

Abstract

The Brassicaceae (Cruciferae) comprises 49 tribes, 321 genera and 3660 species, and belongs to the largest plant families. Whole-genome sequencing of the model plant *Arabidopsis thaliana* fuelled the interest of scientists in the mustard family as well as rapid development of comparative phylogenomics and cytogenomics, including the invent of chromosome painting in *A. thaliana* and comparative chromosome painting (CCP) in other Brassicaceae species. The Brassicaceae is the only plant family in which large-scale CCP is feasible. CCP provides unique insights into the karyotype and genome evolution in plants by comparing chromosome collinearity, identification of chromosome rearrangements, construction of comparative cytogenetic maps, and reconstruction of ancestral karyotype structures.

This PhD thesis deals with the karyotype evolution in the Brassicaceae family uncovered by comparative chromosome painting. The introductory part is divided into four chapters. The first chapter introduces chromosomes, karyotypes, karyotypic variation, and the role of chromosome rearrangements and polyploidy in the karyotype and genome evolution. In the methodical second part, principles of chromosome painting are described. The core third chapter focuses on comparative cytogenomics in the Brassicaceae, and summarizes the current knowledge on karyotype and genome evolution in this family. The final chapter provides comparison of karyotype evolution in the Brassicaceae with evolutionary trends in other plant families. Eight publications document author's contribution in the following research areas: 1) Optimization and application of the large-scale CCP in Brassicaceae. 2) Identification of the mechanisms responsible for chromosome number reduction. 3) Evaluation of the role of polyploidy in karyotype and genome evolution. 4) Re-examination of the role of ancient chromosome rearrangements in plant speciation.