



Edraianthus tarae (Campanulaceae), an intriguing taxon from the Balkan Peninsula: evidence from a morphometric and genome size study

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Abstract

Edraianthus tarae, a taxonomically intricate stenoendemic plant species from the canyon of the river Tara (Montenegro), is reviewed using morphological and genome size data. Several morphological features distinguish this taxon from typical members of *Edraianthus*, which led to its segregation into its own genus, *Protoedraianthus*. Our formal morphometric analysis clearly indicates its morphological distinctiveness in relation to all other representatives of *Edraianthus*, supporting the idea of separation of this species into its own genus. However, our phylogenetic analyses, based on plastid DNA (*trnL-F* region and *rbcL-*atpB** spacer) and nuclear ribosomal ETS sequences, revealed that although *E. tarae* forms an isolated lineage, positioned as a sister group to the rest of the *E. graminifolius*-complex, it makes a natural group within *Edraianthus* s.s. The genome size analysis largely corresponds with molecular results, further supporting the fact that, despite its morphological distinctiveness, *E. tarae* is clearly nested within *Edraianthus* and should be treated as congeneric. Given that the name *Edraianthus tarae* was not validly published, nomenclatural and taxonomical standings are discussed and re-evaluated. *Edraianthus tarae* is validated, a new differential diagnosis, description and illustrations are provided, and its conservation status is assessed.

Keywords Morphometry · Nomenclature · *Protedraianthus* · Stenoendemic taxa

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Contribution to “Plants of the Balkan Peninsula in Space and Time”.

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Introduction

The genus *Edraianthus* Candolle (1839: 448) (Campanulaceae) includes perennial herbs with the centre of distribution in the Balkan Peninsula and a small disjunction in the Apennines, Sicily and southern Carpathians (Wettstein 1887; Janchen 1910; Lakušić 1974; Stefanović et al. 2008). This genus has been the subject of numerous studies over the last decade, spanning anatomy and morphology (Rakić 2010; Rakić et al. 2012), cytogenetics (Međedović et al. 2007; Siljak-Yakovlev et al. 2010), molecular phylogeny and phylogeography (Stefanović et al. 2008; Surina et al. 2011, 2014; Glasnović et al. 2018), and taxonomy (Lakušić et al. 2009, 2013, 2016; Surina et al. 2009; Surina and Lakušić 2010).

One of the most intriguing taxa of this genus is “*Protoedraianthus tarae*”, a stenoendemic plant from the canyon of the river Tara (Fig. 1), described but invalidly published by R. Lakušić (1987). Several morphological features separate this taxon from typical members of *Edraianthus*. Its flowers are exclusively white and unusually large (3–5 cm long),

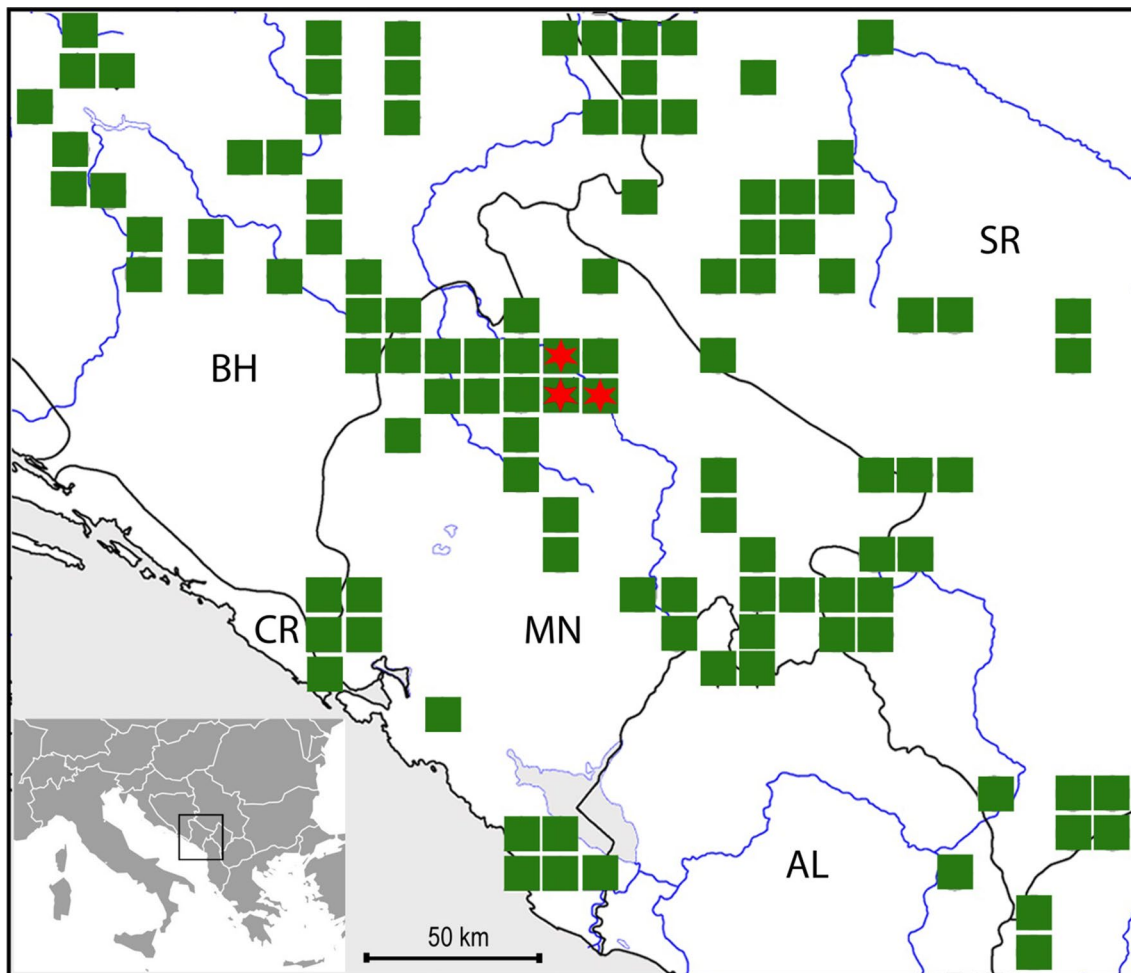


Fig. 1 Distribution of taxa of the *Edraianthus graminifolius*-complex across the central and western Balkan Peninsula. Green squares indicate the range of *Edraianthus graminifolius* s.l. and red asterisks the

range of *E. tarae*. Country abbreviations: *AL* Albania, *BH* Bosnia and Herzegovina, *MN* Montenegro, *SR* Serbia

but more importantly are pedicellate (not sessile) and are arranged in terminal dichasia or polychasia, as opposed to the single flowers or sessile flowers arranged in a terminal capitulum found in other *Edraianthus* species. This inflorescence type is therefore unusual not only in comparison with other *Edraianthus* spp. but also represents a curiosity for the Campanulaceae as a whole. Finally, the fruit dehiscence represents perhaps the most distinct feature found in *E. tarae*. Its capsules open by 3–4 irregular pores at the calyx base, as opposed to the lateral openings found in most campanuloid taxa or the apical openings found in all other members of the genus (Fig. 2). For all these reasons, this taxon was segregated by R. Lakušić, first as a subgenus *Protoedraianthus* (Lakušić 1987) and finally as its own genus (Lakušić 1988).

A broad-scale molecular phylogeny of *Edraianthus* based on plastid markers identified several distinct monophyletic groups (Stefanović et al. 2008). One of them is the *E. graminifolius*-complex, the largest and most diverse

group of the genus. Within this group, *E. tarae* forms an isolated lineage, positioned as a sister group to the rest of the *E. graminifolius*-complex. The genus *Protoedraianthus* itself, as circumscribed by R. Lakušić (1987, 1988), with several species (*P. glisicii*, *P. majae*, *P. serpyllifolius*, *P. pilosulus*, *P. sutjeskae*, *P. tarae*, *P. vesovicii*) was found to be not monophyletic, and the question of their taxonomical position remains open.

The results of the phylogenetic study by Stefanović et al. are consistent with the broad molecular studies of Mansion et al. (2012) and Jones et al. (2017), indicating that *Edraianthus* is a member of a large and well-supported clade, CAM17. The main goal of our study is to provide a formal taxonomic treatment of the species *Edraianthus tarae* based on a comprehensive analysis of morphological, molecular and genome size data.

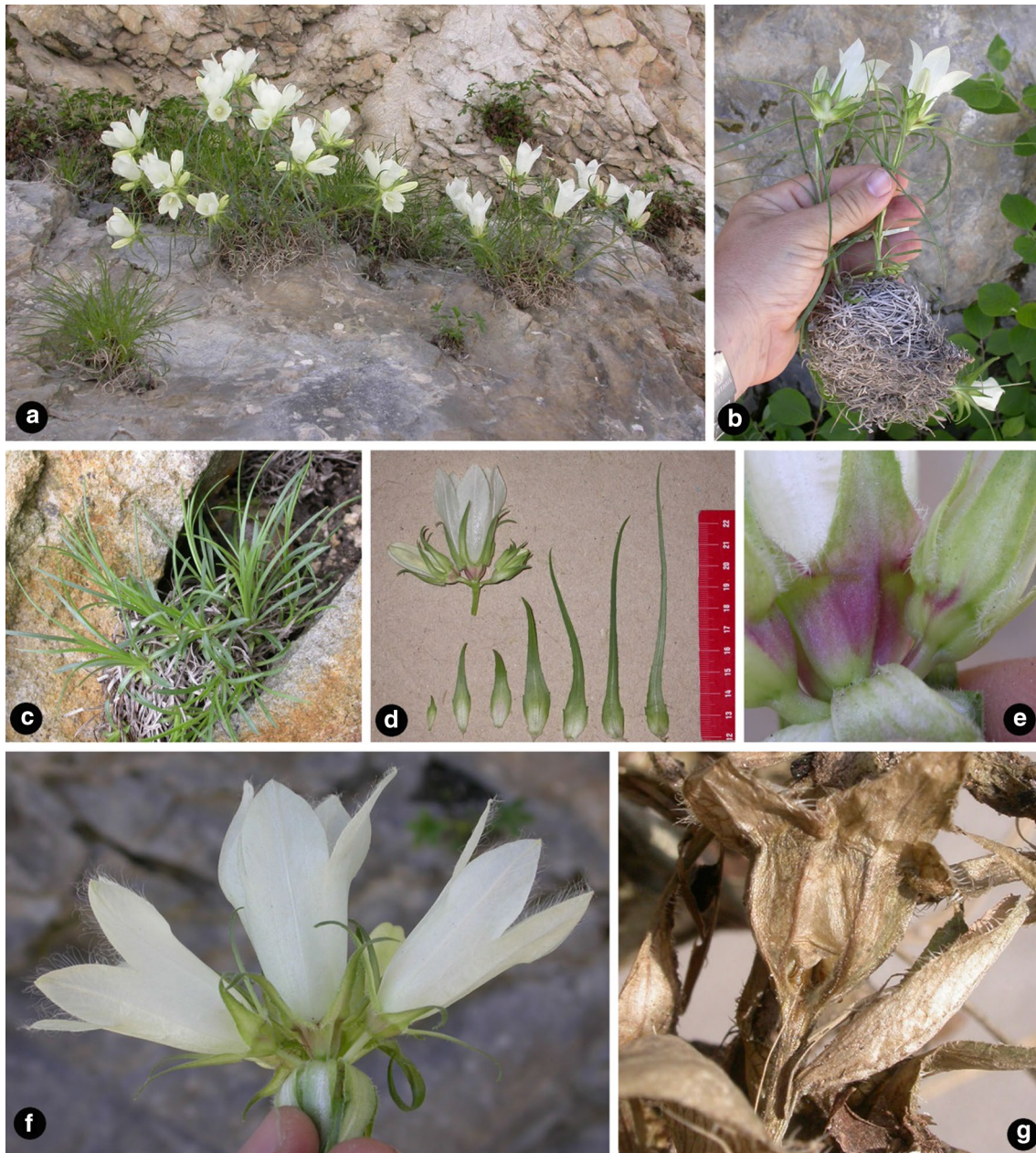


Fig. 2 *Edraianthus tarae* Lakušić ex D.Lakušić & Surina, sp. nov. (from the type locality). **a, b** Flowering individuals. **c** Rosette leaves. **d** Dissected inflorescence with terminal dichasia and a series of involucral bracts. **e** Calyx with small setulose appendages. **f** Inflorescence

arranged in terminal dichasia with one central sessile and two lateral pedicellate flowers. **g** Capsules with basal lateral pores. (Photos: D. Lakušić)

Materials and methods

Material and morphometric analyses

Morphometric analyses were performed on the material collected in the field and preserved in a 96% ethanol and glycerol solution (1:1, v/v). Morphological studies were also carried out on herbarium specimens deposited in B, BEO, BEOU, NHMR, P, PAD, WU (herbarium

abbreviations follow Thiers 2019). The morphometric study included 1224 specimens belonging to 18 species and subspecies collected in the central and western Balkan Peninsula at a wide range of elevations (100–2500 m a.s.l.). From each population, 15 plant samples were used for analysis. Voucher specimens have been deposited in the Herbarium of the Institute of Botany and Botanical Garden, Faculty of Biology, University of Belgrade (BEOU). Morphological characters used in

Table 1 Characters used for morphometric analysis and a summary of discriminant function analysis

Character	Abbreviation	Wilks' Lambda	F-remove (3,1178)	p-level
<i>Stem</i>				
Stem height	St_H0	0.031	7.790	0.000
<i>Rosette leaf</i>				
Base width	Lb_W0	0.031	7.451	0.000
Maximal width	Lb_W1	0.032	18.113	0.000
Total length	Lb_L	0.032	17.852	0.000
<i>Cauline leaf</i>				
Maximal width	Le_W1	0.032	18.150	0.000
Width in the upper quarter	Le_W2	0.031	3.499	0.015
Total length	Le_L0	0.033	29.057	0.000
Distance between the largest leaf width point and the leaf base	Le_L1	0.033	38.523	0.000
<i>Inflorescence</i>				
Number of involucre bracts	No_B	0.036	78.638	0.000
Number of flowers in capitulum	No_F	0.031	12.942	0.000
Pedicle length	PdL	0.034	42.388	0.000
<i>Inner involucre bract</i>				
Maximal width	B1_W1	0.031	10.828	0.000
Width in the upper quarter	B1_W2	0.033	36.508	0.000
Total length	B1_H0	0.030	2.499	0.058
Distance between the largest width point and the base	B1_H1	0.032	16.863	0.000
Distance between apex base and the bract base	B1_H2	0.031	5.452	0.001
<i>Central involucre bract</i>				
Maximal width	B2_W1	0.031	3.377	0.018
Width in the upper quarter	B2_W2	0.030	0.845	0.469
Total length	B2_H0	0.030	1.369	0.251
Distance between the largest width point and the base	B2_H1	0.030	0.329	0.805
Distance between apex base and the bract base	B2_H2	0.031	3.422	0.017
<i>Outer involucre bract</i>				
Maximal width	B3_W1	0.031	10.063	0.000
Width in the upper quarter	B3_W2	0.031	3.176	0.023
Total length	B3_H0	0.030	0.807	0.490
Distance between the largest width point and the base	B3_H1	0.030	2.088	0.100
Distance between apex base and the bract base	B3_H2	0.030	2.473	0.060
<i>Calyx</i>				
Diameter	Ca_W0	0.032	16.391	0.000
Width of lobe base	Ca_W1	0.031	11.145	0.000
Width of lobe base in the upper quarter	Ca_W2	0.032	19.356	0.000
Lobe length	Ca_H1	0.032	19.552	0.000
<i>Corolla</i>				
Maximal width	Co_W1	0.031	4.859	0.002
Width of lobe base	Co_W2	0.031	5.051	0.002
Total corolla height	Co_H1	0.031	9.509	0.000
Lobe height	Co_H2	0.031	3.448	0.016
<i>Style</i>				
Length	St_L	0.031	3.066	0.027
<i>Anther</i>				
Anther length	An1_L	0.031	12.084	0.000
Filament length	An2_L	0.031	10.730	0.000
Height of filamentum base	An3_L	0.031	9.414	0.000

Table 1 (continued)

Wilks's lambda is a multivariate generalization of the univariate F-distribution; F-remove represents a measure of the extent to which a variable makes a unique contribution to the prediction of group membership; *p*-level values < 0.05 are shown in boldface

the morphometric analysis are listed in Table 1. General procedures for selection of morphological characters and protocols of morphometric analyses are outlined in Rakić (2010) and Rakić et al. (2012) and are followed here. Morphological characters were measured using a Leica Q Win and ImageJ 1.38x software. In the morphological descriptions, value ranges correspond to the mean \pm standard deviation, with the minimum and the maximum values in brackets.

A total of 38 morphological characters were measured and used in a canonical discriminant analysis (CDA) to test the hypothesis of the morphological distinctiveness of *E. tarae* in relation to all other members of the genus *Edraianthus*. CDA was performed on four a priori identified groups of individuals, revealed by Stefanović et al. (2008) as distinct monophyletic groups: 1. *E. graminifolius*-complex (*E. jugoslavicus* Lakušić, *E. canescens* D.Lakušić, Niketić & Stevan., *E. caricinus* Schott, Nyman, & Kotschy, *E. montenegrinus* Horak, *E. vesovicii* Lakušić), 2. *E. serpyllifolius*-complex (*E. glisicii* Cernjav. & Soska subsp. *glisicii*, *E. glisicii* subsp. *majae* Lakušić, *E. pilosulus* (Beck) Surina & D.Lakušić, *E. pulevicii* Surina & D.Lakušić, *E. serpyllifolius* A.DC., *E. sutjeskae* Lakušić), 3. *E. tenuifolius*-complex (*E. tenuifolius* A.DC., *E. × lakusicii* Stevan. & D.Lakušić, *E. wettsteinii* Halácsy & Bald. subsp. *wettsteinii*, *E. wettsteinii* subsp. *lovcenicus* E.Mayer & Blečić, *E. serbicus* Petrović, *E. stankovicii* (Lakušić) D.Lakušić & Surina), 4. “*Protoedraianthus*” (only *E. tarae*). Canonical scores for each case were calculated to estimate the distances between individuals that were used to visualize the relationship among the a priori defined groups.

Discriminant function analysis was used to estimate the contribution of individual characters to overall discrimination. Finally, the UPGMA (Unweighted Pair Group Method with Arithmetic Mean) cluster analysis based on Mahalanobis distances between all analysed populations was computed. Statistical analyses of data were performed in Statistica 5.1 for Windows (StatSoft In., Tulsa, USA, 1996).

Flow cytometry for genome size assessment

DNA amount (2C value) was determined by flow cytometry following Marie and Brown (1993). The general protocols for genome size assessment used are outlined in Siljak-Yakovlev et al. (2010) and Lakušić et al. (2016).

Results

Morphometrics

The canonical discriminant analysis, conducted on the four a priori groups showed that all groups were morphologically distinct and statistically well supported (Fig. 3). “*Protoedraianthus*” was positioned in the negative part of the first axis and fully separated from the rest of the analysed individuals. Representatives of the other three groups were positioned in distinct parts of the DA1–DA2 space, with little overlap in the central part of the discriminating space. Scores of the *E. serpyllifolius*-complex were grouped in the positive part of the second axis, while scores of *E. tenuifolius*-complex and *E. graminifolius*-complex are grouped in the negative part of the second axis, yet separated along the first axis.

The UPGMA cluster analysis revealed their differentiation into two large groups: one corresponds to “*Protoedraianthus*”, whereas the second one includes all other investigated complexes (Fig. 4).

Discriminant function analysis revealed 18 out of 38 tested characters (An1_L—anther length; An2_L—filament length; B1_H1—distance between the largest width point and the base of basal bract; B1_W1—maximal width of basal bract; B1_W2—width in the upper quarter of basal bract; B3_W1—maximal width of inner bract; Ca_H1—calyx lobe length; Ca_W0—diameter of calyx; Ca_W1—width of calyx lobe base; Ca_W2—width of calyx lobe base in the upper quarter; Lb_L—total length of rosette leaf; Lb_W1—maximal width of rosette leaf; Le_L0—total length of cauline leaf; Le_L1—distance between the largest cauline leaf width point and the leaf base; Le_W1—maximal width of cauline leaf; No_B—number of involucre bracts; No_F—number of flowers in capitulum; PdL—pedicel length), as dominant for the overall morphological discrimination (Table 1). This would suggest that the detected discrimination was predominantly based on reproductive characters (i.e. inflorescence and flowers), although leaf dimensions also play an important role in segregation among these groups.

Genome size

Our analyses have shown that the nuclear DNA amount (2C value) of “*Protoedraianthus*” ranged from 3.03 to 3.30 pg, with the mean value of all investigated individuals of 3.11 pg. While “*Protoedraianthus*” fits completely

Fig. 3 Position of canonical scores for each case belonging to different molecular groups of genus *Edraianthus* (according to Stefanović et al. 2008) on DA based on canonical discriminant analysis (CDA) of morphometric data

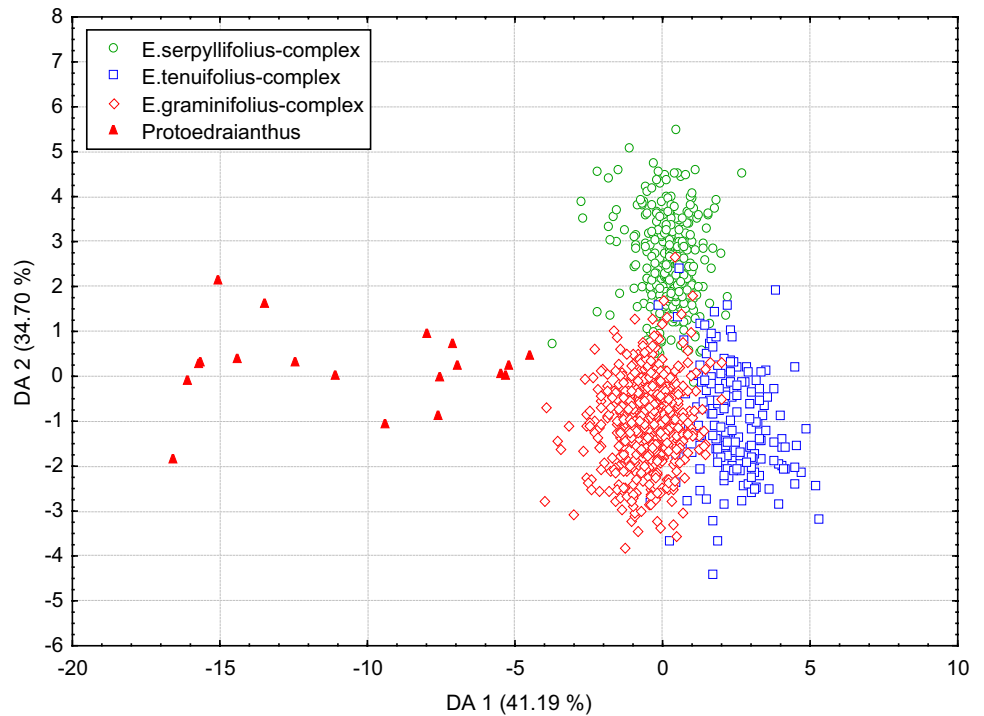
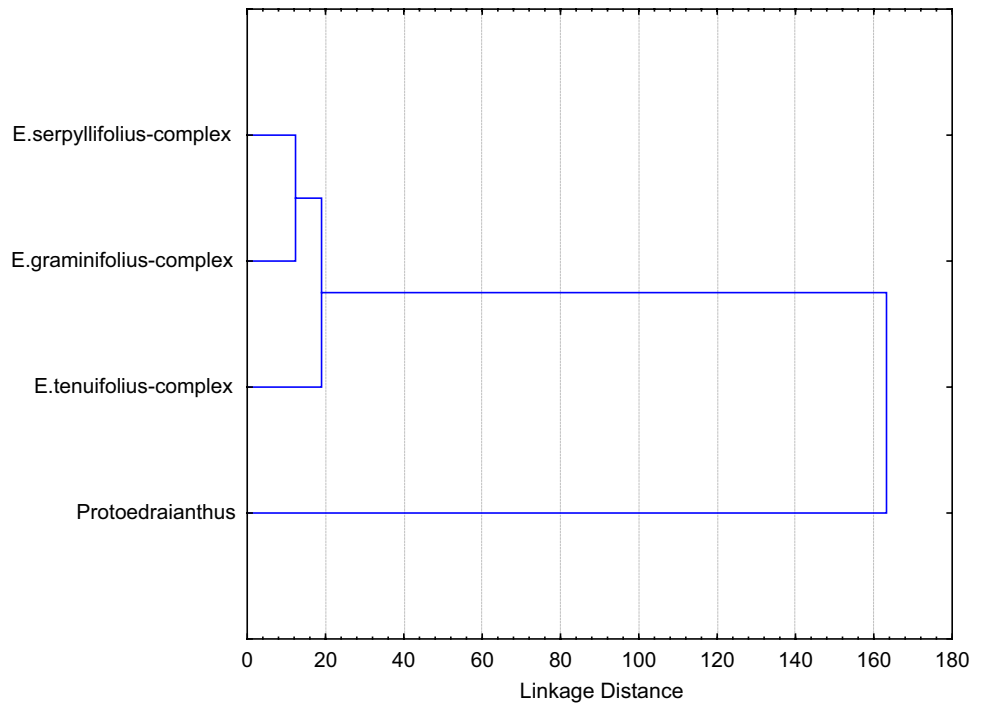


Fig. 4 Overall similarities among molecular groups of genus *Edraianthus* (according to Stefanović et al. 2008) based on the UPGMA agglomerative clustering method of morphometric data

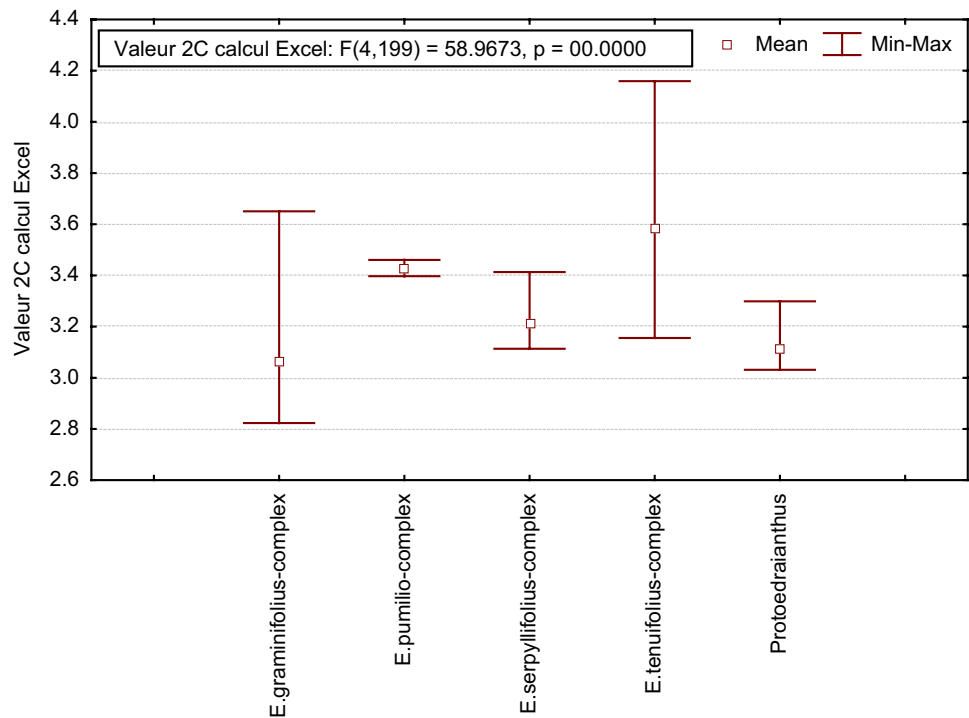


with the genome size range of the *E. graminifolius*- and *E. serpyllifolius*-complexes (Fig. 5), given these values, it is statistically significantly distinct from the genome size range of the *E. tenuifolius*- and *E. pumilio*-complexes.

Discussion

Edraianthus tarae, a species whose populations inhabit cliffs in the canyon of the river Tara in Montenegro, clearly shows its morphological distinctiveness in relation to all

Fig. 5 Genome size of molecular groups of genus *Edraianthus* (according to Stefanović et al. 2008)



other representatives of the genus *Edraianthus* (Lakušić 1987, 1988; Stefanović et al. 2008). This is based on several qualitative features, such as pedicellate flowers, inflorescence arranged in terminal dichasia or polychasia, and capsules opening by basal pores as well as some quantitative morphological properties (e.g. specifically large flowers, bracts and total plant size). This morphological uniqueness is confirmed by the formal morphometric analysis, which grouped all analysed species into two large groups—one corresponding to *Edraianthus tarae* and the other including populations of all remaining investigated taxa, strongly supporting the idea of segregation of *E. tarae* into its own genus *Protoedraianthus* (Lakušić 1988).

However, in contrast to the findings of the morphometric analysis, the nuclear ribosomal ETS sequences (results not shown) as well as previously reported results of the phylogenetic analyses based on plastid DNA (Stefanović et al. 2008) confirm the monophyly of *E. tarae*. Furthermore, molecular data have revealed that this species is not only nested deeply within *Edraianthus* s. str. but also belongs to the *E. graminifolius*-complex, the largest and the most diverse group of *Edraianthus*. Within this group, *E. tarae* forms an isolated lineage, positioned as a sister group to the rest of the *E. graminifolius*-complex. The genome size data largely corroborate the results of molecular analyses and support the notion that *E. tarae* should be treated as congeneric with *Edraianthus*, despite the morphological distinctiveness of this species.

Interestingly, the most important diagnostic features of *E. tarae* are not exclusively confined to this taxon but can

occur, albeit very rarely, within some other representatives of *Edraianthus*. The examples of this include: (1) pedicellate flowers and terminal dichasia or polychasia have been registered as teratological in some individuals of *E. graminifolius* s.l. in subalpine populations on Mt. Kopaonik in Serbia and sub-Mediterranean populations in the canyon of the Morača River in Montenegro (personal field observation by DL and BS); (2) capsule opening by basal lateral pores with a prominent axicorn protruding through the wall of the capsule has been observed as a diagnostic feature in *E. canescens* from the *E. graminifolius*-complex (Lakušić et al. 2013) and is common in *E. glisicii* from the *E. serpyllifolius*-complex (Stefanović et al. 2008); (3) white flowers have been seen as diagnostic features in *Edraianthus graminifolius* subsp. *niveus* (Beck) Janch. from Mt. Vranica in central Bosnia and Herzegovina (Janchen 1910; Lakušić 1974; Lakušić and Abadžić 1982), as well as a rare phenomenon in some subalpine populations of *E. graminifolius* s.l. in Serbia and *E. tenuifolius* in Montenegro (personal field observation by DL and BS); and finally (4) unusually large flowers and scattered bracts have been registered as diagnostic features in *E. glisicii* from the *E. serpyllifolius*-complex (Lakušić 1987, 1988; Rakić 2010).

At the same time, *E. tarae* shares some very important qualitative features with other representatives of the *E. graminifolius*-complex. Those include the long-linear graminoid rosette leaves, hairs at leaf and bract margin directed towards the base, and calyx teeth commonly with small setulose appendages.

Although morphologically very specific and easily recognizable with respect to all other species within the genus, *E. tarae* is still not accepted as a “good species” in the most relevant contemporary floristic literature (Lammers 2007; Castroviejo et al. 2010; Campanula Portal 2013+). Instead, it is either completely neglected or included within *E. graminifolius*. Given that our morphometric, molecular and genome size data allow us to confirm *Edraianthus tarae* as a stenoendemic species of the canyon of the river Tara in Montenegro, formal taxonomic clarification is given here below. Also, despite the fact that morphometric analyses strongly distinguished species *E. tarae* from all other representatives of *Edraianthus* (Figs. 3, 4), taken in aggregate, the morphological differences are not sufficient enough to allow for the acceptance of the proposed genus *Protoedraianthus* (Lakušić 1988).

Taxonomic treatment

According to the ICBN rules (Turland et al. 2018), the binomial *Edraianthus tarae* has not been validly published. Namely, in the original publication the specific epithet was not attached to the genus *Edraianthus*, but rather to the subgenus *Protoedraianthus* (Art. 23). Furthermore, the type specimen has not been validly selected because the collector and date (or collection number) were not properly stated (Art. 40.2). The protologue quote “Lakušić 1968” does not refer to the collector and the year of collection but to the author and the year of publication of the name of vegetation alliance *Amphoricarpion austrati* Lakušić 1968. Consequently, we validly publish the name here, by providing a type citation and a clear indication of the rank. Furthermore, a new expanded species description is provided here because recent research has yielded new insights into the phylogeny and systematics of the genus with significant changes in the taxonomic status of several taxa.

Edraianthus tarae Lakušić ex D.Lakušić & Surina, **sp. nov.**

— TYPE: Montenegro: in faucibus fl. Tara inter vic. Donja Dobrilovina et Djurdjevića Tara [UTM CN67] - in rupium fissuris calcar., 680 m a. s. l., 25 Jun 1981, *E. and M. Mayer* 348 (NHMR) sub *Edraianthus glisicii* agg. (holotype **designated here**: NHMR 348!) (Figs. 2 and 6).

– *Protoedraianthus tarae*, Lakušić, **nom. inval.**, Bilten Društva Ekologa BiH, Ser. A 4: 108. 1987.

Note: During the siege of Sarajevo from 1991 to 1995, the herbarium at the Institute of Biology, University of Sarajevo (IBUS) was completely destroyed. Consequently, we could not trace the type specimen deposited in IBUS that was indicated by Lakušić (1987: 108). The specimen we have chosen as the type is the oldest well-preserved and representative specimen collected by *E. and M. Mayer*. Although

this specimen was originally determined as *E. glisicii*, we found that it fully corresponds to the description of *E. tarae* published by Lakušić (1987: 108).

Expanded species description: Caespitose perennial with herbaceous stems. *Rhizome* stout, somewhat woody, with a branched caudex. *Stem* simple (8.8-) 10.4–20.9 (-26.5) cm, ascending, leafy, glabrous, with a nest-like structure of the dense dried leaves at the base (Fig. 2b). *Leaves* narrowly linear (graminoid), with flat margin, pointed at the tip, glabrous, entire, with raised slightly curved short hairs at leaf margin directed to the leaf base; rosette leaves up to 20 cm long and 1–2 mm wide, rigid end erect, form a globular cushion from which grow out several stems (Fig. 2a, c); cauline leaves sessile, (0.3-) 0.4–0.7 (-0.8) cm × (4.6-) 5.6–12.9 (-17) cm, rarely with a narrowed amplexicaul base. *Inflorescence* with (1-) 3 (-5) flowers arranged in terminal dichasia or polychasia, composed of one central sessile, and 2 to 4 lateral pedicellate flowers (Fig. 2d, e, f); pedicel (3.1-) 4.4–6.9 (-7.1) mm long; flowers surrounded by large scattered bracts. *Involucral bracts* (5-) 6–8 (-9), extremely long (up to 15 cm), much longer than flowers, glabrous, entire, slightly denticulate, green, scattered subtend the flower; inner bracts lanceolate, (0.6-) 0.7–1.1 (-1.3) cm × (2.1-) 3–6 (-7) cm, outer bracts subovate-lanceolate, long attenuate, (0.5-) 0.8–1.2 (-1.3) cm × (5.6-) 6.7–12.9 (-14.7) cm (Fig. 2b, d). *Calyx* pale purplish to green, shiny, glabrous, (5.5-) 6.8–12.3 (-15.7) mm in diameter; calyx teeth narrowly lanceolate, slightly denticulate pointed at the tip, bent outwards, 2–4 times as long as the ovary, (3.3-) 3.6–6.5 (-9.2) mm × (16.8-) 20.2–33.8 (-38.2) mm, glabrous with ciliate margin, commonly with small setulose appendages (Fig. 2e). *Corolla* campanulate, white, glabrous, with long hirsute hairs on margin of corolla lobes (Fig. 2f), extremely large (16.4-) 19.7–31.6 (-35.5) mm × (28.2-) 33.8–45.2 (-47.5) mm; corolla lobes (7.3-) 8.9–13.1 (-14.7) mm × (10.9-) 13.1–19.1 (-21.8) mm. *Style* (20-) 22.5–27.7 (-30.5) mm long, 3 lobed. *Stamens* 5, inserted on disc; anthers (6.8-) 7.2–10.3 (-12.4) mm long; filaments (2.3-) 3.1–6 (-7.9) mm long, in lower part distinctly dilated to deltoid-shaped structure. *Capsule* pale brownish, open by irregular apical rupture and basal lateral pores; axicorn prominent, protruding through the wall of the capsule (Fig. 2G). Flowering May to July.

Chromosome number: $2n = 32$ (estimated based on the genome size and chromosome counts of other *Edraianthus* taxa).

Phenology: Flowering specimens have been observed from May to July.

Etymology: The species is named according to the name of the canyon of the river Tara where the only known populations occur.

Fig. 6 Lectotype of *Edraianthus tarae* R.Lakušić ex D.Lakušić & Surina, sp. nov. (NHMR 348)



Distribution and ecology: *Edraianthus tarae* is distributed in a very narrow area, restricted to the upper part of the canyon of the river Tara, only between Bistrica and Đurđevića Tara, at localities Sokolovina c. 780 m a. s. l. [UTM CN76] and Dobrilovina c. 680 m a.s.l. [UTM CN66 and CN67] (northern Montenegro). *Edraianthus tarae* is a south-eastern Dinaric (Illyrian) narrow endemic (Fig. 1).

Edraianthus tarae inhabits calcareous rocky crevices between 680 and 780 m a. s. l. (Lakušić and Redžić 1989). It is one of the most characteristic rock dwellers growing together with *Bellidiastrum michelii* Cass., *Dianthus*

bertisceus (Rech.f.) E.Mayer & Trpin, *Potentilla caulescens* L., *Micromeria croatica* Schott, *Amphoricarpos autariatus* Blečić & E.Mayer, *Inula ensifolia* L., *Daphne malyana* Blečić, *Edraianthus graminifolius* (L.) A.DC., *Hieracium waldsteinii* Tausch., *Moehringia bavarica* (L.) Gren., *Saxifraga crustata* Vest, *Sesleria interrupta* Vis., *Asplenium ruta-muraria* L., *A. trichomanes* L., *Micromeria thymifolia* (Scop.) R.M.Fritsch, *Seseli rigidum* Waldst. & Kit., *Achnatherum calamagrostis* (L.) P.Beauv., *Asperula scutellaris* Vis., *Silene saxifraga* L., *Solidago virgaurea* L., etc.

Conservation status: *Edraianthus tarae* is known only from its type locality. It is restricted to four microsites, with an area of occupancy of 12 km² extending over 449 km². The population size was estimated to be between 250 and 1000 mature individuals. Therefore, according to the criteria and categories of the IUCN Standards and Petitions Subcommittee (2017), it should be regarded as Endangered, EN C2a(ii).

This species is included in the “List of protected species of Montenegro” (Sl. list RCG 76/2006. Decision on the protection of plant and animal species. Službeni list Republike Crne Gore br. 76/2006 [in Serbian]). All of its known populations are located within the territory of National park and UNESCO MAB reserve “Durmitor and canyon of river Tara”.

Additional specimens examined: Montenegro "in faucibus fluminensis Tara prope vicum Dobrilovina", 700 m a. s. l., in rupium fissuris calcareum, 25 Jun 1981, E. and M. Mayer 349 sub *Edraianthus glisicii* agg. (NHMR!); "in faucibus fl. Tara inter vic. Donja Dobrilovina et Đurđevića Tara", cca 680 m a. s. l., in rupium fissuris calcar., 25 Jun 1981, E. and M. Mayer 346 sub *Edraianthus glisicii* agg. (NHMR!); "in faucibus fluminensis Tara prope vicum Dobrilovina", 650 m a. s. l., in declivibus lapidosis solo calcareo, 25 Jun 1981, E. and M. Mayer 347 sub *Edraianthus glisicii* agg. (NHMR!); "in faucibus fluminensis Tara prope vicum Dobrilovina", 700 m a. s. l., in declivibus lapidosis solo calcareo, 17 May 1982, E. and M. Mayer 345 sub *Edraianthus* (NHMR!); Tara canyon, 6 Jun 2004, Stevanović 22141 (BEOU!); Tara canyon, between Dobrilovina and Đurđevića Tara, calcareous bedrock, 4 Sep 2005, V. Stevanović 19951 (BEOU!); Tara canyon, between Dobrilovina and Đurđevića Tara, calcareous bedrock, 9 Oct 2005, Stevanović and D. Lakušić 19953 (BEOU!); between Donja and Gornja Dobrilovina - calcareous rock crevices, 700 m a. s. l., 27 May 2006, Ž. Modrić and B. Surina 323 (NHMR!); "in faucibus fluminensis Tara", 17 Jun 2006, V. Pulević 350 (NHMR!); Tara canyon between Mojkovac and Đurđevića Tara, between Gornja & Donja Dobrilovina, calcareous rock crevices, exp. N, incl. 80°, *Potentilletum caulescentis*, 29 Jun 2006, Modrić, Vincek and Surina (NHMR!); Tara canyon, calcareous bedrock, *Asplenietea rupestris*, 16 Jul 2006, D. Lakušić 20896 (BEOU); Tara canyon (Dobrilovina), c. 700 m a. s. l., calcareous bedrock, *Asplenietea rupestris*, 16 Jul 2006, Stevanović and D. Lakušić 20955 (BEOU!); Tara canyon, 709 m a. s. l., calcareous bedrock, 5 Jun 2012, D. Lakušić, Kuzmanović and Đurović 35868 (BEOU!); Tara canyon WP 448, 875 m a. s. l., calcareous bedrock, 6 Jun 2013, D. Lakušić, D. Kuzmanović and Kabaš 39733 (BEOU!).

Chorological note: While reviewing herbarium material at BEOU, we found that the north-westernmost point of *E. tarae* presented on the map of the distribution of *E.*

graminifolius-complex (Fig. 6 in Stefanović et al. 2008), showing the locality Ćurovac in the middle part of the Tara Canyon, is incorrect, and that it refers to the species *Edraianthus glisicii* (Crna Gora: Durmitor Tara - kanjon (Ćurovac), 27.09.1991, Stevanović, Lakušić, Niketić 2466/91, sub: *Protoedraianthus tarae* ? – BEOU!).

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