The genus *Crepis s.l.* (Asteraceae) comprises about 200 plant diploid species, that differ significantly in genome size and the basic chromosome number (x = 3, 4, 5, 6 and 11). *Crepis* chromosomes are relatively large and morphologically well-differentiated within one karyotype. These features make *Crepis* a suitable model for studying chromosome evolution in plants. The first comprehensive interpretation of *Crepis* karyotype evolution was performed in the 1930s and 1940s. These studies suggested that chromosomal rearrangements are the driving force of the speciation in this genus. Interpretation of karyotype evolution in *Crepis* remains of special importance since it is often cited as the most prominent example of chromosomal evolution in angiosperms, however, the latest molecular phylogenetics analyses contradict previous hypotheses. Modern cytogenetic methods along with molecular phylogenetic analyzes greatly facilitate the understanding of trends in the karyotype evolution. The aim of this doctoral research was the comparative analysis of *Crepis* karyotypes in the phylogenetic background, which allowed for a better understanding of trends in the evolution of *Crepis* chromosomes.

Phylogenetic analyzes were performed on three data sets: nuclear markers such as nrITS and 5S rDNA NTS and four plastid markers (cpDNA). Analyzes based on the nrITS marker and chloroplast markers allowed to distinguish two evolutionary lineages of *Lagoseris* and *Crepis sensu stricto*. In *Crepis s.s.* four clades of closely related species were distinguished. The analysis of the 5S rDNA NTS marker, due to the interspecies polymorphism of the nucleotide sequences, did not allow for the unequivocal reconstruction of *Crepis* phylogenetic relationships. The analysis of the karyotype structure included: the basic chromosome number, the morphology of the chromosomes and the asymmetry index. A large differentiation in the basic chromosome number and karyotype formulas was shown. Descending dysploidy was the dominant trend in the evolution of the genus *Crepis*. Analysis of genome size evolution revealed that both increases and reductions in genome size accompanied evolution in genus *Crepis*. The conducted analyzes showed that the changes in the karyotype structure and genome size accompanied the evolution of individual species, and rarely the evolution of entire clades.

Fluorescence *in situ* hybridization with 25S and 5S rDNA probes was used to analyze the chromosomal organization of rDNA loci in *Crepis* genomes. A high interspecific polymorphism in rDNA loci chromosomal organization was observed, but most of the species possessed a chromosome with both rDNA loci (5S rDNA and 35S rDNA) located in the same arm. Analyzes of the chromosomal organization of rDNA loci evolution in the phylogenetic background showed that most of the changes in the number and localization of rDNA loci

accompanied the speciation, not the evolution of entire clades of closely related species. Performed analysis suggested that chromosomal rearrangements such as translocations or inversions may have accompanied speciation in the genus *Crepis*.