Abstract

A large number of papers have been published on the effect of polyploidy on a wide range of biological traits of plants, but still not much is known about its effect on the content of secondary metabolites. To elucidate this issue, the intensively chemically studied *Urtica dioica* agg. was selected. It is also a polyploid complex including the widely distributed tetraploid subspecies *U. dioica* subsp. *dioica* and several diploid subspecies with smaller and often vicariant ranges (*U. dioica* subsp. *sondenii*, *U. dioica* subsp. *subinermis*, *U. dioica* subsp. *pubescens* and *U. dioica* subsp. *kurdistanica*), and the closely related species *U. atrovirens*, serving here as an "outgroup". The work was supplemented with a control in the form of synthetic tetraploids. The thesis also aimed to contribute to the still unresolved evolutionary relationships in this aggregate.

To detect the effect of polyploidy on the content of secondary metabolites in plants, synthetic neotetraploids were generated from diploid *U. dioica* subsp. *subinermis* plants using colchicine. The content of metabolites in the leaves of 83 *Urtica dioica* agg. plants, including neotetraploids, was analysed by a combined liquid chromatography-mass spectrometry (LC−MS) method.

The effect of polyploidy on the content of secondary metabolites was confirmed at the level of synthetic neotetraploids in the context of differentiating a group of diploid plants of the parental generation of *U. dioica* subsp. *subinermis* from neotetraploids. The effect of polyploidy at the level of natural variation in tetraploid cytotype was not reliably confirmed, although a hint of differentiation between diploid and tetraploid plants was observable in the analyses.

The results of this work also suggest that the taxa included in the main sister group (i.e. *U. dioica* subsp. *subinermis*, *U. dioica* subsp. *pubescens*, *U. dioica* subsp. *kurdistanica*, *U. dioica* subsp. *sondenii* and *U. dioica* subsp. *dioica*) of the *U. dioica* agg. are apparently closely related to each other, as they could not be significantly distinguished from each other even at the metabolomic level. Since the recent phylogenetic studies, including this metabolomic one, suggest that the current taxonomic concept does not correspond to the real structure of this broadly defined aggregate, it is likely that this concept should perhaps be revised again.

Key words: Urtica dioica, Urtica dioica *agg., polyploidy, secondary metabolites, liquid chromatography, mass spectrometry, LC−MS, synthetic control, colchicine, flow cytometry*