromosome number, chromosome morphology, genome size and chromosomal organization of different repetitive sequences. rRNA genes are the most extensively used repetitive sequences in karyotype analyses. The coding sequence of rRNA genes are evolutionarily highly conserved regions and once isolated from model species could be used as a DNA probe in fluorescent *in situ* hybridization to chromosome of even distantly related species. Except rDNA also satellite sequences will be used as chromosome markers. The fraction of satellite DNA is very poorly studied in the genomes of *Crepis*. Until now only three satellite repeats are known from *C. capillaris* genome. NGS (new generation sequencing) analyses will be performed in a few selected *Crepis* species to allow the identification and isolation of satellite sequences which will be further tested as a chromosome markers. The combination of molecular phylogenetic analyses and comparative mapping of various chromosomal markers, will allow us to gain in-depth insight into the role of chromosomal and genome restructuring which coinciding with diversification and speciation in plant.