

Abstract

A prerequisite for addressing general questions concerning the evolution of intraspecific variability in space and time is the knowledge of the distribution of variability within the species' range. The development of molecular methods has been a major step forward, allowing various evolutionary questions to be addressed using natural populations of model species and their close relatives. Although wild relatives of *Arabidopsis thaliana* have long been in the focus of plant evolutionary biologists and molecular geneticists, the patterns of genetic diversity and phenotypic variation in their natural populations are often overlooked.

The present work focuses on some of the most studied model species in the Brassicaceae family, *Arabidopsis halleri* and the complex of *A. arenosa*, whose members are widely used to study ecology, physiology and evolution as well as the molecular basis of phytoremediation and parallel adaptation.

The study aimed to determine intraspecific variation at the ploidy level, to reveal phylogenetic relationships and the spatial distribution of genetic diversity across the range, and to propose a new taxonomic concept based on the detected intraspecific genotypic and phenotypic variation.

In order to accomplish this goal, we used DNA flow cytometry, several molecular methods (AFLP, SSR, cpDNA and single/low-copy gene sequencing, ddRADSeq, whole-genome sequencing), and multivariate morphometric methods, all based on dense population sampling across the distributional range of both groups.

In the solely diploid *Arabidopsis halleri*, we identified three major genetic lineages within Europe whose distributions were strongly correlated with major geographic barriers in the Central European mountain systems. Subsequent analysis of individual lineages revealed a further geographical distribution of the revealed diversity, resulting in five stable subgroups differing also on the basis of morphology, which allowed a new intraspecific classification of *A. halleri*.

The *Arabidopsis arenosa* species complex comprised three cytotypes, forming predominantly cytotype-uniform populations. Diploid and tetraploid cytotypes showed a predominantly parapatric distribution with three secondary contact zones. In the *A. arenosa* complex, five diploid and five tetraploid genetic lineages were found, with lineages with the same ploidy being geographically isolated (correlating with the biogeographic subdivision of Central Europe). The revealed intraspecific genetic lineages do not correlate with the current taxonomic concept of the *A. arenosa* species complex, which should be thoroughly re-evaluated.

Key Words

Arabidopsis halleri, *Arabidopsis arenosa*, phylogeography, genetic diversity, autopolyploidy, taxonomy