## Chromosome number and DNA ploidy level reports from Central Europe -1

Patrik Mráz\*, ed.

Abstract: This is the first part of an intended series of chromosome number and DNA ploidy level reports from Central Europe, including the whole Carpatho-Pannonian region. Here, the chromosome counts/estimations of DNA ploidy level using flow cytometry are given for 10 taxa: Asplenium cuneifolium (n=36II) by S. Jeßen & H. Rasbach from Slovakia (no. 1); Tephroseris papposa (2n=48) and T. capitata (2n=96) by J. Kochjarová from Slovakia and Romania (nos. 2–3); Allium fussii (2n=16), Brachyactis cilliata (2n=14), Campanula gentilis (2n=34), C. moravica  $(2n\sim4x)$ , C. rotundifolia s. l.  $(2n=68, 2n\sim4x)$ , C. tatrae  $(2n\sim4x)$ , Potentilla aurea subsp. chrysocraspeda (2n=14) and Tephroseris papossa (2n=48) by P. Mraz from the Czech Republic, Hungary, Romania, Slovakia and Ukraine (nos. 4–11). For the first time the chromosome count is given for Allium fussii (A. paniculatum group). One existing chromosome number for Tephroseris papposa given in the literature (2n=40) is with high probability incorrect.

Key words: Alliaceae, Aspleniaceae, Asteraceae, Campanulaceae, cytotaxonomy, FCM, Rosaceae, Senecio.

## **Editorial**

The series of chromosome number and DNA ploidy level reports is expected to be published once or twice per each volume of Biologia, Bratislava, depending on the amount of contributions received. Although, this series is a part of large project "Database of chromosome counts of pteridophytes and flowering plants of the Slovak Republic" (APVT-51-006002), the main goal is the stimulation of karyotaxonomical research mainly in the regions with very scarce karyological data (e.g. Romania, Ukraine). The geographical area comprises the whole Carpathian mountain range and Pannonian basin (covering the whole area of Slovakia and almost all Hungary, most part of Romania and some parts of Austria, Bosnia and Herzegovina, Croatia, Czech Republic, Poland, Serbia, Slovenia and Ukraine, see Fig. 1., KLIMENT 1999), and adjacent part of Central Europe including the following countries: Austria, Czech Republic, Germany, Hungary, Poland, Slovenia and Switzerland. New and first chromosome counts/estimations of DNA ploidy level may be accepted. Nomenclature should follow the main compendia devoted to these regions (national floras and checklists, Flora Europaea, Atlas Florae Europaeae, Liste der Gefäßpflanzen Mitteleuropas, etc.), however in wellfounded cases the author(s) may use different taxonomic concept. Author abbreviations should follow Authors of Plant Names (BRUMMITT & POWELL, 1992; for the current version see http://www.ipni.org). Each count should be accompanied with full description of the locality (geographical co-ordinates are welcomed, as well as the code of Central European grid mapping project for the relevant countries, cf. Niklfeld, 1971), the name of the person who counted chromosome number/performed FCM analysis and the voucher specimen reference (herbarium acronyms following Holmgren et al., 1990; for updated version see: http://www.nybg.org/bsci/ih/ih.html). If herbarium specimen is missing, the reason should be given. In case of the report on DNA ploidy level, internal standard of the previously counted taxon (preferably the same taxon or closely related) and the ratio between nuclei fluorescence intensity of internal reference and analyzed sample should be included. Drawings, photographs (with scale bars) and references may be added following the Instructions for authors used in Biologia, Bratislava (see also http://ibot.sav.sk/Biologia/index.html). Authors, following the layout of the present reports, are invited to submit their manuscripts in English exclusively to the editor of this report preferably by email.

<sup>\*</sup> Address: Institute of Biology & Ecology, P.J. Šafárik University–Faculty of Science, Mánesova 23, SK–04352 Košice, Slovakia, e-mail: mrazpat@kosice.upjs.sk.

I am thankful to Dolores LLEDÓ for checking English in this report and to Karol MARHOLD for valuable comments on the manuscript.