Abstract

This MSc. thesis deals with morphological, karyological, and molecular variations of selected apomictic hybridogenous hawthorns (*Sorbus* L.) endemic to the Czech Republic. The genus is represented by 17 taxa in the Czech Republic, eight of which rank among the (sub)endemics (i.e., *S. alnifrons* KOVANDA, *S. bohemica* KOVANDA, *S. eximia* KOVANDA, *S. gemella* KOVANDA, *S. hadeggensis* KOVANDA, *S. rhodanthera* KOVANDA and *S. sudetica* (TAUSCH) BLUFF, NEES et SCHAUER). Two morphologically-distinct populations of unknown taxonomic position as well as selected parental taxa were also studied.

DAPI and propidium iodide flow cytometry, chromosome counting using rapid squash techniques, multivariate statistics (PCA, cluster analyses, discriminant analyses), and molecular approaches (microsatellite variation) were employed. All native populations of above-mentioned (sub)endemic taxa were included into the study (i.e., 29 populations and over 450 individuals).

DNA ploidy screening, using leaf tissue of mature individuals, revealed triploidy in majority of hybridogenous taxa (often in contrast to previous reports). Exceptions included tetraploid *S. quernea* and *S. sudetica*, and diploid *S. hardeggensis*. Flow cytometric data were mostly confirmed by chromosome counts. Low, but statistically significant, between-species differences in genome size were often observed. Remarkably, triploid and pentaploid embryos were observed during flow cytometric investigation of the mode of reproduction.

Morphometric analyses revealed low intraspecific variation in most taxa, *S. eximia* with two distinct morphotypes being an exception. Species-specific sets of morphological features, which allowed reliable species identification, were identified.

Molecular variation in hybridogenous taxa (both within and among populations of the same taxa) was low while between-species differences were high. Generally, single-locality species were more uniform than their counterparts occurring in several localities. Increased variation in *S. sudetica, S. eximia* and *S. hardeggensis* may be explained by their multiple origins and/or facultative apomixis. Genetic variation of putative parental taxa was, according to expectations, significantly higher.