

ABSTRACT

This thesis aims to elucidate evolution of the members of the selected species groups of the genus *Cardamine*, which is a species-rich genus with cosmopolitan distribution and very complex evolutionary history. The studied species were represented by hygrophytic perennials, with the focus laid on their diversity in the Balkan Peninsula and Southwestern Asia, with the emphasis put on the Anatolica-Caucasus region. These regions harbour global biodiversity hotspots and important glacial refugia, yet, they have been largely understudied in terms of knowledge of evolutionary mechanisms and environmental factors that have played there a role of plants diversification and speciation drivers. In this thesis, questions concerning the phylogeny and taxonomy of the studied groups were addressed, with aim to determine the role of polyploidy and hybridization in their evolution. Hyb-Seq was the majorly applied method, representing a technique based on next-generation sequencing, which has proven to be a very efficient and versatile method for resolving evolutionary questions. An integrative approach was employed, combining Hyb-Seq with a variety of other karyological, molecular, cytogenetic and ecological niche modelling methods, which provided a very complex insight into the addressed topics. This thesis resolves the phylogenetic relationships among the target lineages as well as between the taxa distributed in both studied regions, revealing the evidence of historic Balkan-Anatolian biogeographic links. In contrast to the situation in other parts of Europe, the results showed that the evolutionary history of the studied species was only minorly affected by interspecific hybridization and polyploidization events, even though the exceptions were found, being represented by the two allopolyploid species. The ecological divergence and biogeographic isolation were identified to be among the most crucial factors driving speciation in the target complexes. The reports of conflicts between genetic, morphological and ecological patterns found in previous studies were presumably caused by incorrect interpretation due to the relatively recent and rapid diversification of the studied groups, along with high intraspecific variability observed in part of the species.

Keywords: *Cardamine*; Hyb-Seq; allopolyploidy; endemism; hygrophytic species