

# Abstract

Habitat fragmentation can adversely affect species populations due to reduced genetic diversity and increased population differentiation due to habitat isolation, reduced population size, and disruption of gene flow. Many species suffer from habitat fragmentation and isolation, and *Campanula glomerata* is a good example of a species that is noticeably declining in many places due to changes in landscape management. The question is how the model species responds to these changes and whether the changes are reflected in genetic diversity and population structure. The aim of this work is to determine the degree of genetic diversity and to reveal the genetic structure of populations of the model species *C. glomerata* on a small regional scale in the White Carpathians. This system will allow us to compare populations from two different regions that have been affected to varying degrees by agricultural intensification and fragmentation in the last century. It is a southwestern and northeastern part of the region, which differs from each other in the history of management in the landscape, but also in the continuity of meadows, species composition and environmental conditions. For this purpose, I developed and optimized a total of 16 usable microsatellite markers, 4 of which come from related species of the genus *Campanula* and 12 are newly developed for the species *C. glomerata*. The results suggest that recent habitat fragmentation has not led to a significant loss of genetic diversity. The species probably has sufficient dispersive capabilities to maintain gene flow and population connectivity in a landscape that has been affected by fragmentation in recent history. Nevertheless, some difference was found between the southwestern and northeastern regions, where genetic diversity was slightly lower, there were fewer rare alleles, and populations were more or less differentiated. The explanation may be the higher isolation of populations due to more intense fragmentation in this area. However, the forces that determined the formation of *C. glomerata* populations in the studied region may have been rather ancient historical processes. The effect of environmental factors on genetic diversity has also been tested in several ways. The most important were the location of the populations in the region and the degree of incident sunlight. *C. glomerata* is an example of a species that is more associated with grasslands with a long period of continuity, as demonstrated during data collection in the northeastern region. There are a number of restored meadows, in which, however, *C. glomerata* practically did not occur. It is therefore important to maintain the original meadows with appropriate management, as many of them occur in less accessible places where there is a risk of overgrowth.

**Key words:** *Campanula glomerata*, genetic diversity, microsatellites, habitat fragmentation, continuity of grasslands, gene flow, environmental factors.