Abstract

Eight of fifteen species in genus *Anthoxanthum* (Poaceae) can be found in Europe. Five of them are perennials forming *A. odoratum* complex, the remaining three are annual, more or less mediterranean taxa (*A. aristatum*, *A. ovatum* and *A. gracile*). Within the *A. odoratum* s. l. complex the following taxa are distinguished: widely spread *A. odoratum* s. str. (4x; 2n = 20), arcto-alpine *A. alpinum* (2x a 4x; 2n = 10 and 20), Madeiran endemic species *A. maderense* (2x; 2n = 10), endemic species of Balkan mountains *A. pauciflorum* (2x; 2n = 10) and the Iberian peninsula endemic *A. amarum* (?x; 2n ~ 90). The aim of this thesis is to clearify the unknown evolutionary relationships between the taxa, between the annuals and perennials, diploids and polyploids.

The following questions should be answered in this study: 1) What is the origin and distribution of the rediscovered diploid perennial taxon and what is its relationship to the other members of the group; 2) What is the distribution pattern of the perennial taxa of the genus *Anthoxanthum* in Europe and what is their haplotype differenciation (overall distribution of the taxa and haplotypes and the existence of their sympatric occurence); 3) What evolutionary ties exist among the species and what is the origin of allotetraploid taxon *A. odoratum* s.str.

The assessment of ploidy levels and absolute genome sizes of the studied taxa was carried out using flow cytometry. To reveal evolutionary ties among the taxa and their haplotype differenciation a sequencing of non-coding segments of chloroplast (*trnL-trnF, rpl32-trnL*) and nuclear (single-copy gen GBSSI) DNA was used.

Flow cytometry revealed species-specific genome size in most of the European taxa, which enables their independent and objective determination. Moreover, using flow cytometry, a known (mentioned in literature), but probably not validly described diploid mediterranean taxon was found, a possible parrental species of the allotetraploid *A. odoratum* s. str. But its close relationship to other medieterranean diploid taxa (both perennial and annual) doesn't allow to distinguish real source of genetic diversity of *A. odoratum*. On the other hand, the second parrent is more clear and most probably is composed of *A. alpinum* or its direct ancestor. This hypothesis is supported by molecular data from both chloroplast and nuclear DNA. Analysis of the gene GBSSI revealed high rate of differenciation in genome structure of individual plants of one taxon (especially in the case of *A. odoratum*), which supports the hypothesis of multiple and polytopic origin.