

**GENETIC DIVERSITY OF *MELICA TRANSSILVANICA* SCHUR (POACEAE)
AT ITS NORTHERN RANGE LIMIT**

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Geographically marginal populations are expected to have low genetic variability, which potentially can affect their viability. In Poland *Melica transsilvanica* Schur reaches the northern limit of its continuous geographical range. Genetic diversity and population genetic structure were analyzed in 15 of its marginal and more central populations using AFLPs. Overall, genetic diversity parameters did not differ significantly, and comparable patterns of genetic variation were found in central and marginal populations. All AFLP phenotypes were unique to particular populations. Unique alleles were fixed in some central and some marginal populations. The percentage of polymorphic loci varied from 1.30 to 5.19 (3.24 average) in central populations and from 0.43 to 5.63 (2.36 average) in marginal ones. Hierarchical analyses of molecular variance (AMOVA) for each species/region combination revealed highly significant differentiation between populations and showed similar partitioning of molecular variance in marginal and central populations of *M. transsilvanica* (diversity between populations: 93.24% and 93.18%, $p < 0.001$, respectively). The scattered distribution of suitable species habitats and the predominant selfing breeding system of the species strengthen the effect of selection pressure on fixation of unique loci in individual populations. Marginal populations of *M. transsilvanica* with unique alleles considerably expand the genetic variation of the species and are therefore valuable for conservation of genetic diversity.

Key words: AFLP, genetic diversity, marginal populations, *Melica transsilvanica*, range limit.