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Contribution to plant genome size knowledge: first assessments in five genera and 30 species of angiosperms from western Balkans

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ABSTRACT: The first assessments, done by flow cytometry, of nuclear DNA amount for five genera and 30 species of angiosperms (three monocots, 27 eudicots) from the western Balkan Peninsula, including eight taxa with some degree of endemism to this area, are presented here. These data complement the substantial existing information on plant genome size in this region, now accounting for 670 species and subspecies studied for this character.

Key words: 2C-value, the Balkans, flow cytometry, nuclear DNA amount, vascular plants.

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INTRODUCTION

Genome size is a highly relevant character of living organisms, showing relationships with many other biological and non-biological parameters (Bennett & Leitch 2005). Since the coining of the term C-value by Swift (1950) to define the DNA content of the unreplicated gametic chromosome set of an organism, much effort has been made to clarify the concepts and terms in this field (Greilhuber *et al.* 2005) and to understand their biological significance. This includes, of course, to increase the number of taxa for which this parameter is known and to analyse its relationships with other biotic and abiotic factors (Bennett & Leitch 2011). Among the diverse methods used for plant nuclear DNA amount estimation, flow cytometry is now dominant due to its reliability, ease

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and relatively low cost (Doležel *et al.* 2007 and references therein). Despite the many active research groups and published contributions to this field, the proportion of angiosperms currently with known genome size is still ridiculously small, below 2%: around 6,300 species with information on nuclear DNA amount (Bennett & Leitch 2011) relative to some 360,000 species belonging to this group, the largest in plants (Thorne 2002).

The Balkan region is one of the 250 centres for plant diversity identified in the World (Davis *et al.* 1994) and one of the most important plant biodiversity hotspots in Europe, together with the Iberian and Apennine peninsulas (Krystufek & Reed 2004; Médail & Diadema 2009). Within its floristic richness, the number of endemic plants is remarkable: around 2,600 taxa, representing more than a quarter of its total vascular flora (Stevanović 2005). The good level of knowledge of plant biology proper to this region, such as floristics, ecology or systematics, was in contrast with the sparse information of plant genome size until recent studies focused on the western Balkan area (Siljak-Yakovlev *et al.* 2010, Pustahija *et al.* 2013, and references therein).

Galbraith *et al.* (2011) considered genome size as one of the pillars of the global angiosperm genome census, encouraging research in this field. Likewise, Bennett & Leitch (2011) also proposed work on this field with a target of DNA amount assessment in 2,500 angiosperm species in the period 2012-2016. In recent years, studies to increase knowledge of plant genome size have often developed more or less large data sets based on systematic (Pellicer *et al.* 2010), life-form (Veselý *et al.* 2012), usefulness (Sliwinska & Thiem 2007), geographical (Bai *et al.* 2012) or ecological (Dolenc Koce *et al.* 2008) characters. Many other publications have contributed on various themes or isolated data (Bennett & Leitch 2011, references therein and databases indicated below). The western Balkan Peninsula has been intensively studied from this point of view in the last decade, particularly with two works dealing with some 600 taxa, including a focus on flora of serpentine soils (Siljak-Yakovlev *et al.* 2010; Pustahija *et al.* 2013). A companion study of 2C-values in 225 taxa of Lebanese flora has also been made (Bou Dagher-Kharrat *et al.* 2013).

Following these recommended objectives and with a focus both on Balkan endemic taxa and on widely distributed ones, the aim of this paper was to extend the knowledge of plant nuclear DNA amounts in the Balkan region. With this purpose, only plants with unknown nuclear DNA content were taken into account in this study. To attribute this status, we used the two mentioned papers with large data sets on Balkan plant DNA contents (Siljak-Yakovlev *et al.* 2010; Pustahija *et al.* 2013) and three comprehensive and updated genome size databases, all of them accessed on July 2013: Kew plant DNA C-values database (http://data.kew.org/cvalues), FLOWer, a plant DNA flow cytometry database (http://botany.natur.cuni.cz/flower/index.php), and GSAD, genome size in the Asteraceae database (www.asteraceaegenomesize.com).

MATERIALS AND METHODS

Materials. Fresh leaf material of the investigated taxa was collected for genome size measurements from natural populations in Herzegovina (Bosnia and Herzegovina) and Dalmatia (Croatia), preserved in slightly humidified tissue paper and kept in the refrigerator until their processing on the cytometer, less than one week after collection. In addition, material for herbarium vouchers was also collected, pressed and deposited in the herbarium of Faculty of Forestry, University of Sarajevo. Data on plant origin and collection are provided in Table 1.

Flow cytometry. Genome size was assessed at the *Institut des Sciences du Végétal*, CNRS, Gif-sur-Yvette (France) using one of five internal standards (available from SCB or MB) in order to cover the range of DNA contents: *Solanum lycopersicum* L. 'Montfavet 63-5' (2C = 1.99 pg, Lepers-Andrzejewski *et al.* 2011), *Petunia hybrida* Vilm. 'PxPc6', *Pisum sativum* L. 'Long Express', *Triticum aestivum* L. 'Triple Dirk' (2C = 2.85 pg, 8.37 pg and 30.90 pg, respectively, Marie & Brown 1993), and *Artemisia arborescens* L. (origin: Crete, 2C = 11.43 pg, Garcia *et al.* 2006).

Whenever available, five individuals per population were examined; on average, 4.1 individuals have been studied per taxon, the number ranging from one (in a single case) to five (in the majority, see Table 1). Leaf tissue of the target plant was chopped with a razor blade together with leaf tissue of the appropriate internal standard in 1000 µl of cold Galbraith isolation buffer (Galbraith *et al.* 1983) modified by addition of 1% polyvinylpyrrolidone 10000, 5 mM sodium metabisulphite and raising to 60 mM MOPS (3-(N-morpholino)propanesulfonic acid): respectively, these act to absorb polyphenols, as anti-oxidant and to counter excess plant acids. This buffer was also supplemented with 100 µg/ml of ribonuclease A (RNase A, Roche, France). After filtration of the nuclear suspension through 50 µm CellTrics (Partec), the sample was kept on ice, stained with propidium iodide (stock 1 mg/ml, Sigma-Aldrich, France) to a final concentration of 50 µg/ml or 100 µg/ml for genomes with 2C>20 pg, and analysed in a flow cytometer with a 532 nm 30 mW laser (CyFlow SL3, Partec, Munster, Germany). The instrument was set up with the following configuration: gate on nuclei through a biparametric histogram of Side-Scatter versus Fluorescence, and take propidium fluorescence on both

linear and 3-order log scales using two photomultipliers and a 50/50 beam-splitter. While the linear scale is ideal for calculations, the log scale provides an overview of endoreplication series, parasites, etc. The cytometer linearity was supervised by checking the relative positions of 2C and 4C nuclei found in many tissues. This ratio was always close to the theoretical value of 2, but can drift down when very large nuclei are assessed with a relatively small laser beam. To minimise this possibility, the laser focus was slightly advanced on-axis, and the internal standard was chosen to be close to the unknown, avoiding extrapolation where possible.

To calculate the total holoploid nuclear DNA content (2C) when using an intercalating fluorochrome, we assumed a linear correlation between the fluorescent signals from the stained nuclei of the unknown specimen, the known internal standard, and the DNA amount (Marie & Brown 1993). So, 2C-value was calculated multiplying the known DNA content of the internal standard by the peak (modal) position in the histogram of fluorescence intensities of the target species and dividing the result by the peak position of the internal standard. The mean 2C-value from the individuals of each taxon studied as well as the standard deviation of the mean and its coefficient of variation (%) were calculated.

RESULTS AND DISCUSSION

Data on nuclear DNA content (mean 2C-values per taxon studied), including standard deviations and coefficients of variation, are presented in Table 1, together with information on life cycle type and life growth form of the studied taxa. The coefficients of variation of these means range from 0.37 to 3.80% (mean value, 1.20, standard deviation, 0.71), indicating reproducible estimates and uniform populations. Two taxa, *Rorippa lipizensis* Reichenb. and *Silene otites* Sm., showed strong endoreduplication in the foliar tissue. The summary of available genome size data concerning Balkan flora is recorded in Table 2. Unfortunately, due to the collection period, we could not obtain seeds or fruits in order to determine chromosome number of the populations studied. Given that several ploidy levels have been reported for many taxa considered, we preferred not to include chromosome numbers from the literature, and the discussion of this aspect will hopefully be done in further works.

According to the above-mentioned sources (see Materials and methods section), these values are the first genome size data for all the species considered. In one case, *Inula verbascifolia* (Willd.) Hausskn., the 2C-value would be novel for the typical subspecies (since it is known for subsp. *aschersoniana* (Janka) Tutin, described as *I. aschersoniana* Janka, Sliwinska & Thiem 2007), and for the species *I. candida* (L.) Cass. in case the former taxon is considered as a subspecies of the latter (see Table 1). In another case, ploidy level, but not genome size, of *Doronicum caucasicum* M. Bieb. has been determined by flow cytometry, in a population quoted by the name *D. orientale* Hoffm., considered as synonym of the former (Suda & Trávníček 2006). In addition, genome size has been estimated for the first time in one monocot genus (*Listera*) and four eudicot genera (*Ajuga*, *Bunium*, *Cynoglossum*, *Haplophyllum*). For *Ajuga*, ploidy level, but not nuclear DNA amount, had been estimated by flow cytometry in another species, *A. reptans* L. (Suda & Trávníček 2006).

Most of these 2C-values are rather small, placing most studied taxa in the lowest groups of the plant classification done on genome size basis. According to the categories established by Leitch *et al.* (2005), 17 out of the 30 genome sizes estimated here (57%) are very small (2C < 2.8 pg), eight (27%) are small (2.8 ≤ 2C < 7), four (13%) are intermediate (7 ≤ 2C < 28), only one (3%) is large (28 ≤ 2C ≤ 75) and none is very large (2C > 75).

The present data set comprises three monocotyledonous and 27 dicotyledonous (eudicot) taxa. Eight of the species studied are endemic to relatively small areas within the Balkan region: either western Balkans or Italian and Balkan peninsulas or those peninsulas plus parts of Turkey or of Turkey and Russia (Table 1). Amongst these, *Rorippa lipizensis* is, in addition, included in the IUCN global red list, with the LC (least concern) status (Bilz *et al.* 2011). Also some plants that are very abundant and/or have a very large distribution area, such as for instance *Anthemis cotula* L., *Astrantia major* L. and *Lonicera implexa* Aiton, have been studied: genome size information is apparently lacking even for very common plants.

The vascular flora of Croatia is estimated to comprise 188 families, 1,087 genera, and 4,517 species (5,004 counting species and subspecies) (Flora Croatica Database, http://hirc.botanic.hr/fcd/Search.aspx, updated January 2012, accessed July 2013). That of Bosnia and Herzegovina is reported to encompass 161 families, 874 genera, and 3,298 species (Redžić *et al.* 2008). According to these floristic data, given that a large part of the flora is common to both territories and taking the data of Croatian flora (the largest) for the calculations, the present paper contributes genome size data for 20 families, 29 genera and 30 species, i.e. roughly for 10%, 3% and 0.6% at familiar, generic and specific levels, respectively. Considering the 670 taxa resumed in Table 2, the current coverage of this Balkan flora is approximately 70% of families, 35% of genera and 15% of species.

Table 1. Provenance, life cycle type and life growth form, and nuclear DNA content of the taxa studied.

Taxon[1,2] (family)	Population and collection data[3]	Life cycle type[1,4], life growth form[1,5]	Endemism and conservation status[1,6]	Number of individuals studied	2C in pg (standard deviation)	Coefficient of variation for this mean (%)	1C in Mbp[7]	Internal standard[8]
Ajuga genevensis L.** (Lamiaceae)	1	P, H	-	5	2.48 (0.04)	1.50	1210	*Solanum*
Anthemis cotula L.* (Asteraceae)	1	A, T	-	2	8.35 (0.15)	1.83	4080	*Artemisia*
Aristolochia pallida Willd.* (Aristolochiaceae)	1	P, H	-	4	0.57 (0.01)	1.61	279	*Solanum*
Armeria canescens Boiss.* (Plumbaginaceae)	1	P, H	1	5	9.30 (0.11)	1.16	4550	*Artemisia*
Astragalus illyricus Bernh. [*A. monspessulanus* L. subsp. *illyricus* (Bernh.) Chater]* (Fabaceae)	2	P, H	1	5	2.11 (0.08)	3.80	1030	*Petunia*
Astrantia major L.* (Apiaceae)	1	P, H	-	3	2.48 (0.01)	0.47	1210	*Petunia*
Bunium alpinum Waldst. & Kit. subsp. *montanum* (B.D.J. Koch) P.W. Ball. [*B. montanum* (B.D.J. Koch)]** (Apiaceae)	3	P, G	1	5	2.28 (0.02)	0.87	1120	*Petunia*
Corylus colurna L.* (Betulaceae)	1	P, Ph	-	5	0.85 (0.02)	2.05	416	*Solanum*
Cynoglossum officinale L.** (Boraginaceae)	4	B, H	-	3	1.82 (0.01)	0.37	890	*Petunia*
Dactylis hispanica Roth [*D. glomerata* L. subsp. *hispanica* (Roth) Nyman] * (Poaceae)	1	P, H	-	5	8.46 (0.10)	1.15	4140	*Petunia*
Dianthus sanguineus Vis.* (Caryophyllaceae)	5	P, C	-	5	0.97 (0.02)	1.85	474	*Petunia*
Doronicum caucasicum M. Bieb.* (*D. orientale* Hoffm.) (Asteraceae)	1	P, H	-	5	5.61 (0.02)	0.40	2740	*Artemisia*
Euphorbia myrsinites L.* (Euphorbiaceae)	3	P, H	-	5	4.03 (0.03)	0.64	1970	*Solanum*
Euphorbia spinosa L.* (Euphorbiaceae)	3	P, C	-	5	2.74 (0.03)	1.18	1340	*Solanum*
Genista sylvestris Scop. subsp. *dalmatica* (Bartl. & H.L. Wendl.) H. Lindb.* (Fabaceae)	4	P, C	2	5	3.35 (0.03)	0.96	1640	*Solanum*
Haplophyllum biebersteinii Spach [*H. suavelolens* (DC.) D. Don]** (Rutaceae)	1	P, H	3	4	1.18 (0.01)	0.47	577	*Solanum*
Inula verbascifolia (Willd.) Hausskn. subsp. *verbascifolia* [*Inula candida* (L.) Cass. subsp. *verbascifolia* (Willd.) Hayek]* (Asteraceae)	3	P, H	1	5	2.97 (0.02)	0.73	1450	*Solanum*
Laserpitium siler L.* (Apiaceae)	3	P, H	-	4	4.20 (0.06)	1.32	2050	*Solanum*
Listera ovata (L.) R. Br. [*Neottia ovata* (L.) Bluff & Fingerh.]** (Orchidaceae)	4	P, G	-	1	33.3 (-)	-	163000	*Triticum*
Lonicera implexa Aiton* (Caprifoliaceae)	3	P, Ph	-	5	1.88 (0.02)	0.88	919	*Petunia*
Paronychia kapela A. Kern.* (Caryophyllaceae)	3	P, H	-	5	1.28 (0.01)	0.81	626	*Solanum*
Phyteuma spicatum L.* (Campanulaceae)	1	P, H	-	2	2.43 (0.03)	1.03	1190	*Pisum*
Plantago holosteum Scop. (*Plantago carinata* Mert. et Koch)* (Plantaginaceae)	3	B, H	-	4	2.79 (0.02)	0.77	1360	*Solanum*
Poa vivipara (L.) Willd.* (Poaceae)	4	P, H	-	3	4.98 (0.02)	0.35	2440	*Pisum*
Potentilla rupestris L. [*Drymocallis rupestris* (L.) Soják]* (Rosaceae)	1	P, H	-	2	0.46 (0.01)	2.03	225	*Solanum*
Rorippa lipizensis Reichenb.* (Brassicaceae)	1	P, H	4	4	0.43 (0.01)	1.59	210	*Solanum*
Saxifraga rotundifolia L.* (Saxifragaceae)	1	P, H	-	3	3.28 (0.04)	1.24	1600	*Solanum*
Senecio scopolii Hoppe & Hornsch. ex Bluff & Fingerh. (*S. lanatus* Scop. non L., *S. arachnoideus* Sieber. ex DC.)* (Asteraceae)	1	P, H	1	5	7.93 (0.14)	1.71	3880	*Petunia*
Silene otites Sm.* (Caryophyllaceae)	1	P, H	-	5	5.15 (0.05)	1.00	2520	*Petunia*
Thalictrum minus L.* (Ranunculaceae)	4	P, H	-	4	1.38 (0.02)	1.15	675	*Pisum*

[1] Systematic status, life cycle type and life growth form of each taxon, and endemism and conservation status were determined according to Mueller-Dombois & Ellenberg (1974), Bilz *et al.* (2011), Stevanović (2012), Euro+Med Plantbase project (http://www.emplantbase.org/home.html), Flora Europaea digital version (http://rbg-web2.rbge.org.uk/FE/fe.html), IOPI digital base http://plantnet.rbgsyd.nsw.gov.au/iopi/iopihome.htm, The International Plant Names Index (http://www.ipni.org/ipni/plantnamesearchpage.do), and Tropicos (http://www.tropicos.org/NameSearch.aspx); all databases were accessed on June 2013.

[2]One and two asterisks indicate a genome size report new for a species or for a genus, respectively.

[3]Locations, collectors and dates are as follows: **1)** Bosnia and Herzegovina, Herzegovina, Mt. Prenj, Borašnica, N. Bašić, F. Pustahija, J. Vallès, 5 June 2013; **2)** Bosnia and Herzegovina, Herzegovina, Baško polje, E. Šolić, June 2011; **3)** Croatia, Dalmatia, Mt. Biokovo, F. Bogunić, A. Hajrudinović, E. Šolić, J. Vallès, 8 June 2013; **4)** Bosnia and Herzegovina, Herzegovina, Mt. Prenj, Rujište, N. Bašić, F. Pustahija, J. Vallès, 5 June 2013; **5)** Bosnia and Herzegovina, Herzegovina, Rakitno polje, F. Bogunić, S.C. Brown, A. Hajrudinović, S. Siljak-Yakovlev, J. Vallès, 9 June 2013.

[4]A: annual; B: biennial; P: perennial.

[5]Ph: phanerophyte; C: chamaephyte; H: hemicryptophyte; T: therophyte; G: geophyte.

[6]1: Italian and Balkan peninsulas; 2: western Balkan Peninsula; 3: Italian and Balkan peninsulas plus parts of Turkey and Russia; 4: Italian and Balkan peninsulas plus parts of Turkey, with LC (least concern) conservation status (all the others without conservation status).

[7]1 pg = 978 Mbp (Doležel *et al.* 2003).

[8]See the materials and methods section for details.

Table 2. Data concerning Balkan vascular flora with available genome size values.

	Number of taxa with known nuclear DNA amount		
	Previous works[1]	Present work[2]	Total
Species and subspecies	640	30	670
Pteridophyta	14	-	14
Gymnosperms	20	-	20
Monocots	60	3	63
Eudicots	546	27	573
Genera	370	5	375
Pteridophyta	10	-	10
Gymnosperms	6	-	6
Monocots	40	1	41
Eudicots	309	4	313
Families	133	-	133
Pteridophyta	10	-	10
Gymnosperms	4	-	4
Monocots	18	-	18
Eudicots	101	-	101

[1]See references in the text.

[2]In this table we include only those taxa considered in the present work for which DNA content has not been assessed previously (all the 30 studied species and five out of 29 genera, but not one of the 20 families).

The most represented families in the present paper are Asteraceae (13% of assessments), followed by Apiaceae and Caryophyllaceae (each with 10%). Apart from the Asteraceae being one of the biggest plant families, these three families are numerous in taxa and widespread in the Balkan flora (cf. the above-quoted Flora Croatica Database, Redžić *et al.* 2008 and references therein). All 2C-values obtained in taxa of these three families fall within their known genome size ranges. Those of Asteraceae range, in the current paper, from 2.97 to 8.35 pg, whereas those of the 2,770 taxa included in the Genome size in the Asteraceae database (http://www.asteraceaegenomesize.com, updated July 2013, accessed July 2013) range from 0.72 to 142.0 pg, with a mean value of 7.13 and a median value of 5.52. For the Apiaceae, they range from 2.28 to 4.2 pg, those of the 97 data available in the RBG Kew Angiosperm DNA C-values database (http://data.kew.org/cvalues, updated December 2012, accessed July 2013) being between 0.94 and 13.14 pg, with a mean of 5.25 and a median of 4.53. Concerning Caryophyllaceae, our values are comprised between 0.98 and 5.16 pg, whereas the 115 present in the above-mentioned Kew's database range from 0.84 and 8.66 pg, with a mean value of 3.40 and a median value of 2.60. The distributions of all categories of plant taxa show skew towards lower values. Accordingly, the median is a more representative parameter than the mean.

Concerning life cycle type, 90% of the 30 taxa studied are perennial, 7% biennial and the remaining 3% annual. Hemicryptophytes largely dominate as a life growth form (73%), followed by chamaephytes (10%), phanerophytes and geophytes (7% each), and only 3% are therophytes.

The 2C-values provided here for some genera fall within the range of their families, according to Kew's genome size database. *Ajuga* has a nuclear DNA amount (2.48 pg) practically identical to the mean value in the Lamiaceae (2.44 pg). Similarly, *Cynoglossum*'s value (2.82 pg) is very close to the mean for the Boraginaceae (2.50 pg). Values for *Haplophyllum* (1.18 pg) and *Bunium* (2.28 pg) are much lower - less than half - than the mean of their respective families, Rutaceae (2.62 pg) and Apiaceae (5.04 pg), but above their minimal values (0.40 pg, 0.94 pg). Finally, our single sample of *Listera ovata* (L.) R. Br. exhibited a genome size (2C = 33.3 pg) more than twice that of the mean of Orchidaceae (15.5 pg), but within the range of this large and diverse family, which shows an almost 65-fold variation in 2C-values, from 0.60 to 38.8 pg.

As for species, the values fall as well within the range of variation known for their respective genera. We provide examples of the taxa belonging to the major family reported here, the Asteraceae. The 2C-value of *Senecio scopolii* (7.93 pg) is very close to the mean of the genus (7.23 pg) according to the above-mentioned database "Genome size in the Asteraceae", which includes many

nuclear DNA assessments for this genus (83 species). The *Anthemis cotula* value (8.35 pg) is also close to the mean of the 11 species of the genus with available data (9.49 pg). Several ploidy levels have been reported in both these genera (Watanabe, K. Index to chromosome numbers in Asteraceae, http://www.lib.kobe-u.ac.jp/infolib/meta_pub/G0000003asteraceaee, updated June 2013, accessed July 2013). According to the information contained in the databases on Asteraceae chromosome numbers and genome size, the *Anthemis* taxon considered here would probably be diploid, whereas the number of chromosome sets for the studied *Senecio* is less clear. As stated above, data on chromosome number in the present paper's populations are necessary for definite conclusions on this aspect. In *Inula*, our value (2.97 pg) is lower than the mean of the 11 species of the genus with known data (4.39 pg), but the ploidy level cannot be surmised since in the two databases consulted there are quite different nuclear DNA contents for the same ploidy level. For *Doronicum*, the value here (5.61 pg) is lower than the only other one available for the genus (7.69 pg in *D. hungaricum* Rchb., Veselý *et al.* 2012), also known to comprise different ploidy levels.

CONCLUDING REMARKS

The present paper has focused on nuclear DNA content for those taxa of the Balkan flora where no such information existed. Together with those of the two comprehensive works on this subject (Siljak-Yakovlev *et al.* 2010; Pustahija *et al.* 2013) and with some other papers focused on genome size in western Balkan plants (Shuka *et al.* 2010; Temsch & Greilhuber 2010; Tan *et al.* 2011; Sánchez-Jiménez *et al.* 2012; Koutecký 2012; Olšavska *et al.* 2012; Niketić *et al.* 2013), this kind of information is now available for a total of 133 families, 375 genera and 670 species and subspecies (Table 2), i.e. ca. 70%, 35% and 15% of the vascular flora of the region (according to the Flora Croatica website, see above) at each of these taxonomic levels. This paper expands the Balkan flora genome size database initiated by Siljak-Yakovlev *et al.* (2010), but at the same time makes it evident that for still many genera such information is inexistent. Given the relevance of this area in terms of biodiversity, it is fortunate that genome size is better known in Balkan vascular plants (around 13%, as argued above) than currently at the global level (less than 2% in angiosperms, Bennett & Leitch 2011). Adding the relatively scarce assessments in ferns and gymnosperms does not change this generalisation. Nevertheless, a majority of taxa, including of course rare or endemic, but also many common and widespread easily available ones, has never been studied from this viewpoint. This situation should stimulate further studies in order to increase the availability of this very relevant biological parameter. In parallel, efforts should be made to count chromosome numbers in the populations lacking these data and with known nuclear DNA amount, so that ploidy levels and 1Cx-values might be established in a reliable manner.

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Botanica SERBICA

REZIME

Prilog poznavanju veličini genoma biljaka: prvi podaci za pet rodova i trideset vrsta cvetnica sa područja zapadnog Balkana

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U radu su predstavljeni prvi podaci dobijeni tečnom citometrijom za sadržaj količine nuklearne DNK kod pet rodova i trideset vrsta cvetnica (tri monokotile i 27 dikotila) sa područja zapadnog Balkana, uključujući osam taksona sa izvesnim stepenom endemizma. Predstavljeni podaci doprinose bazičnom poznavanju veličine genoma kod biljaka iz ovog regiona. Sa ovim podacima ukupno je pokriveno 670 vrsta iz regiona.

Ključne reči: 2C-vrednost, Balkan, tečna citometrija, količina nuklearne DNK, vaskularne biljke.