ABSTRACT

Nuclear DNA content (genome size) is one of the basic characteristics of living organisms. In the Angiosperms, the range of genome size is 2,300-fold, which raises questions about the causes and consequences of this tremendous variation. This thesis deals with genome size in plants from the level of intraspecific homoploid variation, through intraspecific ploidy variation, to interspecies comparisons. On various study systems we investigated the dynamics and ranges of genome size variation, tried to reveal possible associations between genome size and selected biological traits, and assessed the extent to which differences in genome size are manifested at the ecological and evolutionary level.

As a means of estimating genome size we applied flow cytometry (FCM). In *Taraxacum stenocephalum* we conducted a detailed study of its enormous genome size variation. We carried out crossings of parents with various genome sizes and compared these parental genome sizes with those of F1 offspring. We also attempted to reveal the association of genome size with various growth traits. In *Galium valdepilosum* and *Arabidopsis arenosa* we carried out an extensive flow-cytometric ploidy level screening and compared the distribution and ecological preferences of detected cytotypes. We studied the Andean genus *Lasiocephalus* growing in different habitats spanning a wide range of elevations. Using FCM we determined both relative and absolute genome size across the genus, and, with the use of ITS sequencing, attempted to identify the sources of genome size variation within it. On the set of allien species we studied the relationship of genome size and invasiveness. Last but not least, we attempted to overcome the need for fresh samples in flow-cytometric genome size measurements. We modified the protocol of nuclei preservation in glycerol and verified the new protocol in a time-scale laboratory experiment and a field experiment.

We have confirmed the existence of substantial genome size variation within the species *Taraxacum stenocephalum* and found a strong correlation between parental and F1 genome size. We have also found correlations between genome size and certain biological traits that might influence the establishment of populations. The two ploidy-variable species under study differ in the ecological preferences of their cytotypes. In *Lasiocephalus* the main factor determining genome size variation is phylogeny. We found the association of genome size and invasiveness. We designed a new protocol for the preservation of nuclei which enables to estimate genome size in samples from remote areas.

This thesis unambiguously shows that genome size is associated with various aspects of the lives of plants and that it therefore represents a useful marker in plant studies. Genome size can not only indicate important species-forming processes, such as polyploidization, selection and hybridization, but it can also help us better understand the evolution of taxa. The effect of genome size differs from species to species and at different levels (e.g. anatomical, morphological, phenological or ecological), and to answer particular questions it is necessary to select a suitable model system and to meaningfully set the scope of the study.