MOLECULAR TAXONOMICAL COMPARISON OF DIFFERENT *FESTUCA* SPECIES

MOLEKULÁRIS TAXONÓMIAI ÉS POLIMORFIZMUS VIZSGÁLATOK *FESTUCA* FAJOKON

Z. GALLI[1], K. PENKSZA[1], B. WICHMAN[1], E. KISS[1], L.E. HESZKY[1]

[1]SzIU, Institute of Genetics and Biotechnology, 2103 Gödöllő, Páter Károly str. 1.
[2]SzIU, Department of Nature Conservation and Landscape Ecology, 2103 Gödöllő, Páter Károly str. 1.
galli.zsolt@mkk.szie.hu

Classification of some species from genus *Festuca* is still a controversial question. The goal of our experiments was the molecular comparison of the most questionable *Festuca* species to supply new data for the conventional taxonomy. There was no available molecular analysis regarding the most examined *Festuca* species before our experiments. Examinations were executed at molecular marker and sequence levels, as well.

Among the tested 47 RAPD and 19 AP-PCR primers, eight and six showed polymorphic patterns, respectively. For the determination of genetic distance between the examined species, the binary codes of 111 fragments of these 14 polymorphic primers were used. The examined *Festuca* species were classified into three well-separable groups on the basis of these results.

It has been proved that the separate *Festuca rupicola* groups independently of their separation based on the shape and size of their leaves, compose uniform species at molecular level. It has been proved that the sub-Mediterranean tetraploid *F. pallens* (4x) differs genetically from the subalpine diploid *F. pallens* (2x), which may modify the present classification. The species *F. javorkae* and *F. rupicola* can be differentiated from each other at the molecular level based on the result conducted by the PAL1 primer. It is worthy of note that the species *F. wagneri* based on our molecular classification was placed in a different group than its supposed parent species (♀: *F. vaginata*, ♂: *F. valesiaca* or *F. pseudovina* or *F. rupicola*).

After the above experiments based on PCR techology, comparison of internal transcribed region (ITS) and the chloroplast origin *trn*L intron have been executed at sequence level in the studied species. The amplification and sequencing of the ITS and *trn*L intron regions was achieved in 27 specimens of 10 species. The determined sequences were placed into the NCBI Genbank where among the 10 species in 8 cases this meant the first entry. Intraspecific ITS variation was detected only in *F. rupicola.* In the other 9 species there was no detectable difference between their individuals even if they originated from different locations. In these species polymorphism was manifested only in intragenomic differences which can be explained by the high number of copies of rDNA and the possible differences between them. Among the sequences of the *trn*L intron even intragenomic polymorphisms were not detected in any of the *Festuca* species studied.

Kulcsszavak: *Festuca ovina* csoport, RAPD, AP-PCR, ITS, *trn*L intron