

Abstract

For understanding extant species diversity, knowledge about processes acting at the population level is crucial. Besides mutations generating de novo genetic variation, three major processes, i.e., polyploidy, hybridization and local adaptation, notably impact population structure and cause evolutionary novelty. *Campanula rotundifolia* agg. was chosen as a model group for the joint study of these processes because it represents a polyploid complex with three major cytotypes (2x, 4x, 6x), a hitherto unknown ability to hybridize, and a pleiad of putative species that have undergone local adaptation to different conditions. In particular, polyploidization in the complex is acknowledged for generating morphological variation, facilitating long-distance dispersal and shifts in the environmental niche. It also creates a reproductive barrier, thus enabling sympatric speciation. Prerequisites for local adaptation are morphological variation and strong selection pressures leading to adaptive divergence and the rise of many endemic taxa, mainly at the extremes of environmental gradients. On the other hand, for locally adapted or endemic taxa, hybridization with a widespread taxon is one of the main existential threats.

Here, I focused on *C. rotundifolia* agg. populations in Central Europe – its hypothetical centre of origin and a region where all cytotypes coexist either in sympatry, parapatry or allopatry. The assessment and comparisons of current cytotype distribution, morphological variation and environmental niche, illustrated the dominant role of polyploidy in reproductive isolation among diploids and tetraploids, either in sympatry or parapatry. Due to the higher permeability of the postzygotic reproductive barrier among higher polyploids, environmental niche shift played an important role as a prezygotic reproductive barrier preventing interploidy gene flow.

Morphological variation in all analysed characters was affected by both, the ploidy level and environment, however, generative characters were influenced dominantly by ploidy. To disentangle the effect of polyploidy from the adaptive changes to local conditions, morphological variation in tetraploid populations along elevational gradients in the Western Carpathians was studied in the field and cultivation. As the morphological variation may also be influenced by hybridization among putative alpine endemic and widespread lowland taxa, genome size, genetic and morphological variation were assessed. High within-population genetic variation, shared gene pool, and phenotypic plasticity detected in the experimental cultivation point out the possibility of high adaptive potential but challenge the classical taxonomic concept of the group based primarily on characters without species specificity.

A general insight into the evolutionary history of mountain taxa from *C. rotundifolia* agg. was obtained by comparing phylogenies reconstructed for six clades with diversification centres in the European mountains. Multiclade comparative models detected asymmetrical migrations from silicate alpine elevational habitats to lowland, and mostly calcareous, refugia. The repeated migrations buffered extinction during Pleistocene glaciation cycles but prevented speciation along elevational gradients due to repeated range oscillations. Allopatric speciation driven by adaptation to different bedrocks within the same mountain ranges promoted diversification.

To elucidate the discrepancies between reconstructed evolutionary history and morphology-based taxonomy, genetic, genome size and morphological variation among Central European mountain endemics from the Alps, the Krkonoše and the Jeseníky were compared with local populations of diploid and tetraploid *C. rotundifolia* s. str. Morphological and genetic similarity between *C. bohémica* from the Krkonoše and *C. scheuchzeri* from the Alps supports its hypothesised vicariant origin. In contrast with the current taxonomic treatment, the genotype of putative stenoendemic *C. gelida* was present in most populations of another putative endemic taxon, *C. rotundifolia* subsp. *sudetica*. On the other hand, *C. rotundifolia* subsp. *sudetica* does not form a separate genetic group, nor does it cluster with the genotype of *C. rotundifolia* s. str.

Campanula rotundifolia agg. represents a remarkable polyploid complex with a recent evolutionary origin followed by rapid radiation. High morphological and genetic variation and phenotypic plasticity provide adaptive potential, on the other hand, they challenge taxonomists using classical approaches relying on minute morphological differences.

Keywords: *Campanula rotundifolia* agg., adaptive divergence, elevational gradient, flow cytometry, polyploidy, gene flow, morphological variation, niche modelling, phenotypic plasticity, phylogenetic comparative methods population genetics.