ABSTRACT

Although European flora belongs among the best explored, there are still several marginally studied groups. One striking example is the polyploid complex of *Urtica dioica*, with multiple rare diploid taxa, which are often found in remote and partly relict geographic ranges, in contrast to cosmopolitan tetraploid individuals, which occur in a variety of synanthropic habitats and have an unknown evolutionary history. The thesis primarily deals with the evolution of diploid taxa recognized in Europe and contiguous areas of Southwest Asia (*Urtica dioica* subsp. *kurdistanica*, *U. d.* subsp. *pubescens*, *U. d.* subsp. *sondenii*, *U. d.* subsp. *subinermis*). This can lay the foundation for understanding phylogenetic relationships and revealing the evolutionary history of polyploids (*U. d.* subsp. *dioica*). The study also concerns itself with other related species outside of the complex *U. dioica*, especially from the Mediterranean area. An extensive dataset of 7012 samples from 1317 populations in a cytogeographical study has been analyzed, which covers most of the currently accepted diploid subspecies of *U. dioica*. From the entire dataset, a set of 279 plants (evenly representing the geographical and morphological variation) was used to estimate the extent of phylogenetic and morphological differentiation. The distinct dominance of tetraploids over diploids (87% of tetraploids and 13% of diploids) has been revealed, and for the first time, the rare triploid and pentaploid ploidy levels have also been detected, both in adults and in seeds. Subsequent analyses of absolute genome size showed uniform Cx-value among all studied diploid subspecies while differing significantly from Cx-values of other species related to *U. dioica* (*Urtica bianorii*, *U. cypria*, *U. kioviensis*, *U. rupestris*), which may be indicative of genetic distance. All revealed ploidy levels were verified by exact chromosome counts. A combination of molecular approaches was used to understand the basic phylogenetic relationships. The data evaluation took place first at the diploid level and then on the whole dataset; this approach was also used for morphometrics. Diploid subspecies form more or less separate clusters in morphological analyses, but molecular evaluation did not reveal any structure. Moreover, tetraploids merged with diploids in both morphological and molecular analyses. To reveal specific habitat requirements and ecological preferences of the cytotypes, the correlation with geographic parameters (latitude, longitude, and altitude), Bioclim modeling, and affinity to human-affected habitats has been applied. The diploid populations usually prefer lower altitudes, have a narrower ecological niche, and occur in less human-affected habitats in comparison to the ubiquitous, synanthropic tetraploid cytotype.