

## Abstract

Presented thesis evaluates the risk of ongoing hybridization (antropohybridization) in highly endangered *Prunus fruticosa* in the Czech Republic and selected adjacent countries. Absolute genome size analysis (estimated by flow cytometry) combined with both numeric and geometric morphometrics were used for evaluation of hybridization.

*Prunus fruticosa* frequently hybridize with naturalized *Prunus cerasus* (emerging tetraploid hybrid *Prunus ×eminens*) and native *Prunus avium* (forming triploid hybrid *Prunus ×mohacsyana*). Discrimination between *P. ×eminens* and *P. ×mohacsyana* is difficult, when using leaf morphology characters only, so the occurrence of triploid hybrids was strongly underestimated in the Czech Republic (only tetraploid hybrids were reported). Both hybrids are surely differentiated using flow cytometry analysis (based on different ploidy level). The majority of analyzed populations is formed by either individuals of pure *P. fruticosa* or one of the mentioned hybrids. Only four populations were mixed. Continuous variability in absolute genome size was found in two of them, which may indicate hybrid swarm forming (incl. primary hybrids and backcrosses). Our findings can be considered only as indirect evidence for introgression, which needs to be confirmed by molecular markers (for example microsatellites).

Morphological and karyological variation of *P. avium* a *P. cerasus* cultivated in horticultural collections was also evaluated and compared with natural populations. Absolute genome size variation observed in *P. cerasus* was markedly broader than the expected (or previously published) one.

**Key words:** *Prunus fruticosa*, *P. cerasus*, *P. avium*, interspecific hybridization, absolute genome size, flow cytometry, numeric morphometrics, geometric morphometrics