

New nomenclature combinations in the green alder species complex (Betulaceae)

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Abstract

The name *Alnus viridis* (Chaix) DC., based on *Betula viridis* Chaix (1785), has traditionally been attributed to green alders although it is based on a later basionym. *Alnus alnobetula* (Ehrh.) K. Koch based on *Betula alnobetula* Ehrh. (1783) is the correct name for green alders. In light of the increasing use and recognition of the name *Alnus alnobetula* (Ehrh.) K. Koch in the literature. I herein propose new nomenclatural combinations to account for the Japanese and Chinese subspecies respectively: *Alnus alnobetula* subsp. *maximowiczii* (Callier ex C.K. Schneid.) J. Chery and *Alnus alnobetula* subsp. *mandschurica* (Callier ex C.K. Schneid.) J. Chery. Recent phylogenetic analyses place these two taxa in the green alder species complex, suggesting that they should be treated as infraspecific taxa under the polymorphic *Alnus alnobetula*.

Keywords

Green alders, *Alnus viridis*, *Alnus alnobetula*, Betulaceae

Introduction

Characteristic to the genus, *Alnus alnobetula* (Ehrh.) K. Koch is an anemophilous shrub with carpellate catkins that develop into woody strobili. It has a circumpolar distribution with subspecies in Europe (Greuter and Raab-Straube 2011, Flora Euro-

pea [<http://rbg-web2.rbge.org.uk/FE/fe.html> – accessed 22.07.2015], North America (Furlow 1979, Furlow 1990, Fl. North. Amer. North of Mexico Editorial Committee 1997), and Asia (Löve 1968, Li and Skvortsov 1999, Ohba 2006). A phylogeny using nuclear ribosomal DNA ITS sequences generated a polytomy containing five taxa within the green alder species complex due to low sequence divergence among the individuals (Chen and Li 2004). Ren et al. (2010) found the green alder species complex to be a monophyletic clade with the unique character state of a thymine at position 192 of the ITS region. Banaev and Adel'shin (2009) also found close affinity of green alder species using molecular data.

The name *Alnus viridis* (Chaix) DC. has long been attributed to green alders; however a closer look at the literature reveals the name *Alnus alnobetula* (Ehrh.) K. Koch has priority (Pouzar 1982, Holub 1986). Appropriate nomenclatural combinations have recently been published for *A. alnobetula* subsp. *crispa* (Aiton) Raus, *A. alnobetula* subsp. *sinuata* (Aiton) Raus (Greuter and Raab-Straube 2011), and *A. alnobetula* subsp. *suaevolens* (Req.) Lambinon & Kerguélen (Lambinon and Kerguélen 1988). Subspecies names for the Japanese green alder and Chinese green alder are assigned here.

Nomenclature history

The confusion lies in the appropriate basionym of this taxon. The name *Betula viridis* Chaix dates from 1785 (unable to access original text; revisited in Perret and Burdet 1981). No type specimen was designated. Two years earlier, *Betula alnobetula* Ehrh. was published by Ehrhart (in Gartenkalender 1783) describing a shrub in which “the homeland is unknown to me” (translated from German). In Ehrhart (1788), he republished his work where the name *Betula alnobetula* Ehrh. reappeared.

As *Betula* species were transferred to *Alnus*, authors were evidently unaware of the original 1783 publication of the name *B. alnobetula* Ehrh., so *B. viridis* Chaix was thought to be the older name and was taken to be the basionym for green alders. *Alnus alnobetula* Ehrh. has consistently been associated with the 1788 reproduced work and thus listed as a later synonym of *A. viridis* (Chaix) DC.

Major databases such as plantlist.org [accessed 22.07.2015], list the name *Alnus viridis* (Chaix) DC. as a synonym of *A. alnobetula* (Ehrh.) K. Koch. Other databases seem to be waiting for formal action to account for all subspecies names. For example, USDA, Germplasm Resources Information Network (GRIN 2015) [<http://www.ars-grin.gov/cgi-bin/npgs/html/taxon.pl?2483>], states: “the name *A. alnobetula* (Ehrh.) K. Koch, based on *Betula alnobetula* Ehrh. (1783) has priority over *A. viridis* (Chaix) DC., based on *B. viridis* Chaix (1786); nevertheless, *A. viridis* is retained here until all infraspecific taxa are accounted for under *A. alnobetula*”. Other major databases have incomplete citation list for synonyms such as Fl. North Amer. North of Mexico Editorial Committee [http://www.efloras.org/flora_page.aspx?flora_id=1 – accessed 22.07.2015]. Flora Europea [<http://rbg-web2.rbge.org.uk/FE/fe.html> – accessed 22.07.2015] omits citations for green alder names.

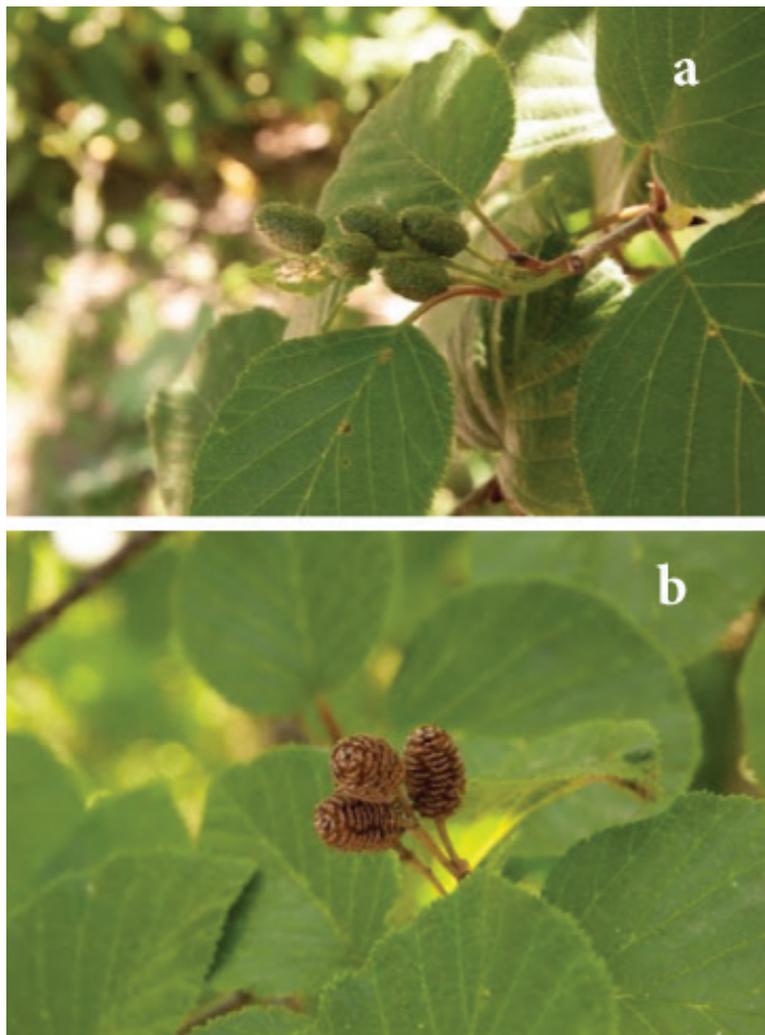


Figure 1. *Alnus alnobetula* subsp. *maximowiczii* – images (taken by Jordan Wood) from Arnold Arboretum 1462-77*E **a**) developing infructescences; **b**) old infructescences.

Conclusions

The close relatedness of the green alder species complex members is supported by recent phylogenetic analyses. The use of a single nrDNA marker, ITS, generated a weakly supported clade of *A. mandshurica*, *A. firma*, *A. pendula* and *A. sieboldiana* embedded within a greater polytomy that includes all other green alders (see strict consensus parsimony tree by Chen and Li 2004). In more recent phylogenetic analysis, *A. maximowiczii* and *A. mandshurica* always form a monophyletic clade with the rest of the green alders (Ren et al. 2010, Banaev and Adel'shin 2009). Given this evidence, it is appropriate to change the rank of these taxa to subspecies of the green alders. The

proposed nomenclature changes utilize the correct species epithet and recognize their phylogenetic placement as lineages of a polymorphic *Alnus alnobetula*.

Intraspecific rankings of plants, specifically subspecies and variety, have been used rather interchangeably (Hamilton and Reichard 1992). The green alder species complex has historically been separated into subspecies due to geographic and morphological distinctiveness. I here agree with this subspecies concept and propose two new nomenclatural combinations to account for the Japanese and Chinese green alder subspecies. This change provides the proper nomenclature for future taxonomic and phylogenetic studies in the green alder species complex.

***Alnus alnobetula* subsp. *maximowiczii* (Callier ex C.K. Schneid.) Chery, comb. n.**
urn:lsid:ipni.org:names:77149153-1

Alnus maximowiczii Callier ex C.K. Schneid., *Illustr. Handb. Laubholz*. 1: 122. 1904: typified by the plate accompanying the protologue (Basionym).

Alnus crispa subsp. *maximowiczii* (Callier ex C.K. Schneid.) Hultén, *Acta Univ. Lund. Avd.* 2. 40(1): 590. 1944.

Alnaster maximowiczii (Callier) Czerep., *Bot. Mater. Gerb. Bot. Inst. Komarova Akad. Nauk. S.S.S.R.* 17: 97. 1955.

Alnaster crispus subsp. *maximowiczii* (Callier ex C.K. Schneid.) Murai, *Bull. Gov. Forest Exp.Sta.* 154: 62. 1963.

Duschekia maximowiczii (Callier ex C.K. Schneid.) Pouzar, *Preslia* 36: 339. 1964.

Alnaster maximowiczii (Callier) Czerep., *Fl. Arct. URSS Fasc.* 5, 133 in obs. 1966.

Alnus viridis subsp. *maximowiczii* (Callier ex C.K. Schneid.) D. Löve, *Taxon* 17: 89. 1968.

Alnus viridis subsp. *maximowiczii* (Callier ex C.K. Schneid.) H. Ohba, *Fl. Japan* 2a: 27. 2006.

Distribution. Temperate Asia: Russian Federation - Khabarovsk, Kurile Islands, Primorye, Sakhalin; Japan - Hokkaido, Honshu; Korea

***Alnus alnobetula* subsp. *mandschurica* (Callier ex C.K. Schneid.) Chery, comb. n.**
urn:lsid:ipni.org:names:77149155-1

Alnus fruticosa var. *mandschurica* Callier ex C.K. Schneid., *Illustr. Handb. Laubholz*. 1:121. 1904: Lectotype: Nadelholzzone des Tschangpei-schan, immer vereinzelt, 1600–1800 m (Fenze 262); designated by Hand.-Mazz., not seen) (Basionym).

Alnus fruticosa var. *mandschurica* Callier ex Kom., *Acta Hort. Petr.* 22: 59. 1903.

Alnus fruticosa var. *mandschurica* f. *normalis* Callier, *Fedde, Rep. Spec. Nov.* 10: 227. 1911.

Alnus fruticosa var. *mandschurica* f. *grandifolia* Callier, *Fedde, Rep. Spec. Nov.* 10: 227. 1911.

Alnus mandschurica (Callier ex C.K. Schneid.) Hand.-Mazz., Oesterr. Bot. Z. 81: 306–307. 1932.

Alnus crispa (Aiton) Pursh subsp. *mandshurica* (Callier) Hara, J. Fac. Sci. Univ. Tokyo III, -6, (2): 32. 1952.

Alnus mandschurica var. *pubescens* Baranov, in T. N. Liou, Illustrated Flora of Ligneous plants of N. E. China 206, t. 75, fig. 112, t. 76, figs 1–4. 1955.

Duschekia mandschurica (Callier ex C.K. Schneid.) Pouzar, Preslia 36(4): 339. 1964.

Alnaster crispa (Aiton) ssp. *mandshurica* (Callier) Murai, Bull. Gov. For. Expt. Sta. Jap. 171: 34. 1964.

Distribution. Russian Federation: Khabarovsk, Primorye; China: Heilongjiang, Jilin, Liaoning, Nei Monggol; Korea

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Problematic specimens turn out to be two undescribed species of *Bignonia* (Bignoniaceae)

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Abstract

Bignonia comprises 29 species of lianas characterized by eight phloem wedges, leaves usually 2-foliolate, mostly simple tendrils and opaque seed wings. The analysis of herbarium specimens in preparation for a taxonomic revision of the genus led to the recognition of two new species: (i) *Bignonia cararensis* from Costa Rica, characterized by a thyrses with lateral compound dichasia and lack of interpetiolar ridge, and (ii) *Bignonia sanctae-crucis* from Bolivia and Brazil, distinguishable by its membranous leaflets, membranous calyx and small fruits. We provide detailed descriptions, illustrations, distribution maps, initial conservation status assessments, and comparisons of the newly described taxa with closely related species.

Keywords

Amazonia, Costa Rica, Bignoniaceae, Lianas, Neotropical Flora

Introduction

Bignonia L. is the fifth largest genus in the Neotropical tribe Bignonieae (Bignoniaceae), with 29 species distributed from Argentina to USA (Zuntini et al. 2015). The genus comprises lianas with eight phloem wedges, leaves usually 2-foliolate, prophylls of the axillary buds foliaceous and bromeliad-like (small, decussate, triangular prophylls

resembling a bromeliad), mostly simple tendrils and opaque seed wings (Lohmann and Taylor 2014). Additionally, these plants have showy rather large flowers, pink corollas, and septicidal capsules that contain numerous seeds, usually winged. Molecular studies have found that *Bignonia* is a highly supported clade that combines previously recognized genera, such as *Clytostoma* Miers ex Bureau and *Cydista* Miers (Lohmann 2006). The species of these two former genera share a variety of morphological features, such as variously cylindrical or quadrangular stems, a cupular calyx, dorso-ventrally flattened corollas, and a reduced nectariferous disk, which made their generic identification sometimes difficult. While preparing a monograph of *Bignonia* (Zuntini, Taylor and Lohmann, in prep.), more than 4,000 collections were analyzed and several problematic specimens that had been previously identified in a variety of Bignoniaceae genera were found to belong to *Bignonia*. However before these materials were finally identified to genus, the identity of these specimens was so unclear that they were confused with four different genera, and the flowering and fruiting specimens of each of these new species were considered to belong to different genera. Once identified as *Bignonia*, it became clear that these specimens represent two undescribed species.

These two new species are *Bignonia cararensis* Zuntini from Costa Rica and *Bignonia sanctae-crucis* Zuntini from Bolivia and western Brazil. Within *Bignonia*, these new species are not very similar and are not closely related to each other, however, these species are each similar to previously described species.

With these two new species, *Bignonia* is now composed of 31 species, with no morphological or geographical changes in the circumscription of the genus. Our results highlight the importance of large diverse herbarium collections for understanding the systematics of tropical plants, and also of broadly surveying all the specimens of a group before finalizing monographic studies rather than studying only a selected set of specimens of a given genus.

Methods

Specimens from the following herbaria were examined: CR, F, INB, MO, NY, SPF, USJ (acronyms following Thiers 2015). The morphology descriptions follow mainly Lohmann and Taylor (2014), with additional terminology from Leaf Architecture Working Group (1999), Radford et al. (1974) and Weberling (1989). For indumentum, we follow Nogueira et al. (2013) with each trichome type described separately; peltate glandular trichomes are described according to their density as sparsely, moderately or densely lepidote, and patelliform glandular trichomes are presented here as “glands.” In the descriptions, terms inside parentheses denote rare conditions. The conservation status assessments follow IUCN guidelines (IUCN 2012), with the evaluation of geographic range based on the extent of occurrence (EOO). Distribution maps were prepared using the specimen database that was compiled as part of an ongoing monographic study of the whole genus (Zuntini, Taylor and Lohmann, in prep).

Taxonomic treatment

Bignonia cararensis Zuntini, sp. nov.

urn:lsid:ipni.org:names:77149637-1

Type. Costa Rica. Puntarenas: Reserva Biológica [Parque Nacional] Carara, Sector Quebrada Bonita. Sitio Area administrativa, 09°45.6'N, 084°36.0'W, 20 m, 9 February 1990, *R. Zúñiga 90* (holotype: CR-145925, mounted in two sheets!; isotypes: F!, INB!, MO!). Figure 1.

Diagnosis. This new species is closely related to *Bignonia uleana* (Kraenzl.) L.G.Lohmann, but differs by the absence of interpetiolar ridges, inflorescences with compound dichasia (vs. simple dichasia in *B. uleana*) and fruits up to 14 cm long with cylindrical and delicate spines (vs. longer than 16 cm with triangular and rough spines in *B. uleana*). Table 1.

Description. Lianas. **Stems** solid, cylindrical, not winged, with lenticels, without interpetiolar gland fields, without interpetiolar ridge, puberulous at least at nodes, sparsely lepidote; foliaceous prophylls caducous, cymbiform, ascending, sessile, symmetrical, 1.7–2.0 mm × ca. 1.4 mm, ciliate, sparsely lepidote, without glands; bromeliad-like prophylls present. **Leaves** 2-foliolate; petiole semi-cylindrical, 35.9–46.5 mm, without simple trichomes or puberulous, sparsely lepidote; petiolules semi-cylindrical, 25.0–45.3 mm, without simple trichomes or puberulous, sparsely lepidote; blades concolorous to slightly discolorous, chartaceous, matte, symmetrical, elliptic to widely elliptic, shortly acuminate apically, rounded basally, 17.1–23.4 × 11.0–12.8 cm, on adaxial surface puberulous at base, sparsely lepidote, with glands clustered at apex and few scattered, on abaxial surface without simple trichomes or puberulous on mid and secondary veins, sparsely lepidote, with a few scattered glands; venation pinnate, with tertiary venations mixed opposite-alternate percurrent; tendrils rarely present, simple, without simple trichomes, sparsely lepidote, with simple apex. **Inflorescences** thyrses, terminal, multi-flowered, with lateral dichasia compound and pedunculate, without simple trichomes, sparsely to moderately lepidote, primary axis ca. 255.0 mm long; bracts caducous, narrowly triangular, 1.8–2.1 × 0.5–0.6 mm, without simple trichomes, sparsely lepidote, without glands; pedicels 6.7–14.4 mm, without simple trichomes, sparsely lepidote, without glands. **Flowers** with calyx cupular, 5-toothed, sub-chartaceous, 3.7–5.9 × 4.7–6.4 mm wide at apex, ciliate, moderately lepidote, with a few scattered glands, teeth 0.6–1.4 mm; corolla purple outside, inside color unknown, infundibuliform, dorso-ventrally flattened, membranous, 40.8–75.0 mm, externally sericeous, sparsely lepidote, without glands, internally sericeous at lobes, not lepidote, with stipitate glandular trichomes at base, tube 28.4–52.5 × 2.7–3.3 mm wide at base and 10.9–14.1 mm wide at apex, lobes sub-circular, 9.7–22.0 × 10.7–15.5 mm; androecium didynamous, with stamens included, the largest 16.4–18.6 mm, the shortest 11.2–11.3 mm, without simple trichomes, not lepidote, with stipitate glandular trichomes at base, thecae 3.3–3.5 mm, staminode ca. 4.2 mm; gynoecium 25.5–27.9 mm, ovary cylindrical, verrucose, without simple trichomes, not lepidote, ovules in 2

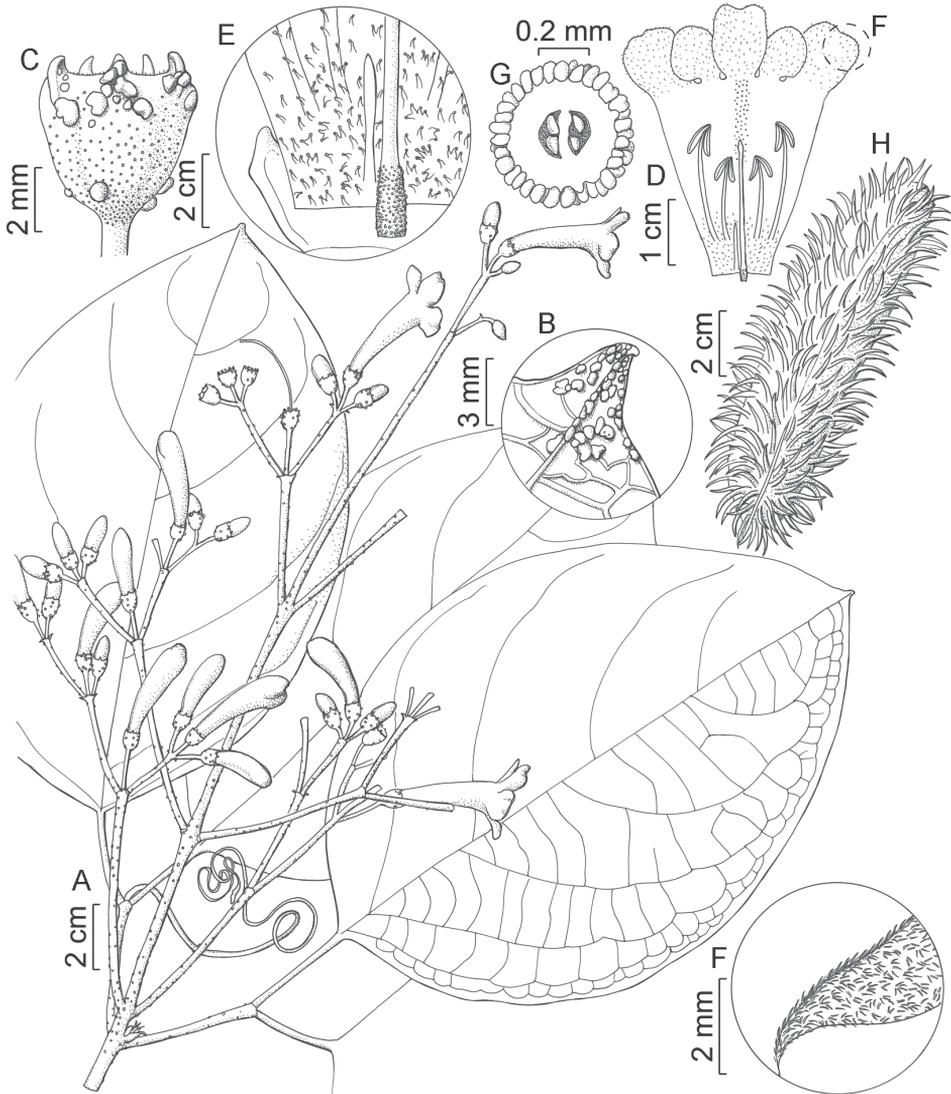


Figure 1. *Bignonia cararensis* Zuntini **A** Flowering branch **B** Gland cluster at leaflet apex on adaxial surface **C** Calyx **D** Opened flower **E** Detail of internal flower base, showing the glandular stipitate trichomes at corolla **F** Detail of the internal sericeous indument of the corolla lobes **G** Ovary cross-section **H** Fruit. Illustrated from *Zuniga 90* (MO) [**A–G**] and *Weinberg s.n.* (MO-3842040) [**H**].

series per locule, style not lepidote; nectariferous disk reduced. **Fruits** inflated, narrowly elliptic, 11.2–14.5 × 3.1–4.0 wide × ca. 1.4 cm thick, valves woody, without ridges, moderately echinate, without simple trichomes, not lepidote, without glands; spines cylindrical, 8.2–13.4 mm. **Seeds** unknown.

Distribution. This species is known only from Parque Nacional Carara, in Puntarenas, Costa Rica, between 20 and 100 m elevation (Fig. 2).

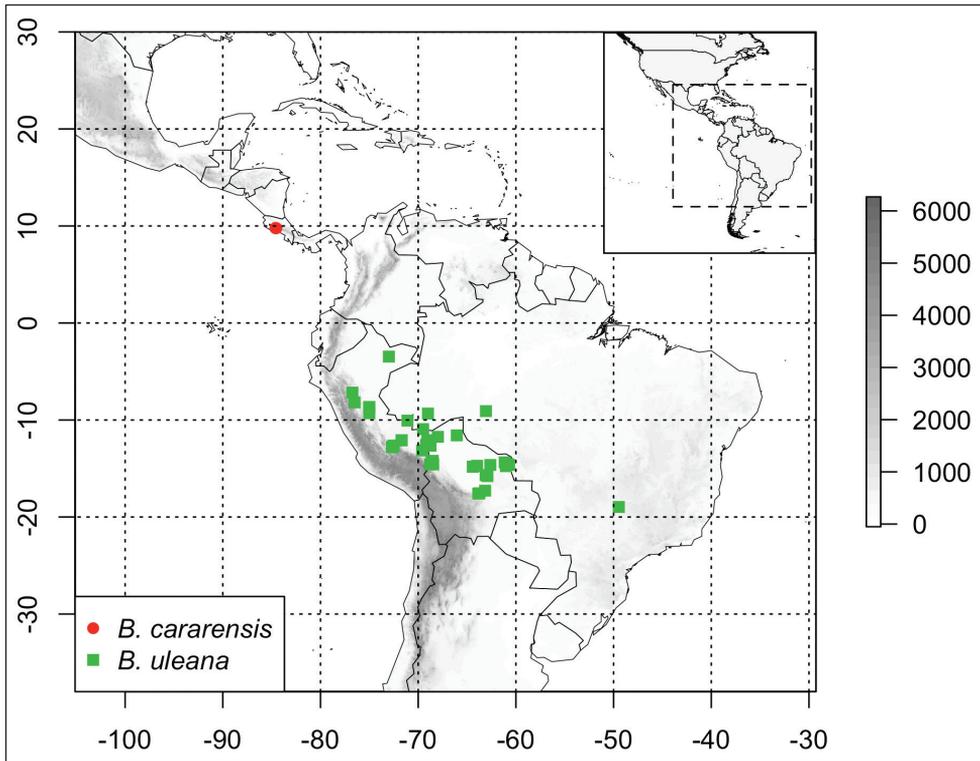


Figure 2. Distribution of *Bignonia cararensis* (red circles) and *B. uleana* (green squares). Elevation in meters, following the scale on the right.

Phenology. Three fertile collections are documented for *Bignonia cararensis*: a single flowering specimen was collected in February and two fruiting specimens were collected in February and October.

Etymology. The name is a reference to the type locality.

Conservation status. The collections from the main herbaria of Costa Rica (CR, INB and USJ) were consulted, but so far this species is only documented from Parque Nacional Carara. Since *B. cararensis* is known exclusively from the type locality, its full distribution cannot be accurately assessed and is here listed as Data Deficient (DD). Additional fieldwork is necessary to estimate the number of mature individuals and to assess the full extend of the species' distribution.

Discussion. This species is similar to *B. uleana*, a species from Bolivia, central western Brazil and Peru. *Bignonia cararensis* can be recognized by the absence of interpetiolar ridges (vs. present in *B. uleana*), the inflorescences in lateral compound dichasia (vs. lateral simple dichasia in *B. uleana*), and the fruit up to 14 cm and with cylindrical delicate spines (vs. longer than 16 cm with triangular rough spines in *B. uleana*) (Table 1).

The flowering collection *Zuñiga 90* was previously identified as *Cydista lilacina* A.H.Gentry [\equiv *B. lilacina* (A.H.Gentry) L.G.Lohmann] (Burger and Gentry 2000,

Table 1. Contrasting characters of *Bignonia cararensis* and *B. uleana*.

Character	<i>B. cararensis</i>	<i>B. uleana</i>
Interpetiolar ridge	Absent	Present
Inflorescence lateral structure	Compound dichasia	Simple dichasia
Fruit length (cm)	11.2–14.5	16.8–26.0
Fruit spines	Cylindrical, moderately distributed	Triangular, sparsely distributed
Distribution	Costa Rica	Bolivia, Brazil and Peru

Hauk 1997, *in sched.* at CR, INB and MO), and so was the sterile specimen *Acosta Vargas* 826 (*in sched.* at INB and MO). *Bignonia lilacina* is similar to *Bignonia cararensis*, with which it shares cylindrical stems, large leaflets, and inflorescences in thyrses with compound lateral dichasia. However, *Bignonia cararensis* differs from *B. lilacina*, an Amazonian species, by its glabrous and verrucose ovary (vs. densely lepidote and smooth in *B. lilacina*), sparsely lepidote stems, inflorescences and flowers (all of these structures are densely lepidote in *B. lilacina*), gland clusters borne on the adaxial surface of leaflet apices (vs. basal gland clusters on the abaxial leaflet surface in *B. lilacina*) and buds with straight apices (vs. curved apices in *B. lilacina*).

In contrast, the fruiting collection *Jiménez* 2042 was previously identified as *Clytostoma pterocalyx* Sprague ex Urb. [\equiv *B. pterocalyx* (Sprague ex Urb.) L.G.Lohmann] (*in sched.* at INB), and as *Clytostoma sciuripabulum* Bureau & K.Schum. [\equiv *B. sciuripabulum* (Bureau & K.Schum.) L.G.Lohmann] (*in sched.* at CR and INB). The other fruiting material of this new species (*Weinberg* s.n.) was also identified as *C. sciuripabulum* (*in sched.* at MO). However, *Bignonia cararensis* differs from *B. pterocalyx* by its puberulous stems and inflorescences (vs. pilose in *B. pterocalyx*), 2-foliolate leaves (vs. 1-foliolate in *B. pterocalyx*) and moderately echinate fruit (vs. densely echinate in *B. pterocalyx*). *Bignonia cararensis* differs from *B. sciuripabulum* by the cylindrical stems (vs. quadrangular in *B. sciuripabulum*) and apical gland clusters borne on the adaxial leaflet surface (vs. no apical clusters in *B. sciuripabulum*).

Clytostoma pterocalyx and *Cydista lilacina* were reported as new records for Costa Rica (Burger and Gentry 2000, Hauk 1997, Jiménez and Grayum 2002) based on the specimens studied here, but with the re-identification of these specimens both of these species are now known only from South America. *Bignonia pterocalyx* is found in Venezuela and Colombia, and *B. lilacina* is distributed throughout Amazonia.

The Carara National Park is located in the northern portion of the Tárcoles-Térraba floristic region, which extends through the central portion of Pacific coastal Costa Rica (Hammel et al. 2004). This region has a combination of dry and moist forests, and includes elements from Nicoya and Osa Peninsulas, where *B. cararensis* might also be found.

Additional examined specimens. COSTA RICA. Puntarenas: Carara Biological Reserve, 2.6 km del portón de la entrada del sendero Laguna Meandrica. Primer desviación a mano izquierda entrando, 9°48.0'N, 84°35.16'W, 100 m, 6 Apr 2000, *L.G. Acosta Vargas* 826 (INB, MO); Camino a Coopecarara, 9°47.16'N, 84°36.16'W, 100

m, 11 Oct 1995, *Q. Jiménez 2042* (CR, INB); Carara Biological Reserve. 15 minute walk from entrance of Carara taking trail winding right (counter-clockwise), 9°46'N, 84°31'W, 18 Feb 1991, *R. Weinberg s.n.* (MO-3842040).

***Bignonia sanctae-crucis* Zuntini, sp. nov.**

urn:lsid:ipni.org:names:77149638-1

Type. Bolivia. Santa Cruz: Prov. Ichilo. El Carmen (8 km al SSW de Buena Vista), tramo de 2km al W de la comunidad por el camino al Campamento del Río Saguayo, 17°31.98'S, 63°41.85'W, 400 m, 5 October 1996, *I.G. Vargas C. 5382* & *S. Hurtado P.* (holotype: MO-5878679!; isotypes: K, NY!). Figure 3.

Diagnosis. This new species is similar to *Bignonia potosina* (K.Schum. & Loes.) L.G.Lohmann, but is distinguished by its membranous leaflets with mixed opposite-alternate percurrent tertiary venation (vs. chartaceous with alternate percurrent tertiary venation in *B. potosina*), membranous calyx (vs. chartaceous calyx in *B. potosina*) and fruits shorter than 6.8 cm long (vs. fruits longer than 15 cm in *B. potosina*). Table 2.

Description. Lianas. **Stems** solid, tetragonal, winged or ribbed, with lenticels, without interpetiolar gland field, with interpetiolar ridge, puberulous to pilose at least at nodes, sparsely lepidote; foliaceous prophylls caducous, falcate (subulate), ascending, stipitate, asymmetrical, 0.9–2.3 mm × 0.5–1.5 mm, without simple trichomes, sparsely lepidote, with a few glands on abaxial surface (no glands); bromeliad-like prophylls present. **Leaves** 2-foliolate; petiole semi-cylindrical, (6.1–)15.1–38.9 mm, pubescent, puberulous or pilose, sparsely lepidote; petiolules semi-cylindrical, 9.7–29.8 mm, pilose, sparsely lepidote; blades slightly discoloured, membranous, matte, slightly asymmetrical to asymmetrical, elliptic to widely ovate, acuminate to long acuminate apically, rounded basally (short attenuate), 8.3–13.3(–18.9) × 5.1–8.5(–12.3) cm, on adaxial surface without simple trichomes, densely lepidote, without glands, on abaxial surface pilose along midvein and secondary veins, sparsely lepidote, with a few scattered glands; venation pinnate, with tertiary venations mixed opposite-alternate percurrent; tendrils rarely present, simple, without simple trichomes, sparsely lepidote, with simple apex. **Inflorescences** racemes, terminal, 2–4-flowered, without simple trichomes or puberulent, sparsely lepidote, primary axis 8.3–13.8 mm long; bracts caducous, not observed; pedicels 5.5–10.0 mm, without simple trichomes, moderately lepidote. **Flowers** with calyx cupular, 5-toothed, membranous, 4.5–6.0 × 4.3–5.1 mm wide at apex, ciliate, moderately lepidote, with glands clustered in columns, teeth 0.6–1.5 mm; corolla creamish outside, yellowish inside, infundibuliform, dorso-ventrally flattened, membranous, 30.6–52.8 mm, externally pubescent at lobes, moderately lepidote, without glands, internally with pubescent lobes, not lepidote, with shortly stipitate glandular trichomes at base, tube 19.8–40.0 × 2.1–5.0 mm wide at base and 9.2–16.3 mm wide at apex, lobes rounded or oblong, 9.7–15.4 × 8.8–15.2 mm; androecium didynamous, with stamens included, the largest 10.7–18.0 mm, the shortest 6.4–11.7 mm, without simple trichomes, not lepidote, with shortly stipitate glandular

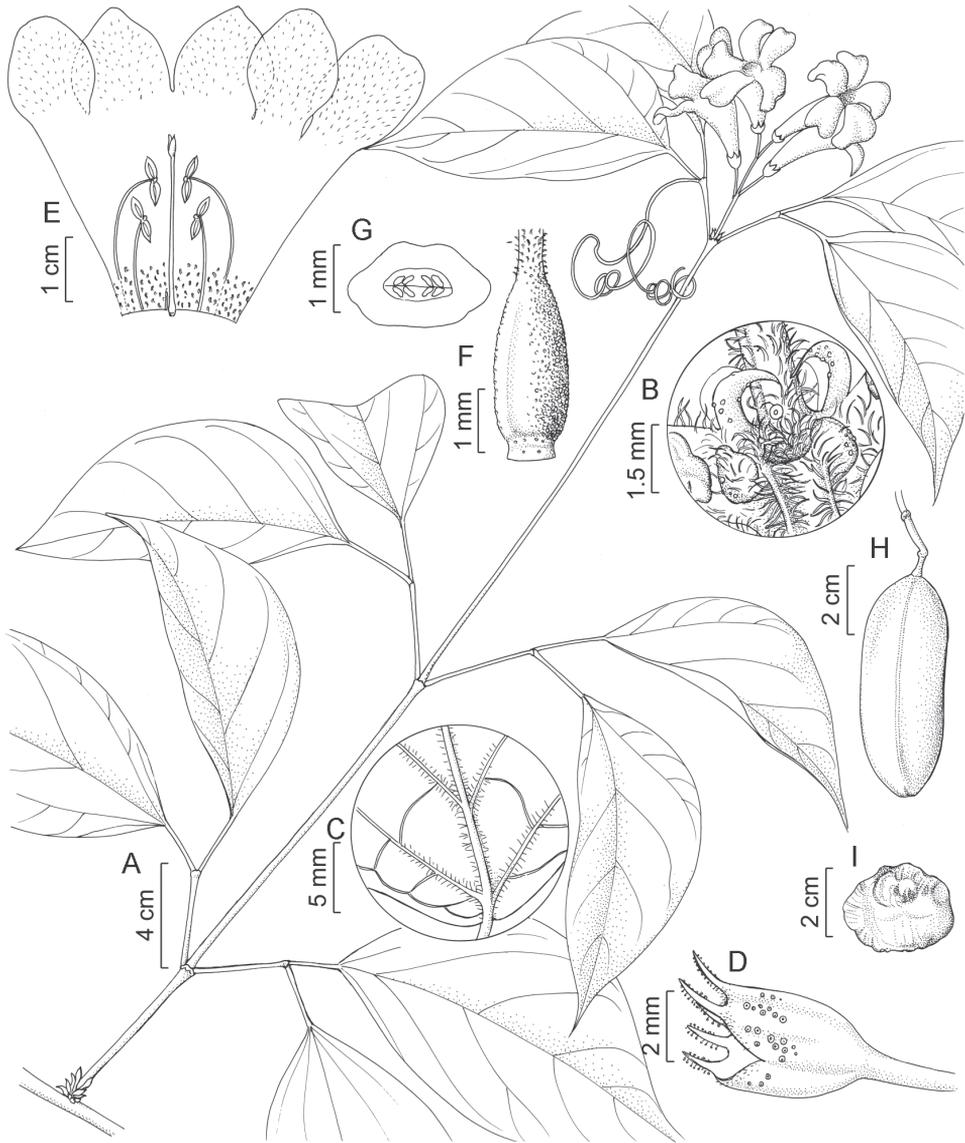


Figure 3. *Bignonia sanctae-crucis* Zuntini. **A** Flowering branch **B** Stem node with prophylls of the axillary buds **C** Detail of the abaxial leaflet surface **D** Calyx **E** Opened flower **F** Ovary side-view **G** Ovary cross-section **H** Fruit **I** Seed. Illustrated from *Vargas* 5382 (NY) [**A,D**], *Saldias* 4775 (NY) [**E–G**] and *Nee* 52361 (NY) [**B, C, H, I**].

trichomes at base, thecae 1.7–3.6 mm, staminode 0.9–2.5 mm; gynoecium 21.5–29.2 mm, ovary ovoid to cylindrical, smooth, without simple trichomes (pilose at apex), densely lepidote, ovules in 4 series per locule, style sparsely lepidote at base; nectariferous disk reduced. **Fruits** inflated, oblong, ca. 6.8 × 2.8 wide × 0.8 cm thick, valves

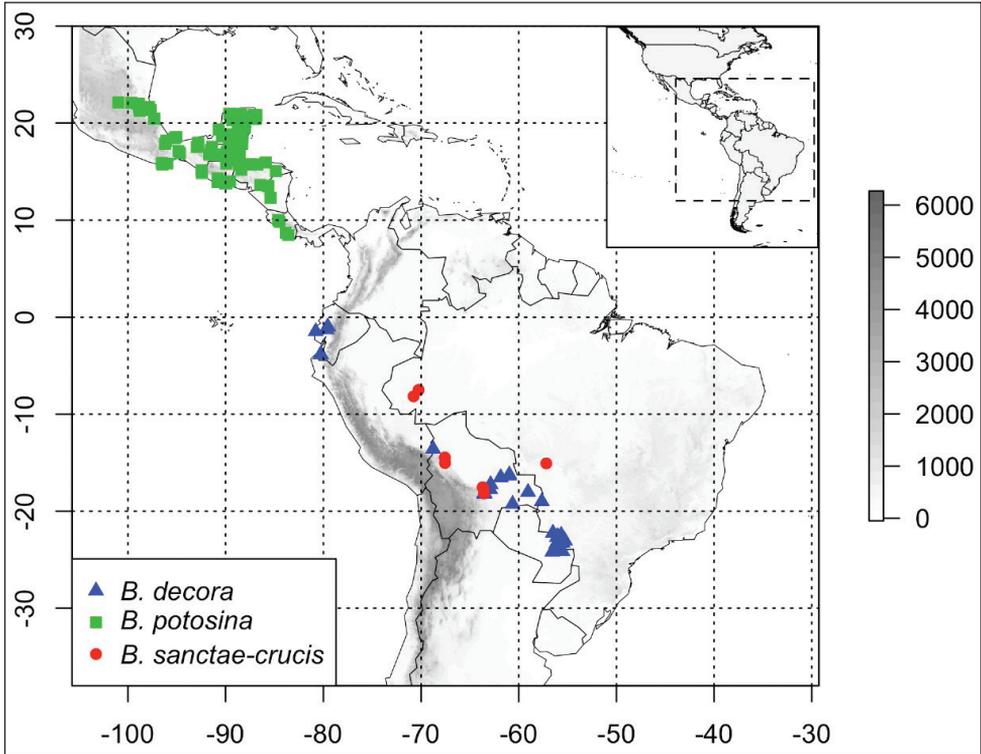


Figure 4. Distribution of *Bignonia sanctae-crucis* (red circles), *B. decora* (blue triangles), and *B. potosina* (green squares). Elevation in meters, following the scale on the right.

woody, without ridges, smooth, without simple trichomes, sparsely lepidote, without glands. **Seeds** beige, thin, transversally elliptic to narrowly transversally oblong, symmetrical, 13.7–24.3 × 28.5–39.4 mm, with two opaque wings; seed body flattened, 0.8–1.2 mm thick.

Distribution. This species is found in evergreen or semideciduous forests in Western Amazonia, occurring in Bolivia (Beni, La Paz and Santa Cruz) and Brazil (Acre, Amazonas and Mato Grosso), between 160 to 700 m alt. (Fig. 4).

Phenology. This species was collected with flowers in June, September, October and November. A single fruiting specimen was collected in July.

Conservation status. *Bignonia sanctae-crucis* is known from only seven locations but is considered Least Concern (LC) given its wide extent of occurrence (over 600.000 km²) and the different physiognomies where it occurs, including secondary formations. The number of locations where this species is known to occur is likely underestimated because *Bignonia* species are usually not densely distributed and because this entire region is not well documented floristically. Additional fieldwork is needed in order to fully document the extent of distribution of this species.

Etymology. The epithet refers to the type locality, the Department of Santa Cruz (Bolivia), where most specimens were collected.

Table 2. Contrasting characters of *Bignonia decora*, *B. potosina* and *B. sanctae-crucis*.

Character	<i>B. decora</i>	<i>B. potosina</i>	<i>B. sanctae-crucis</i>
Prophylls of axillary buds	Foliaceous, persistent and spreading	Falcate, caducous and ascending	Falcate, caducous and ascending
Leaf texture	Sub-chartaceous to chartaceous	Chartaceous to sub-coriaceous	Membranous
Leaf tertiary venation	Alternate percurrent	Alternate percurrent	Mixed opposite-alternate percurrent
Inflorescence	Thyrse	Raceme	Raceme
Calyx texture	Chartaceous	Chartaceous	Membranous
Fruit length (cm)	14.7–37.7	12.0–24.0	Ca. 6.8
Distribution	Bolivia, Brazil, Ecuador and Peru	Central America	Bolivia and Brazil

Discussion. *Bignonia sanctae-crucis* and *B. potosina* share quadrangular and ribbed (winged) stems, prominent interpetiolar ridges, falcate and caducous prophylls, and few-flowered racemes. Apart from being morphologically similar, these species are also closely related and can be confused. However, *Bignonia sanctae-crucis* can be distinguished from *B. potosina* by the membranous calyx (vs. chartaceous in *B. potosina*) and fruits shorter than 6.8 cm long (vs. fruits longer than 15 cm in *B. potosina*) (Table 2). These two species are also geographically widely separated, with *B. sanctae-crucis* found in Bolivia and central to western Brazil while *B. potosina* is widely found in Mexico and Central America but not in South America. *Bignonia sanctae-crucis* can also be confused with the sympatric species *B. decora* (S.Moore) L.G.Lohmann due to the quadrangular stems shared by both species. However, *B. sanctae-crucis* can be recognized by its falcate and caducous prophylls (vs. foliaceous and persistent in *B. decora*), few-flowered racemes (vs. multi-flowered thyrses in *B. decora*) and fruit without ridges (vs. three longitudinal ridges in *B. decora*) (Table 2). Quadrangular stems are also characteristic of *B. sciuripabulum* (Bureau & K.Schum.) L.G.Lohmann, a distantly related species (Zuntini and Lohmann, in prep.) that has a verrucose and glabrous ovary (vs. smooth and lepidote in *B. sanctae-crucis*) and echinate fruits (vs. smooth in *B. sanctae-crucis*); *B. sciuripabulum* is found in Amazonia and the Atlantic forest of Brazil.

The only fruiting material of this new species (*Nee* 52361) was previously identified as *Cydista cf. decora* (S.Moore) A.H.Gentry [\equiv *B. decora*] (*in sched.* at NY), a closely related species. The flowering specimens of *B. sanctae-crucis*, however, were identified as *Clytostoma sciuripabulum* Bureau & K.Schum. [\equiv *B. sciuripabulum*], *Clytostoma uleanum* Kraenzl. [\equiv *Bignonia uleana*], and some other *Clytostoma* species (*in sched.* at MO and NY). The thin-textured corolla probably confused the generic identification, given that most *Cydista*, as previously circumscribed, were characterized by thicker corollas whereas such thin corollas were characteristic of the previously recognized *Clytostoma*. Despite its corolla texture, *B. sanctae-crucis* is not closely related to the species that were included in *Clytostoma*, and does not have the verrucose glabrous ovary that is characteristic of that group.

Additional examined specimens. BOLIVIA. Beni: Rurrenabaque, Rurrenabaque, 14°28'S, 67°34'W, 333 m, 8 Oct 1921, *White 874* (NY). La Paz: Alto Beni, Concesión de San Jose de Papay, 15°02'S, 67°33'W, 500 m, 23 Oct 1987, *E. Vargas 2022* (LPB, MO); San Buena Ventura, 500 m, 29 Nov 1901, *R.S. Williams 363* (NY). Santa Cruz: Cercado, Lomas del Río Cúcha, 450 m, 28 Oct 1925, *J. Steinbach G. 7307* (F, MO); Ibáñez, Gorge of Río Bermejo, 6.5km (by road) W of the checkpoint at Angostura, 18°10'S, 63°33'W, 690 m, 25 Jul 2003, *M.H. Nee 52361* (LPB, NY, USZ). Ichilo, 2 km W of Center of San Carlos, older secondary growth along highway from Buena Vista to Villa Tunari, 17°24.5'S, 63°45'W, 310 m, 31 Oct 1999, *M.H. Nee 50398* (NY); Ichilo, Estância San Rafaél (propiedad de la Unversidad NUR), 16 km SW de Buena Vista, 17°36'S, 63°36'W, 432 m, 1 Oct 1996, *M. Saldias P. 4775* (NY, USZ). BRAZIL. Acre: Tarauacá, 1–3 km east of Rio Tarauacá, 24 Sep 1968, *G.T. Prance 7513* (K, INPA, MG, MO, NY). Amazonas: Envira, Rio Juruá, Basin of Rio Juruá, near mouth of Rio Embira, 7°30'S, 70°15'W, 160 m, 28 Jun 1933, *B.A. Krukoff 5046* (MICH, MO, NY, US). Mato Grosso: Barra do Bugres, Fazenda Ochsenfeld, 23 Oct 1995, *G. Hatschbach 63777* (MBM, SPF).

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A new record of the rare alga *Pachycladella* P. C. Silva (Chlorophyceae) in New England

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Abstract

A rarely reported taxon, the microscopic green alga *Pachycladella*, was found in a pond in Connecticut. Due to an unresolved taxonomic debate within the genus, the species-level identity of the newly discovered population cannot be determined with absolute certainty. However, according to the currently accepted classification the Connecticut specimens best match *Pachycladella zatoriensis*, heretofore only known from Europe. The find represents not only the first record of *Pachycladella* in Connecticut, but also in the entire New England region. This study highlights the need for continuing floristic surveys even in regions previously well explored.

Keywords

Connecticut, floristics, microalgae, plankton

Introduction

USA's New England region, which encompasses the states of Connecticut (CT), Maine, Massachusetts, New Hampshire, Rhode Island and Vermont, has certainly received plenty of floristic attention over the past century. Freshwater algal floristic works in this region, however, have dwindled in recent years. In 1984, a 1020 pages long list of New England algal records and the related literature was compiled by Colt (1984) from previously published works, but relatively few studies have been added since. Yet, even those few have demonstrated the need for continuing floristic work on New England freshwater algae: for example, Vaccarino et al. (2011) added 140 generic records to

the flora of Acadia National Park and Fučíková et al. (2015) reported 65 new species records for Maine. Clearly, much of the freshwater algal diversity still remains to be documented even in this relatively well-studied region.

The genus *Pachycladella* was originally described from Palisades Interstate Park in New York by Smith (1924, as *Pachycladon* G.M. Smith), and remained monotypic for nearly four decades. The type species, *P. umbrina* (G.M. Smith) P.C. Silva, is represented in public culture collections by a single strain (SAG 10.85 and its duplicates in other collections), which has been studied extensively in terms of its morphology, life cycle, and ultrastructure (e.g., Reymond and Hegewald 1990, Friedl and Reymond 1997). This strain was also used in molecular phylogenetic reconstructions. Both molecular data and ultrastructural features indicate that the strain (and presumably the genus) belongs to Chlorophyceae, and molecular phylogenies, e.g., in Škaloud et al. (2013), show it as member of the volvoclean clade Stephanosphaerina.

Pachycladella and the species within it have a somewhat convoluted taxonomic history (Smith 1924, Silva 1970, Reymond 1980, Reymond et al. 1992). Of the five currently recognized species, three are not well understood in terms of morphological variation, occurrence, and ultimately taxonomic status (Reymond et al. 1992, Guiry and Guiry 2015). Through careful morphological examinations and literature review Reymond et al. (1992) clarified the blurry distinction between *P. umbrina* and *P. zatoriensis* (Bednarz & Mrozinska-Webb) Komárek, but the distinctness of *P. chodatii* (Bern.) Hegewald, *P. minor* (Chudybowa & Chudyba) P.C. Silva, and *P. komarekii* (Fott & Kováčik) Reymond still needs to be confirmed (Komárek and Fott 1983).

The present study contributes a new record of *Pachycladella* cf. *zatoriensis* from the USA, and is the first report of the genus *Pachycladella* for CT and for New England. Given the past taxonomic confusion it is difficult to interpret all historical records with certainty, but it is possible that this study also represents the first record of *P. zatoriensis* in the United States. Continuing survey studies will be necessary to understand the occurrence patterns of *Pachycladella* and its species.

Methods

In 2014 and 2015 I conducted a survey of selected lakes, streams, and wetlands in northeastern CT and recorded the algal diversity in these habitats. Samples were collected using a 10 µm mesh plankton net, stored in small Ziploc bags, and examined microscopically using an Olympus BX60 microscope with Nomarski DIC optics equipped with an Olympus DP25 digital camera (Olympus Imaging America, Center Valley, PA, USA). The Olympus CellSens software was used to capture images and measure cell dimensions. Georeferenced records of observed algae, accompanied by micrographs where possible, have been deposited in iNaturalist (<https://www.inaturalist.org/projects/freshwater-algae-of-new-england>). Most algal species were identified using North American and New England taxonomic literature (Conn and Webster 1908, Hylander 1928, Prescott 1964, Whitford and Schumacher 1984).

Results

On August 4th 2015, I collected a plankton sample from a pond on Bonemill Rd., Storrs, CT (41°48'12", -72°16'48") and in it found a population of a species I had not seen in any previous collection, including a 2014 sample from the same pond. I identified the alga as *Pachycladella umbrina* based on the unmistakable reddish-brown cell wall processes (Fig. 1A–F) that were either bluntly or bifurcately terminated (Fig. 1C). Upon later review of the literature it became apparent that the tetrahedral arrangement of the processes (also referred to as appendages in past literature) is characteristic of *P. zatoriensis* rather than *P. umbrina*, the latter of which has predominantly a cruciate arrangement of processes, i.e., all four processes are in the same plane (Reymond et al. 1992).

I collected an additional sample on August 12th. In both samples, *Pachycladella* occurred infrequently but consistently: I usually saw 5–10 specimens on every slide. Other algae abundant in the planktonic community included nonmotile colonial chlorophytes resembling *Chlamydocapsa planktonica* (West & G.S. West) Fott, members of the chlorophycean family Hydrodictyaceae, the large dinophyte *Ceratium hirundinella* (O.F. Müller) Dujardin, alongside diatoms (e.g., *Cymbella* C. Agardh, *Eunotia* Ehrenberg, and *Melosira* C. Agardh), synurophytes (*Mallomonas* Perty and *Synura* Ehrenberg), and euglenoids (*Euglena* Ehrenberg, *Lepocinclis* Perty, *Phacus* Dujardin, and *Trachelomonas* Ehrenberg).

The observed *Pachycladella* cells were spherical and 8–11.5 µm in diameter, and possessed one chloroplast with a single pyrenoid (not always visible). Cell wall was protracted into four (rarely five, Fig. 1D) long, hollow processes arranged in a tetrahedral, exceptionally somewhat irregular manner. Of the ca. 30 specimens observed, none exhibited a cruciate arrangement of processes. The processes were light to dark reddish-brown in color, (26-) 30–42 µm long, 3.5–4.1 µm thick at the base and 1.6–2 µm thick ca. at half their length, and had a rough surface. Process apices were either bluntly pointed or bifurcated (Fig. 1C). Additional micrographs showing the observed morphological variation are available online as Fig. S1.

Discussion

Globally, *Pachycladella* has been reported broadly but infrequently. For some time, the genus and its sole species were only known from North America (e.g., as noted by Bourrelly 1966). The geographically scattered records of the genus now also include several European countries, Argentina, Bangladesh, Brazil, India, Singapore, Taiwan, and possibly Australia (Reymond et al. 1992 and references within, Keppeler et al. 1999, Islam and Alfasane 2005, Pham et al. 2011, Hentschke and Prado 2012). *Pachycladella umbrina* is by far the most commonly reported species, although many reports do not contain enough detail in morphological descriptions or figures to critically evaluate the species-level identifications. Thus, some of these reports may in fact represent the occurrence of another species of *Pachycladella*.

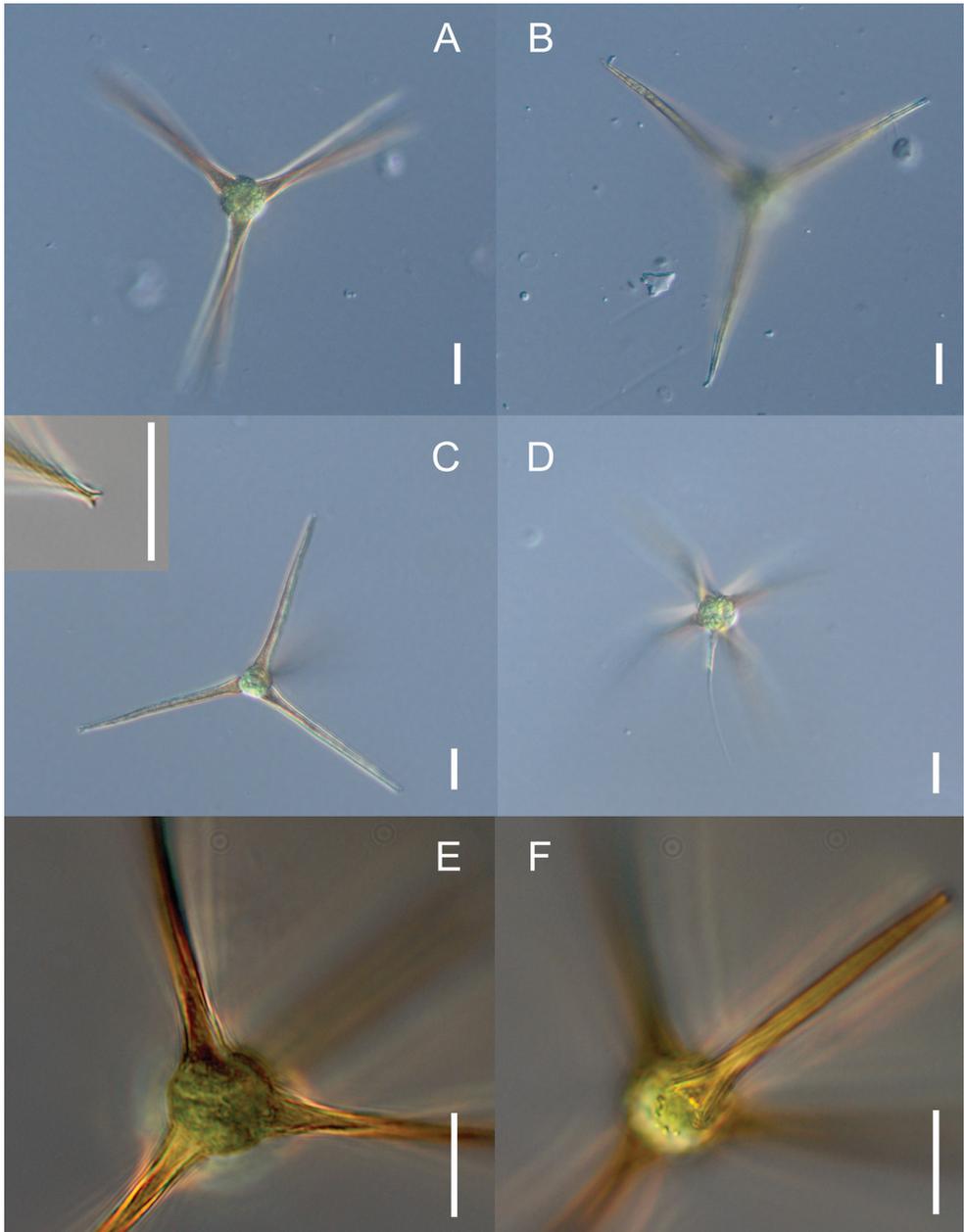


Figure 1. Light micrographs of *Pachycladella* cf. *zatoriensis* found in Connecticut. **A** gross morphology of a vegetative cell **B** same cell as in **A**, with focus on process apices **C** small vegetative cell with a clearly bifurcated process apex (enlarged in the inset) **D** an unusual cell with a fifth, irregularly placed and colorless appendage **E** high-magnification micrograph showing the hollow bases of cell wall processes as well as their dark coloration **F** same cell as in **E** with focus on the cell surface and attachment of the fourth process. Scale bars represent 10 μm in all images.

Based on past records and newly collected data, Reymond et al. (1992) argued that the tetrahedral vs. cruciate arrangement of processes is a stable trait within populations and can be used to distinguish *P. umbrina* (cruciate) from *P. zatoriensis* (tetrahedral). Following this distinction they assigned several previous records of *Pachycladella* to either of the two species, but also left many as uncertain due to lack of information in the reports or because the reported morphological variation spanned both types of appendage arrangement. *Pachycladella zatoriensis* is so far only confirmed to occur in Europe (Reymond et al. 1992). However, Reymond et al. (1992) also suggested that Playfair's (1918) report of *Bernardia tetraedrica* from Australia is in fact the first report of *Pachycladella zatoriensis*. Notably, Playfair (1918) does not mention two of the generic characters assigned to *Pachycladella* by Smith (1924): a common bifurcation of the process apices and the brown tint of the cell wall. Both traits were also extensively documented in *P. zatoriensis* (Bednarz and Mrozinska-Webb 1971, Reymond et al. 1992, 1993). While these characters may be variable and facultative (Wawrik 1977, Reymond et al. 1993), their complete absence in Playfair's description and figure makes the synonymy with *Pachycladella* far less certain.

In the USA, *Pachycladella* has been heretofore reported from Alabama, Kentucky, New York, North Carolina, Tennessee, and from the Great Lakes region, and has been noted to be rare or uncommon (e.g., Prescott 1964, Shubert 2003). The genus was not found during the extensive National Lakes Assessment conducted by the United States Environmental Protection Agency in 2007. Only *P. umbrina* has been reported thus far, but many US records of *Pachycladella* cannot be assigned to species with confidence (Reymond et al. 1992 and references within).

The population of *Pachycladella* newly found in CT morphologically matched the original description of *P. umbrina* except for having appendages consistently in a tetrahedral orientation, rather than being mostly cruciate (Smith 1924). The tetrahedral disposition classifies the CT specimens as *P. zatoriensis sensu* Reymond et al. (1992), which has heretofore not been reported from the USA. The original description of *P. zatoriensis* by Bednarz and Mrozinska-Webb (1971) however reports slightly smaller cells and considerably shorter processes, only up to 20 μm long. The size difference between the two species appears to be consistent across the reports reviewed and assigned to species by Reymond et al. (1992). With their larger size and tetrahedral appendage orientation, the CT specimens fit neither species perfectly, nor do they fit other *Pachycladella* species morphologically or ecologically. However, several reports marked as uncertain by Reymond et al. (1992) suggest a similar trait combination as the CT specimens (e.g., Wawrik 1977, Dillard 1989). Thus, the distinction between the two species may not be as clear-cut as implied by Reymond et al. (1992).

The rarity of *Pachycladella* combined with difficult-to-interpret past records makes species-level taxonomy in this genus quite tricky. DNA barcode data are available only from SAG 10.85, and therefore genetic comparisons of morphologically and geographically distinct populations are not possible at present. A morphological study aided by a molecular phylogeny would help deciding which traits should be considered taxonomically informative. Because even morphologically distinct taxa can be non-monophyletic (e.g., McManus and Lewis 2011), such a study on *Pachycladella* would

also elucidate whether the *Pachycladella*-like morphology has a common origin or represents multiple taxa. For the purposes of this study, I followed the taxonomic scheme of Reymond et al. (1992) and assigned the CT specimens to *P. zatoriensis*. However, it is possible that they represent an unusual population of *P. umbrina*, or possibly even a novel species of *Pachycladella*. Given this uncertainty I am hesitant to proclaim this find the first US record of *P. zatoriensis*, but based on the available literature it is the first report of the genus and species in New England.

It is possible that this interesting alga had been overlooked in past floristic studies or misidentified as another taxon, despite its distinct morphology. *Pachycladella* could conceivably be mistaken for *Treubaria triappendiculata* Bernard, a species reported from Massachusetts by Gustafson (1942). It could also possibly be confused with other species of *Treubaria* (which have been reported from Maine and New Hampshire, Colt 1984 and references within). However, the two genera, despite both bearing tetrahedrally or cruciately arranged processes, are quite morphologically different. When present, the brown cell wall and bifurcate processes give *Pachycladella* away immediately. Furthermore, e.g., Smith (1950) summarizes the differences in cell shape (spherical in *Pachycladella* vs. pyramidal in *Treubaria*), appendage morphology (slender, brown and blunt/bifurcate in *Pachycladella* vs. stout, hyaline, and sharp in *Treubaria*), and chloroplast features (single plastid with one pyrenoid in *Pachycladella* vs. four pyrenoids or even four distinct plastids in older cells of *Treubaria*). Other than the unlikely misidentification for *Treubaria*, no records of *Pachycladella* or its synonyms are listed in Colt's New England checklist (Colt 1984) or subsequent works (e.g., Sheath and Harlin 1988, Vaccarino et al. 2011).

It may be somewhat surprising to see a new genus record in a region so well studied – and particularly in CT, which of all the New England states likely has the best documented freshwater algal microflora, perhaps only rivaled by Rhode Island (Conn and Webster 1908, Hylander 1928, Colt 1984, Sheath and Harlin 1988). However, many of the comprehensive studies are several to many decades old, and given the drastic environmental and habitat changes this region has undergone in the past century, one cannot simply assume that the same biodiversity still occurs here. As shown in the present study, a previously unreported taxon may have expanded its range into New England from more southern states. In other cases, species may have been lost from New England due to habitat deterioration or destruction without this biodiversity loss ever being noticed. With this small study I hope to underscore the importance of continuing survey studies on algae, as they are key players in aquatic ecosystems.

Conclusion

Despite past taxonomic confusion and uncertainty about the classification and specific diversity of *Pachycladella*, this study presents a new record of an alga that matches the original generic description perfectly, best matching the species *P. zatoriensis*. As such, it is the first record of *Pachycladella* in New England and possibly the first record of *P. zatoriensis* in North America.

Acknowledgements

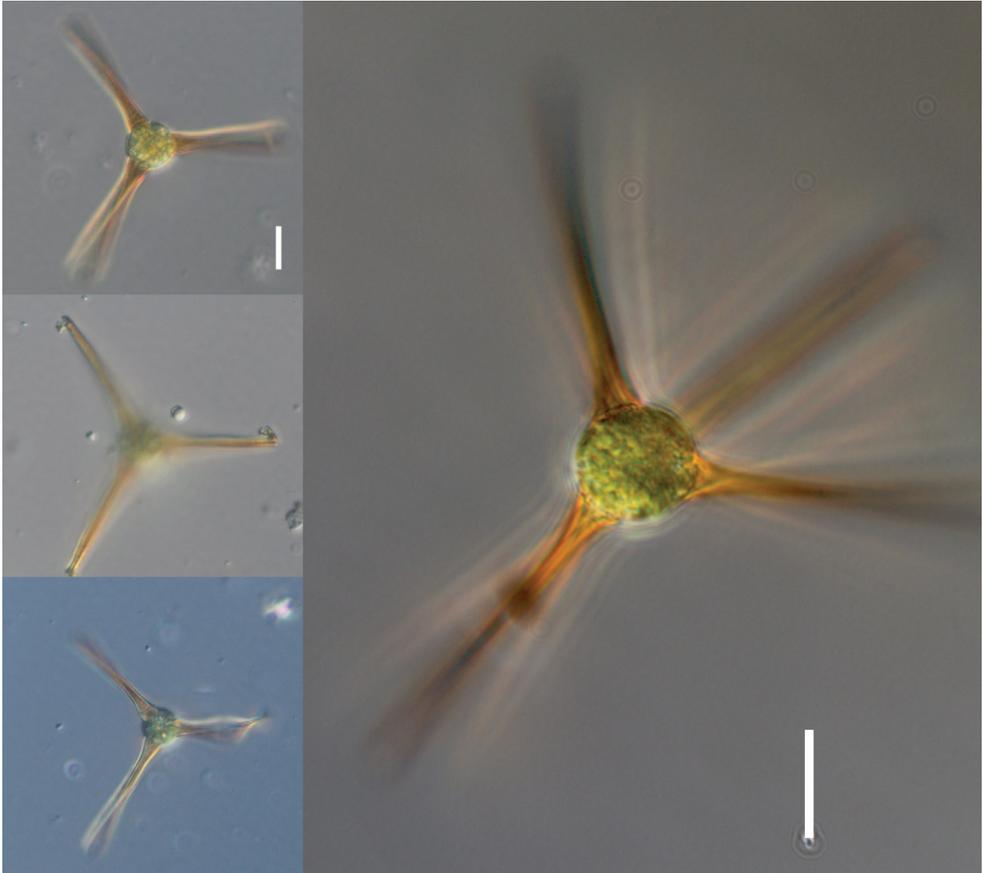
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Appendix



Figures S1. Additional light micrographs showing the morphology of *Pachycladella cf. zatoriensis* found in Connecticut. Scale bars represent 10 μm .

Study of phylogenetic relationship of Turkish species of *Klasea* (Asteraceae) based on ISSR amplification

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Abstract

Klasea is a taxonomically complex genus in which there are many problems, mostly with *Klasea kotschyi* and *K. hakkiarica*. It is challenging to differentiate the genera based on morphological characters alone. Revision studies performed on the basis of molecular data obtained from studies conducted in recent years have made the phylogenetic relationships and systematic positions of the taxa more apparent and reliable. In this study, *Klasea*, *Serratula*, *Jurinea* and *Centaurea* species native to Turkey, were collected from different localities of Anatolia and DNA was isolated from the collected samples. The data were analyzed ordination analyses including UPGMA and PCA using NTSYSpc 2.1. The infrageneric and intergeneric phylogenetic relationships between *Klasea* and other related genera were also characterized. The *Klasea* species were grouped into three clusters. It was determined that taxa *Klasea kotschyi* and *K. hakkiarica* are separate but closely related. Moreover, it was observed that the *Klasea lasiocephala* a separate group within the genera. Clearly the genera *Klasea*, *Serratula*, *Jurinea* and *Centaurea* are phylogenetically differentiated on the dendrogram.

Keywords

Asteraceae, ISSR, *Klasea*, *Serratula*, Molecular systematics, Phylogeny

Introduction

The tribe Cardueae (Asteraceae) is generally accepted to be classified into five subtribes named Echinopinae, Carlininae, Carduinae, Centaureinae and Cardopatiinae (Susanna et al. 2006). Cardueae include perennial, biennial, or monocarpic herbs and shrubs and, less often, annual herbs or small trees (Barres et al. 2013). However, delineation of these taxonomic entities is highly problematic. Beyond the limits of the tribes, the boundaries between these units are also very difficult to establish. Also, some large genera of the tribes have generic delimitation problems: *Carduus* L. (90 species), *Cirsium* Mill. (250 species), *Centaurea* L. (400 species), *Cousinia* Cass. (800 species), *Serratula* L. (70 species), and *Saussurea* DC. (more than 300 species) (Garcia-Jacas et al. 2002). Extensive work conducted recently by Garcia-Jacas et al. (2000, 2001) and Font et al. (2002) have clarified the delineation of *Centaurea*. Limited studies also exist on *Cirsium* and *Carduus* (Haffner and Hellwig 1999), but most of the taxonomic problems persist. The genus *Klasea* Cass. constitutes a taxonomically complex group of plants with generic boundaries are unclear, especially at the generic level surrounding genus *Serratula* (Martins and Hellwig 2005). *Klasea* Cass., traditionally treated as a section within *Serratula* L., is widely accepted at the generic level (Martins 2006). *Klasea* is naturally distributed in Central Asia, Iran, Turkey, China, Himalayas, south east Europe and south Russia. *Klasea* is located within the monophyletic tribe Cardueae, in the subtribe Centaureinae (Susanna et al. 2006).

16 species were reported for the genus *Serratula* in Turkey (Davis and Kupicha 1975; Davis et al. 1988). Then all Turkish *Serratula* species were transferred to *Klasea* except *Serratula tinctoria* (Greuter 2003; Martins 2006). Thus, *Klasea* is represented by 15 species and *Serratula* is represented by one species within the Mediterranean and Irano-Turanian phytogeographic regions of Turkey (Dogan et al. 2012). Five of these species are endemic to Turkey, resulting in an endemism ratio of 33.3% (Dogan et al. 2012).

Currently, morphological revisions of various plant taxa are often supported by molecular data (APG 2003). As compared with morphological data, DNA sequences are not influenced by the environmental conditions in which the plants have grown; hence they serve as a powerful tool in resolving taxonomical and systematical problems. When compared with the phenotypic characters, by using different molecular marker systems, more reliable results were also obtained by a number of researchers that used different plant groups (Yang et al. 1996; Joel et al. 1998; Soranzo et al. 1999; Bremer et al. 2001; Mengitsu et al. 2002; Ash et al. 2003; Jump et al. 2003; Pharmawati et al. 2004; Dogan et al. 2007; Ali et al. 2013).

The RAPD (Randomly Amplified Polymorphic DNA) fingerprinting method is widely used and has a wide range of applications (Williams et al. 1990). However, because RAPD is a highly sensitive method, it should be used with great care. The ISSR (Inter Simple Sequence Repeat) has much higher levels of reproducibility than RAPD, for which reason it is preferable (Zietkiewicz et al. 1994, Prevost and Wilkinson 1999; Dogan et al. 2007; Hakki et al. 2010). The ISSR method is very widely used for the analysis of genetic diversity (Prevost and Wilkinson 1999).

Simple sequence repeats (SSRs), also known as microsatellites, are tandemly repeated di-, tri-, tetra- or penta-nucleotide sequences (mainly within the range of 10–80 repeats of the core unit) that are abundant within eukaryotic genomes. A high level of genomic variation is generated by the more or less evenly distributed microsatellite sequences present within the plant and animal genomes. The high levels of genomic variation are widely used for genetic variation analysis of both wild plants (Wolfe et al. 1998; Dogan et al. 2010; Laosatit et al. 2013; Khalik et al. 2014) and crop plants (Vosman and Arens 1997; Hakki et al. 2001; Mohammadzadeh et al. 2011). Microsatellites can be used in inter- as well as intra-species analyses (Soranzo et al. 1999). However, the technique requires prior sequence information for the locus-specific primers, a feature that renders it difficult to be applied to plants for which no adequate genomic sequencing studies exist. Without considering their difficulty or cost (Hakki and Akkaya 2000), numerous microsatellite loci have been identified for economically important crops such as wheat, rice or maize. In *Klasea*, however, they have not been utilized.

In this study, *Klasea* species, which are difficult to delineate using morphological traits, were collected from their natural habitats in Turkey. DNA was isolated and fingerprinting was performed using a highly reliable and reproducible technique that mimics the application ease of RAPDs. The method employed to assess the genetic diversity and to resolve the genetic relationships among the species is a technique derived from SSR characterization based on PCR amplification of ISSR regions primed by a single oligonucleotide corresponding to the targeted repeat motif. The SSR-containing primers are usually 16-25 base pair long oligonucleotides anchored at the 3'- or 5'-end by two to four arbitrary, and often degenerate, nucleotides (Fang et al. 1997). The primer can be based on any of the motifs found at SSR loci. In these conditions, only sequence regions flanked by the two adjacent identical and inversely oriented microsatellites are amplified. Overall, the technique does not require prior sequence information (an advantage against microsatellites) and its reliability is higher than RAPD's.

The aim of this study was to determine the genetic relationships among selected Anatolian-originated *Klasea*, *Serratula*, *Jurinea* and *Centaurea* species collected from diverse regions of Turkey and to use a DNA-based molecular marker system to resolve the unclear and controversial status of these species based on conventional morphological characters.

Material and methods

Specimen collection

Silica gel dried plant leaf samples belonging to 15 *Klasea* taxa and *Serratula tinctoria*, and 2 out-group taxa (*Jurinea* and *Centaurea*) were collected from the natural flora of Turkey. The species and provinces of their localities are as follows: *Klasea quinquefolia* (Artvin), *K. oligocephala* (Kahramanmaraş), *K. kotschyi* (Bitlis), *K. serratuloides* (Van), *K. erucifolia* (Erzurum), *K. lasiocephala* (Antalya), *K. cerinthifolia* (Kahramanmaraş), *K. grandifolia*

Table 1. List of sampled taxa. Including location data, collectors, and herbarium in which the voucher specimens are accessioned.

Species	Voucher
<i>Klasea serratuloides</i>	Turkey, Van: Van to Gurpinar, 2125 m, 38024.434'N, 0430 23.079'E, 19.07.2009, B.Doğan 2117 & A.Duran (KNYA).
<i>K. lasiocephala</i>	Turkey, Antalya, Gazipasa, Çayır-yaka mountain pasture, 1730 m, 36°30.027'N, 032°32.181'E, 30.06.2009, B.Doğan 2105 & A.Duran (KNYA), Endemic.
<i>K. bornmuelleri</i>	Turkey, Malatya, Darende, near Akçatoprak, 1010 m, 38°30.064'N, 037°33.907'E, 17.07.2009, B.Doğan 2110 & A.Duran (KNYA), Endemic.
<i>K. kurdica</i>	Turkey, Osmaniye, Yarpuz, 1465 m, 37°00.774'N, 036°26.683'E, 15.07.2009, B.Doğan 2106 & A.Duran (KNYA).
<i>K. coriaceae</i>	Turkey, Kars, Tuzluca to Kağızman, 1055 m, 40°06.399'N, 043°29.567'E, 20.07.2009, B.Doğan 2122 & A.Duran (KNYA)
<i>K. cerinthifolia</i>	Turkey, Kahramanmaraş, Ahir mountain, 990 m, 37°36.470'N, 036°52.917'E, 16.07.2009, B.Doğan 2107 & A.Duran (KNYA)
<i>K. grandifolia</i>	Turkey, Antalya, Akseki, Süleymanlı village, 1425 m, 37°17.980'N, 031°46.520'E, 31.07.2009, B.Doğan 2130 & A.Duran (KNYA).
<i>K. haussknechtii</i>	Turkey, Muş, Malazgirt, Karıncalı village, 1840 m, 39°21.219'N, 042°20.010'E, 18.07.2009, B.Doğan 2113 (KNYA).
<i>K. radiata</i> subsp. <i>biebersteiniana</i>	Turkey, Kars, Kağızman, Akçay to Cumaçay, 1830 m, 20.07.2009, B.Doğan 2124 & A.Duran (KNYA).
<i>K. radiata</i> subsp. <i>radiata</i>	Turkey, Kars, Arpaçay, Kardeşköy to Dağköy, 2190 m, 06.08.2010, 40°55.087'N, 043°11.209'E, B.Doğan 2283 & A.Duran
<i>K. hakkiarica</i>	Turkey, Hakkari, Cilo mountain, Kırıkdağ, near dez stream, 2210 m, 37°32.974'N, 043°57.615'E, 07.08.2009, B.Doğan 2132 & A.Duran (KNYA), Endemic.
<i>K. kotschyi</i>	Turkey, Bitlis, Tatvan, Sapur village, 1965 m, 38°26.154'N, 042°24.413'E, 06.08.2009, B.Doğan 2131 & A.Duran (KNYA).
<i>K. quinquefolia</i>	Turkey, Artvin, Ardanuç, Boyalı village, 1210 m, 41°06.967'N, 042°07.283'E, 11.08.2009, B.Doğan 2139 & A.Duran (KNYA).
<i>K. erucifolia</i>	Turkey, Erzurum, Köprüköy, Eğirmez village, 1635 m, 39°57.056'N, 041°51.530'E, 09.08.2009, B.Doğan 2137 & A.Duran (KNYA).
<i>K. oligocephala</i>	Turkey, Kahramanmaraş, Ahir mountain, 995 m, 37°36.475'N, 036°52.947'E, 16.07.2009, B.Doğan 2108 & A.Duran (KNYA).
<i>Serratula tinctoria</i>	Turkey, Bolu, Gerece to Bolu, 28. km, 1105 m, 09.08.2010, 40°45.340'N, 031°54.888'E, B.Doğan 2290 & A.Duran (KNYA).
<i>Jurinea cataonica</i>	Turkey, Erzincan, Old Çayır-lı road, 10. km, 1750 m, 39047.954'N, 039030.343'E, 07.08.2005, B.Doğan 1029 (KNYA). Endemic.
<i>Centaurea ptosimopappoides</i>	Turkey, Adana, Aladağ to Kızıldağ, 890 m, 19. 06. 2010, A.Duran 9042 & M.Öztürk (KNYA).
<i>C. straminicephala</i>	Turkey, Erzurum, Uzundere to Artvin, 1100 m, 26.07.2002, A.Duran 6048 & M.Sağiroğlu (KNYA).

(Antalya), *K. radiata* subsp. *radiata* (Kars), *K. hakkiarica* (Hakkari), *K. haussknechtii* (Muş), *K. coriaceae* (Kars), *K. radiata* subsp. *biebersteiniana* (Kars), *K. kurdica* (Osmaniye), *K. bornmuelleri* (Malatya), *Serratula tinctoria* (Bolu), *Centaurea ptosimopappoides* (Adana), *C. straminicephala* (Erzurum), and *Jurinea cataonica*. For details see Table 1.

DNA extraction

Nuclear DNA of silica gel dried leaf samples were extracted according to the instructions of the Nucleon phytopure plant DNA extraction kit (RPN 8510, Amersham Life Science, England). For each sample, DNA was extracted from 100 mg of leaf. After concentrations were determined using an Eppendorf BioPhotometer, DNA samples were diluted to the working concentration of 25 ng/ μ L. To better quantify the DNA and to assess the quality of the DNA, samples were run on an agarose gel (0.9%), stained with ethidium bromide, against a DNA standard with known concentrations. Stock DNA was kept at -86 °C.

ISSR Amplifications

Of the 20 primers investigated during our initial screening, the primers that gave the most informative patterns (in terms of repeatability, scorability, and the ability to distinguish between varieties) were selected for fingerprinting. The characteristics of the primers used are given in Table 2.

Each reaction contained 2.5 mM MgCl₂, 10 mM Tris-HCl (pH 8.8), 50 mM KCl; 0.8% Nonidet P40, 200 mM of each of dNTP, 0.5 mM primer, 25 ng DNA template and 0.4 units of Taq DNA Polymerase (Bioron, Germany) in a final reaction volume of 25 μ L. After a pre-denaturation step of 3 minutes at 94 °C, amplification reactions were cycled 40 times at 94 °C for 1 minute, at annealing temperature (Table 1) for 50 seconds and 72 °C for one minute followed by a final 10 minutes 72 °C extension in an Eppendorf Mastercycler gradient thermocycler. Upon completion of the reaction, aliquots of PCR products (15 μ L) were mixed with 3 μ L of loading buffer (50% glycerol, 0.25% bromophenol blue and 0.25% xylene cyanol), loaded onto a 2.0% agarose/1x Tris-Borate EDTA gel and electrophoresed at 4 V/cm.

Amplifications were repeated at least twice at different time periods for each primer using the same reagents and procedures.

Table 2. List of the ISSR primers used in this study and their specifications.

Primer	Primer sequence	T _m (°C)	Size (bp)	GC (%)	Number of polymorphic bands
ISSR F1	GAG CAA CAA CAA CAA CAA	49.1	18	38.9	13
ISSR F2	CTC GTG TGT GTG TGT GTG T	56.7	19	52.6	11
ISSR F3	AGA GAG AGA GAG AGA GCG	56	18	55.6	14
ISSR F4	AGA GAG AGA GAG AGA GTG	53.7	18	50	12
ISSR F5	AGA GAG AGA GAG AGA G	49.2	16	50	10
ISSR F6	CCA CCA CCA CCA CCA	53.3	15	66.7	13
ISSR F7	ACA CAC ACA CAC ACA C	49.2	16	50	12

Data collection and cluster analysis

Amplified fragments were visualized under a UV transilluminator and photographed using a gel documentation system (Vilbert Lourmat, Infinity model). All of the amplified fragments were treated as dominant genetic markers. Each DNA band generated was visually scored as an independent character or locus (1 for presence and 0 for absence). Qualitative differences in band intensities were not considered. Every gel was scored in triplicate (independent scorings) and only the fragments consistently scored were considered for analysis. A rectangular binary data matrix was prepared and all the data analysis was performed using the Numerical Taxonomy System, NTSYS-pc version 2.1 (Applied Biostatistic, Exeter Software, Setauket, New York, USA).

In cluster analysis of the samples, the unweighted pair-group method with the arithmetic mean (UPGMA) procedure was followed (Rohlf 1992). The genetic distances were calculated with the SM coefficient. In order to determine the ability of ISSR data to display the inter-relationships among the samples, principle co-ordinate analysis (PCA) of pair-wise genetic distances (Nei 1972) was also conducted using the NTSYS-pc package.

Results and discussion

Silica gel dried plants collected from 19 different natural habitats were taken to the laboratory. The total number of species collected and used in the phylogenetic analysis was 19. DNA extractions were first attempted using a standard 2X CTAB method. Due to the poor DNA quality produced by the CTAB procedure, a commercial kit (Nucleon phytopure) was used in all isolations and repeated extractions were conducted whenever necessary.

From an initial screening of 20 ISSR primers, seven primers revealed high levels of polymorphisms. These primers generated 85 highly polymorphic fragments that were consistently amplified in repeated experiments conducted on separate dates. The GC percentages of the selected primers were within the range of 38.8–66.7%. The characteristics as well as the sequences of the primers revealing a polymorphism are shown in Table 2. The primer ISSR F3 amplified the highest number of polymorphic fragments (14 bands) and primer ISSR F5 yielded the lowest number of fragments (10 bands). In total, the average number of polymorphic fragments per primer used was roughly 12. A representative figure containing ISSR F3 and ISSR F5 banding patterns is given in Figure 1.

A total of 15 *Klasea*, 1 *Serratula*, 1 *Jurinea* and 2 *Centaurea* taxa were used in the scoring analysis. The *Jurinea* and *Centaurea* taxa, which were used as the out-group, formed a cluster that was distinct from the *Klasea* and *Serratula* cluster in the constructed dendrogram. Furthermore the *Klasea* and the *Serratula* taxa form clearly separate clusters among themselves (Figure 2).

The *Klasea radiata* subsp. *radiata* and *Klasea radiata* subsp. *biebersteiniana* taxa were observed to be very closely positioned in the dendrogram. The *K. kotschyi*, *K. hak-*

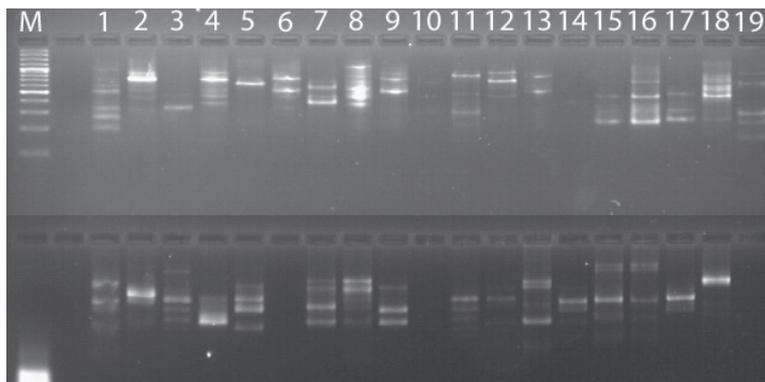


Figure 1. Representative agarose gels where PCR products were amplified with the primers ISSR F5 (highest number of polymorphic bands, top) and ISSR F5 (lowest level of polymorphic bands, down). **1** *Serratula tinctoria* **2** *Klasea quinquefolia* **3** *K. oligocephala* **4** *K. kotschy* **5** *K. serratulooides* **6** *K. erucifolia* **7** *K. lasiocephala* **8** *K. cerinthifolia* **9** *K. grandifolia* **10** *K. radiata* subsp. *radiata* **11** *K. hakkiarica* **12** *K. haussknechtii* **13** *K. coriacea* **14** *K. radiata* subsp. *radiata* **15** *K. kurdica* **16** *K. bornmuelleri* **17** *Centaurea ptosimopappoides* **18** *C. straminicephala* **19** *Jurinea cataonica*, M: marker.

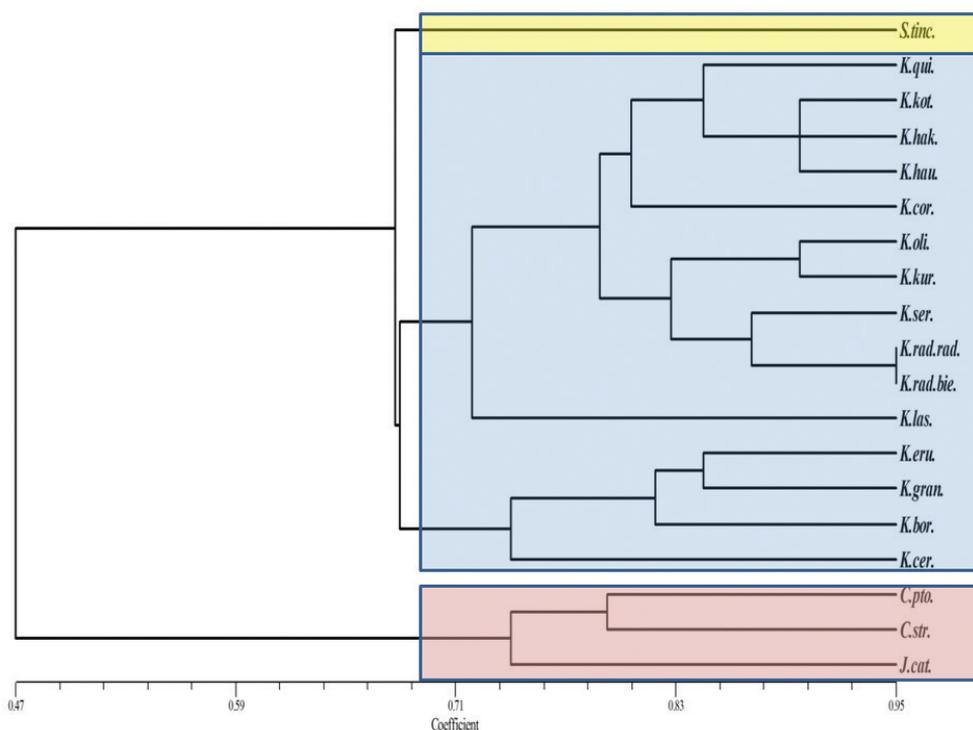


Figure 2. Dendrogram showing genetic relationship of *Klasea*, *Serratula*, *Centaurea* and *Jurinea* species as shown using inter simple sequence repeats. (*Serratula tinctoria*, *Klasea quinquefolia*, *K. oligocephala*, *K. kotschy*, *K. serratulooides*, *K. erucifolia*, *K. lasiocephala*, *K. cerinthifolia*, *K. grandifolia*, *K. radiata* subsp. *radiata*, *K. hakkiarica*, *K. haussknechtii*, *K. coriacea*, *K. radiata* subsp. *radiata*, *K. kurdica*, *K. bornmuelleri*, *Centaurea ptosimopappoides*, *C. straminicephala*, *Jurinea cataonica*)

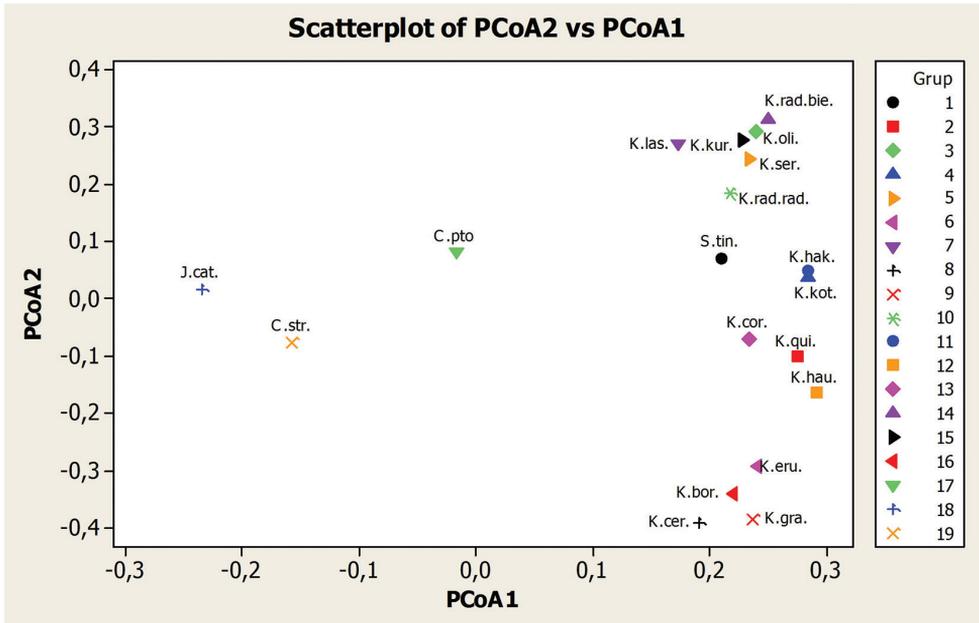


Figure 3. Principal co-ordinate analysis (PCA) of *Klasea*, *Serratula*, *Centaurea* and *Jurinea* species. 1 *Serratula tinctoria* 2 *Klasea quinquefolia* 3 *K. oligocephala* 4 *K. kotschyi* 5 *K. serratuloides* 6 *K. erucifolia* 7 *K. lasiocephala* 8 *K. cerinthifolia* 9 *K. grandifolia* 10 *K. radiata* subsp. *radiata* 11 *K. hakkarica* 12 *K. haussknechtii* 13 *K. coriacea* 14 *K. radiata* subsp. *radiata* 15 *K. kurdica* 16 *K. bornmuelleri* 17 *Centaurea ptosimopappoides* 18 *C. straminicephala* 19 *Jurinea cataonica*

kiarica and *K. haussknechtii* taxa, which have similar leaf characteristics, were also correlated in terms of their molecular data and were located in the same sub-cluster. *K. coriacea* is a taxon, which spreads over distinct areas in the Eastern Anatolia and is distinguished owing to its distinctive height. The *Klasea oligocephala* and *K. kurdica* clustered together. The two taxa are very similar also in terms of morphological properties such as leaf, capitulum and pollen characteristics. *K. serratuloides* taxon has the largest capitulum among the genus. It has a similar profile to the *K. radiata* subspecies with respect to the leaf characteristics and the similarity of overspreading areas. *Klasea serratuloides* and *K. radiata* were also positioned close to one another on the dendrogram.

K. lasiocephala is distinguished within the genus by its very short stems or the absent stems. *K. lasiocephala* differs morphologically from other *Klasea* taxa in having absent or reduced stems and that it is also somewhat genetically distinct from other *Klasea* taxa, as the sole taxon in the cluster in which it is placed. The *K. erucifolia* and *K. grandifolia* taxa have similar leaf characteristics and were also located in the same sub-cluster owing to their molecular characteristics. *K. bornmuelleri* taxon does not have a morphologically close relative in the genus. Its position on the dendrogram confirmed this classification. *K. cerinthifolia* is distinguished by its yellow flowers and semiamplexicaul leaf structure and was also molecularly identified to be distinct. All

these findings were consistent with the morphological classifications made in the Flora of Turkey (Davis and Kupicha 1975; Dogan et al. 2012). Martins and Hellwig (2005) showed that *Klasea* and *Serratula* taxa to belong to separate clusters in a molecular study conducted using the ITS and ETS sequences. The same study reported shorter distances on the dendrogram constructed based on molecular similarities for the taxa, which showed morphological similarities.

The inspection of the dendrogram indicated that molecularly similar taxa were also morphologically similar. This separation was also shown in the PCA plot (Figure 3).

Our study has demonstrated that ISSR is a powerful tool in resolving the genetic relationships within problematic taxonomical entities. In conclusion, the morphologically close taxa were, in the molecular aspect, also located in the same clade. The genera used as out-groups (*Serratula*, *Jurinea*, and *Centaurea*) were clearly separate from the genus *Klasea*. According to our knowledge, this is the first report on the use of ISSR in *Klasea*.

Acknowledgements

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A new species of *Symplocos* (Symplocaceae) from southern Ecuador

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Abstract

A new species from Ecuador, *Symplocos limonensis*, is here described and illustrated. It resembles *S. clethrifolia* but differs by having larger leaves with evident (i.e., not concealed) areoles on lower surface, sessile inflorescences, smaller white corollas, and fewer stamens. The species is only known from three collections in the Andean forests of Morona-Santiago Province in southern Ecuador.

Resumen

Se describe e ilustra una nueva especie, *Symplocos limonensis*, de Ecuador. Se parece a *S. clethrifolia* pero se diferencia por tener las hojas más grandes, con las aréolas evidentes (no ocultas) en el envés, las inflorescencias sésiles y las flores más pequeñas, blancas y con menos estambres. La especie solo se conoce de tres ejemplares de los bosques andinos de la provincia de Morona-Santiago en el sur del país.

Keywords

Symplocos, Ecuador, Andes

Introduction

The genus *Symplocos* Jacq. is represented in Ecuador by ca. 33 species (Ståhl 2010a), the majority of which occur in Andean forests at 2500–3500 m elevation (Ståhl 1995). Thirteen of the species are country endemics (Barriga 2011) and have been described in the last 25 years, significantly increasing the knowledge of this still poorly known genus. In his treatment of the Symplocaceae for the Flora of Ecuador series, Ståhl (1991) described several new species of *Symplocos*, especially from southern Ecuador. One of these, *S. clethrifolia* Ståhl, was based on five collections, one of which (*Ulloa* 487) was indicated to deviate from the remaining four in floral and leaf features. This collection was provisionally treated under *S. clethrifolia* until more material could help elucidate its taxonomic status.

Materials and methods

Recent examination of the *Symplocos* collections in Ecuadorian herbaria revealed additional gatherings from the same general area that have led us to conclude that the *Ulloa* collection, along with some new ones, belong to a previously undescribed species, which is described here. Acronyms of the herbaria follow Thiers (2015).

Description of the new species

Symplocos limonensis Ståhl, C. Ulloa & Minga, sp. nov.

urn:lsid:ipni.org:names:77150152-1

Fig. 1

Diagnosis. *Symplocos limonensis* differs from *S. clethrifolia* Ståhl by having larger leaves (up to 13.5 vs. 9.5 cm) with evident (i.e., not concealed) venation areoles abaxially (vs. densely ferruginous-velutinous with matted hairs concealing areoles), sessile inflorescences (vs. pedunculate), somewhat smaller, white (vs. red to pink) corollas, and fewer stamens (40–50 vs. 60–70).

Type: ECUADOR. Morona-Santiago: road Cuenca-Macas (road Gualaceo-Limón East of the pass), 2700–3400 m, 19 Aug 1987, C. *Ulloa* 487 (Holotype: QCA-209874!; isotypes AAU!, GB!, MO-6500819!).

Tree or treelet to 12 m tall; branchlets reddish brown, sparsely villous to glabrescent, apical buds densely long-villous. Leaves alternate, petiolate; blade oblong to widely elliptic, 8–13.5 × 4–9 cm, the blades exceptionally almost circular and ca. 3 × 3 cm, coriaceous, light green and long-villous beneath, olive green and glabrous above, base rounded or truncate, slightly decurrent on petiole, apex rounded to widely obtuse, mucronulate at the tip, margins denticulate, teeth 3–4 mm apart, lateral veins 8–10 per side, midvein, lateral veins, and veinlets on lower side prominently raised and

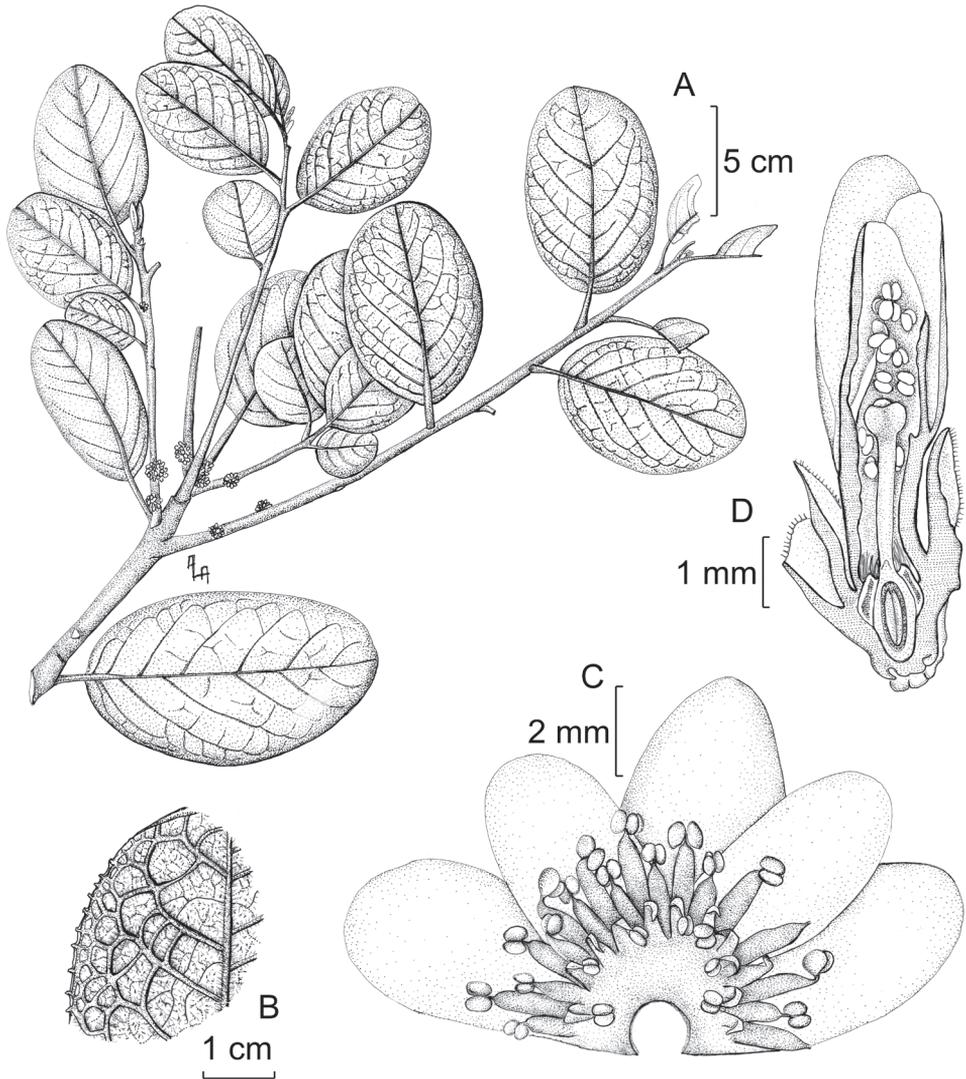


Figure 1. *Symplocos limonensis*. **A** Flowering branch **B** Detail of venation on leaf lower surface **C** Corolla and stamens whorls **D** Young flower in longitudinal section. (**A**, **B** from Jørgensen 92876; **C**, **D** from Ulloa 487). Illustration by A.L. Arbeláez.

verrucose, impressed above; petiole 1–1.5 cm long, rounded and long-villous beneath, flattened and glabrous above. Inflorescences fasciculate, sessile, borne in axils of extant leaves and along branchlets beneath the foliage; flowers 8–10 per inflorescence; bracts 4, very broadly ovate, 2–3 × 2–2.5 mm, strigulose on midvein toward apex, otherwise glabrous, margins ciliate. Flowers with the calyx synsepalous, tube ca. 1.5 mm long, lobes 5, very broadly ovate, 1.5–2.5 × 2.2–2.8 mm, margins ciliate; corolla sympetalous, glabrous, white, 5–6 mm long, lobes 5 to 7, broadly oblong, 1.8–4 mm

wide, margins entire; stamens 40–45 in 3(4) rows, filaments smooth, fused for ca. 2 mm to the corolla tube, those of the inner whorl fused most of their length leaving ca. 0.5 mm of the filaments free, stamens of the outer whorls with free filaments 1–2.8 mm long, more or less flattened and constricted at apex, anthers ca. 0.5 mm long; disc intrastaminal, dome-shaped, densely villous; style ca. 2.5 mm long, glabrous; stigma capitate and irregularly 3-lobed; ovary inferior, 3-locular with 3 or 4 ovules per locule. Mature fruits not seen.

Specimens examined (Paratypes). ECUADOR. **Morona-Santiago:** road Gualaceo-Limón, km 33.3, 03°02'S, 78°35'W, 3010 m, 27 Dec 1990 (fl), *P.M. Jørgensen, C. Ulloa & B. Øllgaard* 92876 (AAU!, QCA!, QCNE!); Collay, Maylas, on road to Limón 03°00.36'S, 78°38.00'W, 3150 m, 14 Jun 2000 (bud), *F. Serrano, D. Minga & A. Verdugo* 1459 (HA!).

Etymology. The name of the species refers to the town of Limón, officially known as General Leonidas Plaza Gutiérrez. The road leading from the Andean town of Gualaceo to Limón, situated at 1400 m altitude on the east Andean slopes, has long been considered an important locality for botanical exploration where many new species have been found.

Distribution and conservation status. The species is known solely from three collections made in disturbed upper Andean forests and scrub páramo on the highest point of the Gualaceo-Limón-Macas road in Morona-Santiago Province of southern Ecuador. The area of occupancy (AOO) of the species is less than 20 km² and falls within the “Área de Conservación Municipal Tinajillas-Río Gualaceño,” a locally managed reserve; however, the category of protection is of lesser status than that of a National Park. Since 2000, we have searched for additional plants but could not locate any, finding only one population of *Symplocos quitensis* Brand (1901: 76), a very different species with a wide Andean distribution. The road was poorly maintained and treacherous until recently, but has now been considerably widened in the process of being paved, and consequently the natural vegetation alongside is heavily destroyed. Ongoing wood extraction for charcoal production, expansion of areas under cultivation, and mining activities for clay, gravel, and metals are threats to the natural habitats in this region. Given current knowledge, we assign a provisional IUCN conservation status of Endangered (IUCN 2014) to this species.

Discussion. *Symplocos limonensis* resembles *S. clethrifolia* Ståhl and *S. golondrinae* Ståhl by having leaves with conspicuous venation, the veins of the lower side being prominent and verrucose and those on the upper side impressed. It differs from *S. clethrifolia*, which also is restricted to southern Ecuador (but from other localities), by having larger leaves (up to 13.5 vs. 9.5 cm) with evident (i.e., not concealed) venation areoles abaxially (vs. densely ferruginous-velutinous with matted hairs concealing areoles), sessile inflorescences (vs. pedunculate), smaller (5–6 vs. c. 8 mm long), white (vs. red to pink) corollas, and fewer stamens (40–50 vs. 60–70). From *S. golondrinae* it differs by the larger size of leaves and flowers, with the leaves being coriaceous (vs. cartilaginous), long-villous abaxially (vs. sparsely strigose) and having longer (1–1.5 vs.

< 1 cm) petioles, and by having a densely villous flower disk (vs. glabrous). Moreover, *S. golondrinae* occurs in northwestern Ecuador, on the opposite side of the Andes.

Symplocos quitensis has been collected in the same area of the new species, but it is readily distinguished from both *S. limonensis* and *S. clethrifolia* by the densely hispid branchlets, smaller (up to 6.5 × 4 cm), membranaceous leaves, and pinkish flowers borne in short racemes.

In the most recent key to Andean *Symplocos* (Ståhl 2010a), *S. limonensis* keys to *S. clethrifolia* (albeit with the inflorescence pedunculate) or to *S. robusta* Ståhl. The latter species is known only from Bolivia and differs from *S. limonensis* in, e.g., its larger (to 14.5 × 8.5 cm), longer-petiolate (to 2 cm) leaves, more numerous flowers (up to 20) per inflorescence, and strigose corollas (vs. glabrous).

Symplocos limonensis has flowers with 5 to 7 petals, but being notoriously unstable in many species of *Symplocos*, and often not studied, the number of petals may show to be of little taxonomic significance.

In the key to infrageneric taxa of the genus (Fritsch et al. 2008), *Symplocos limonensis* falls into the tropical American clade *Symplocos* subg. *Symplocos* sect. *Symplocos* having exerted, monodelphous stamens adnate to the corolla beyond its base, and the filaments flattened and constricted apically.

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SIFlore, a dataset of geographical distribution of vascular plants covering five centuries of knowledge in France: Results of a collaborative project coordinated by the Federation of the National Botanical Conservatories

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Abstract

More than 20 years ago, the French Muséum National d'Histoire Naturelle¹ (MNHN, Secretariat of the Fauna and Flora) published the first part of an atlas of the flora of France at a 20km spatial resolution, accounting for 645 taxa (Dupont 1990). Since then, at the national level, there has not been any work on this scale relating to flora distribution, despite the obvious need for a better understanding. In 2011, in response to this need, the Federation des Conservatoires Botaniques Nationaux² (FCBN, <http://www.fcbn.fr>) launched an ambitious collaborative project involving eleven national botanical conservatories of France. The project aims to establish a formal procedure and standardized system for data hosting, aggregation and publication for four areas: flora, fungi, vegetation and habitats. In 2014, the first phase of the project led to the development of the national flora dataset: SIFlore. As it includes about 21 million records of flora occurrences, this is currently the most comprehensive dataset on the distribution of vascular plants (Tracheophyta) in the French territory. SIFlore contains information for about 15'454 plant taxa occurrences (indigenous and alien taxa) in metropolitan France and Reunion Island, from 1545 until 2014. The data records were originally collated from inventories, checklists, literature and herbarium records. SIFlore was developed by assembling flora datasets from the regional to the national level. At the regional level, source records are managed by the national botanical conservatories that are responsible for flora data collection and validation.

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In order to present our results, a geoportal was developed by the Fédération des conservatoires botaniques nationaux that allows the SIFlore dataset to be publically viewed. This portal is available at: <http://siflore.fcbn.fr>. As the FCBN belongs to the Information System for Nature and Landscapes' (SINP), a governmental program, the dataset is also accessible through the websites of the National Inventory of Natural Heritage (<http://www.inpn.fr>) and the Global Biodiversity Information Facility (<http://www.gbif.fr>). SIFlore is regularly updated with additional data records. It is also planned to expand the scope of the dataset to include information about taxon biology, phenology, ecology, chorology, frequency, conservation status and seed banks.

A map showing an estimation of the dataset completeness (based on Jackknife 1 estimator) is presented and included as a numerical appendix.

Purpose:

SIFlore aims to make the data of the flora of France available at the national level for conservation, policy management and scientific research. Such a dataset will provide enough information to allow for macroecological reviews of species distribution patterns and, coupled with climatic or topographic datasets, the identification of determinants of these patterns. This dataset can be considered as the primary indicator of the current state of knowledge of flora distribution across France. At a policy level, and in the context of global warming, this should promote the adoption of new measures aiming to improve and intensify flora conservation and surveys.

Keywords

Metropolitan France, La Reunion Island, Plantae, Tracheophyta, FCBN, CBN

Data published through

FCBN: <http://www.siflore.fcbn.fr>

Introduction**Taxonomic coverage**

Note: The taxonomic and nomenclatural reference for the first edition of the SIFlore dataset is the fifth edition of the taxonomic repository for the fauna, flora and fungi of metropolitan France and overseas territories, TAXREF, which was developed within the framework of a convention between the French ministry of ecology, the MNHN, the FCBN and Tela Botanica. The overall methodological framework at the basis of the TAXREF repository is presented in Gargominy et al. (2014).

The version originally used for data aggregation is TAXREF v5.0, posted online on July 20th, 2012.

At the time of writing, the current version of TAXREF was v8.0, posted online on December 1st, 2014. Data is available in the taxonomic and nomenclatural reference TAXREF v5.0 on the <http://siflore.fcbn.fr> web atlas. For practical reasons, data has

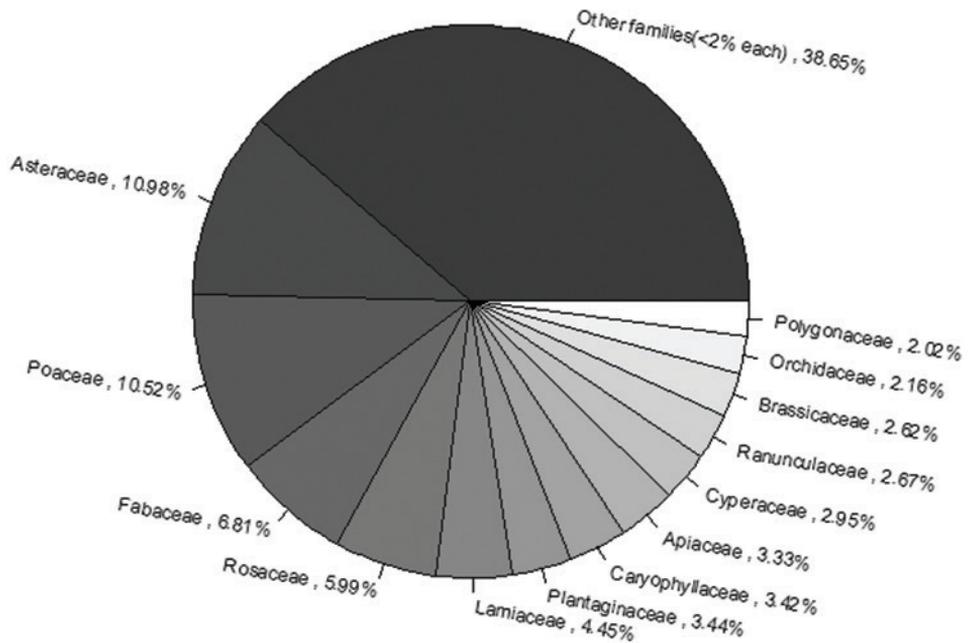


Figure 1. Distribution of the dataset by family.

been automatically linked to TAXREF v8.0 on the GBIF website, which may generate some taxonomic errors. This work was carried out under the responsibility of the Service du patrimoine naturel (SPN/MNHN). In order to prevent any error of interpretation, amended taxa were tagged in the Darwin core archive within the field *datageneralization* as follows: “taxon initially attached to the Taxonomic repository TAXREF v5. This taxon has undergone changes since”.

It has to be noted that the taxonomic coverage of La Reunion Island was incomplete in this 1st version of SIFlore dataset as TAXREF v5.0 did not include most of La Reunion Island taxa. This issue was addressed in TAXREF v7, and subsequent versions, with the integration of the “Index des Trachéophytes de La Réunion (ITR, Boulet & al, 2012)”. Consequently, SIFlore completeness will be improved in the near future by including more taxa originating from La Réunion.

General taxonomic coverage description: The taxonomic coverage of this dataset spans the phylum Tracheophyta (vascular plants) present in metropolitan France (excluding the departments of Alsace and Lorraine) and La Reunion Island. Taxa are first identified at the species level and, if appropriate, subspecies level. The largest number of data records belong to the Asteraceae family (2,317,247 records), followed by Poaceae (2,220,479 records), Fabaceae (1,436,758 records) and Rosaceae (1,264,321 records). The families with the least number of records are Escalloniaceae, Malpighiaceae and Schizaeaceae with one data record each (Figure 1).

Taxonomic ranks

Kingdom: Plantae

Phylum: Tracheophyta

Class: Equisetopsida

Order: Acorales, Alismatales, Apiales, Aquifoliales, Araucariales, Arecales, Asparagales, Asterales, Boraginales, Brassicales, Buxales, Caryophyllales, Celastrales, Ceratophyllales, Commelinales, Cornales, Crossosomatales, Cucurbitales, Cupressales, Dioscoreales, Dipsacales, Ephedrales, Equisetales, Ericales, Escalloniales, Fabales, Fagales, Garryales, Gentianales, Geraniales, Ginkgoales, Gunnerales, Hymenophyllales, Isoetales, Lamiales, Laurales, Liliales, Lycopodiales, Magnoliales, Malpighiales, Malvales, Myrtales, Nymphaeales, Ophioglossales, Osmundales, Oxalidales, Pandanales, Pinales, Piperales, Poales, Polypodiales, Proteales, Psilotales, Ranunculales, Rosales, Salviniaceae, Santalales, Sapindales, Saxifragales, Schizaceae, Selaginellales, Solanales, Vitales, Zingiberales, Zygophyllales

Family: Acanthaceae, Acoraceae, Actinidiaceae, Adoxaceae, Aizoaceae, Alismataceae, Altingiaceae, Amaranthaceae, Amaryllidaceae, Anacardiaceae, Annonaceae, Apiaceae, Apocynaceae, Aponogetonaceae, Aquifoliaceae, Araceae, Araliaceae, Araucariaceae, Arecaceae, Aristolochiaceae, Asparagaceae, Aspleniaceae, Asteraceae, Balsaminaceae, Basellaceae, Begoniaceae, Berberidaceae, Betulaceae, Bignoniaceae, Blechnaceae, Boraginaceae, Brassicaceae, Bromeliaceae, Butomaceae, Buxaceae, Cabombaceae, Cactaceae, Campanulaceae, Cannabaceae, Cannaceae, Capparaceae, Caprifoliaceae, Caricaceae, Caryophyllaceae, Casuarinaceae, Celastraceae, Ceratophyllaceae, Cistaceae, Cleomaceae, Clusiaceae, Colchicaceae, Combretaceae, Commelinaceae, Convolvulaceae, Coriariaceae, Cornaceae, Crassulaceae, Cucurbitaceae, Cunoniaceae, Cupressaceae, Cymodoceaceae, Cyperaceae, Cytinaceae, Dennstaedtiaceae, Dioscoreaceae, Droseraceae, Dryopteridaceae, Ebenaceae, Elaeagnaceae, Elatinaceae, Ephedraceae, Equisetaceae, Ericaceae, Escalloniaceae, Euphorbiaceae, Fabaceae, Fagaceae, Frankeniaceae, Garryaceae, Gentianaceae, Geraniaceae, Gesneriaceae, Ginkgoaceae, Goodeniaceae, Grossulariaceae, Gunneraceae, Haloragaceae, Heliconiaceae, Hydrangeaceae, Hydrocharitaceae, Hymenophyllaceae, Hypericaceae, Hypoxidaceae, Iridaceae, Isoetaceae, Juglandaceae, Juncaceae, Juncaginaceae, Lamiaceae, Lardizabalaceae, Lauraceae, Lecythidaceae, Lentibulariaceae, Liliaceae, Linaceae, Linderniaceae, Lycopodiaceae, Lythraceae, Magnoliaceae, Malpighiaceae, Malvaceae, Marantaceae, Marsileaceae, Martyniaceae, Melanthiaceae, Melastomataceae, Meliaceae, Menispermaceae, Menyanthaceae, Molluginaceae, Moraceae, Moringaceae, Musaceae, Myricaceae, Myrtaceae, Nartheciaceae, Nelumbonaceae, Nephrolepidaceae, Nitrariaceae, Nyctaginaceae, Nymphaeaceae, Oleaceae, Onagraceae, Ophioglossaceae, Orchidaceae, Orobanchaceae, Osmundaceae, Oxalidaceae, Paeoniaceae, Pandanaceae, Papaveraceae, Passifloraceae, Paulowniaceae, Phrymaceae, Phyllanthaceae, Phytolaccaceae, Pinaceae, Piperaceae, Pittosporaceae, Plantaginaceae, Platanaceae, Plumbaginaceae, Poaceae, Polemoniaceae, Polygalaceae, Polygonaceae, Polypodiaceae, Pontederiaceae, Portulacaceae, Posidoniaceae, Pota-

mogetonaceae, Primulaceae, Proteaceae, Psilotaceae, Pteridaceae, Ranunculaceae, Resedaceae, Rhamnaceae, Rosaceae, Rubiaceae, Ruppiaceae, Rutaceae, Salicaceae, Salviniaceae, Santalaceae, Sapindaceae, Sapotaceae, Sarraceniaceae, Saxifragaceae, Scheuchzeriaceae, Schizaeaceae, Scrophulariaceae, Selaginellaceae, Simaroubaceae, Smilacaceae, Solanaceae, Staphyleaceae, Strelitziaceae, Styracaceae, Tamaricaceae, Taxaceae, Theaceae, Thelypteridaceae, Thymelaeaceae, Tofieldiaceae, Tropaeolaceae, Typhaceae, Ulmaceae, Urticaceae, Verbenaceae, Violaceae, Vitaceae, Woodsiaceae, Xanthorrhoeaceae, Zingiberaceae, Zosteraceae, Zygothallaceae

Spatial coverage

General geographic description

This national dataset collates species occurrences from metropolitan France and Reunion Island. Four different climates are covered in the metropolitan area: oceanic, continental, mediterranean and alpine. Reunion Island is an overseas department and region of France, located in the southwest Indian Ocean, in the Mascareignes archipelago, to the east of Madagascar. The island has a tropical climate.

The records documented in the dataset are distributed across 21 (out of a total of 27) administrative regions of France: Aquitaine, Auvergne, Bourgogne, Bretagne, Centre, Champagne-Ardenne, Corse, Franche-Comté, Ile-de-France, Languedoc-Roussillon, Limousin, Midi-Pyrénées, Nord-Pas-de-Calais, Basse-Normandie, Haute-Normandie, Pays de la Loire, Picardie, Poitou-Charentes, Provence-Alpes-Côte d'Azur, La Réunion, Rhône-Alpes.

This geographical zone is characterized by a large range in altitude, from 0 to 4,810 m above sea level, and extends over an area of 516,499 km² representing 74% of Metropolitan France, its overseas departments and other territories.

Geographical method

Reference grids

In France, the Muséum National d'Histoire Naturelle (MNHN) recommends the use of standardized grids for species distribution maps. The grid reference of MNHN is defined according to the French official map projection systems: Lambert 93 in Metropolitan France (grid name "L93_10X10") and UTM 40 S in La Reunion Island (grid name "grille_10km_ZEE_974").

Lambert-93 (EPSG 2154) is a Lambert conic projection using RGF93 geodetic system (compatible with WGS84) and defined by two reference parallels: 44°N and 49°N. The central meridian, 3°E, is the Greenwich meridian and the latitude of origin is 46°30'N. Prime coordinates are 700,000 meters and 6,600,000 meters.

The Universal Transverse Mercator Projection 40 South (UTM 40S) is an adaptation of the standard Mercator projection. This is a cylindrical and conformal projection using RGR92 geodetic system (compatible with WGS84). The central meridian is 57°E and the latitude of origin is 0. Prime coordinates are 500,000 meters and 10,000,000 meters.

Grids are composed of cells of 10 km by 10 km. Continental and maritime metropolitan France (954, 500 sq.km) is divided into 9546 cells and La Reunion Island terrestrial area (2, 512 sq.km) is divided into 34 cells (information on maritime area is not given as it is disproportionate in relation to terrestrial one).

All SIFlore records are georeferenced through the code of the corresponding grid square.

French municipalities repository: The official geographic boundaries of the municipalities and associated data (BD CARTO®) were provided by the National Geographic Institute (IGN) based on the National Institute of Statistics and Economic Studies (Insee) database. Each municipality is referenced by an official geographic code (code Insee) and its name. The records in SIFlore are georeferenced through the code of the corresponding municipality.

The BD CARTO® version originally used for data aggregation was published in 2011.

The current version is BD CARTO® 3.1 which was revised in 2013.

Coordinates

Metropolitan France : 40°0'0"N – 52°0'0"N Latitude; 07°0'0"W – 12°0'0"W Longitude.

La Reunion Island : 20°52'0"S – 21°24'0"S Latitude; 55°10'0"E – 55°50'0"E Longitude.

Temporal coverage

The oldest record in the dataset is from the year 1545 and the most recent records are from 2014. Most records (69.6%) were obtained after 2000 (Figure 2).

Records for which the date of collection is unknown are registered with the year 1500.

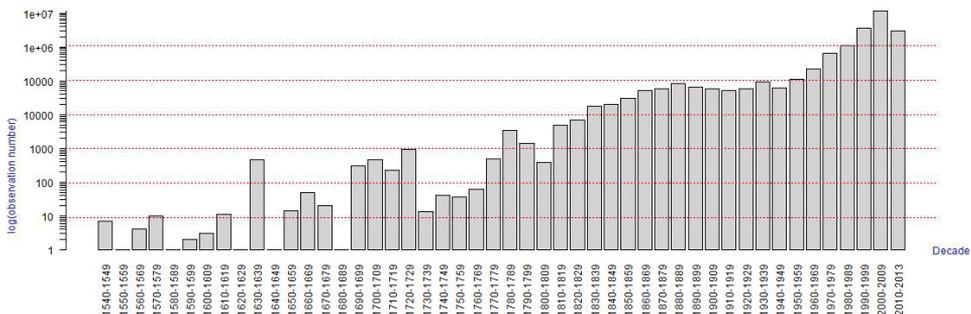


Figure 2. Temporal distribution of records by decade (shown on logarithmic scale).

Project description

Title: «*A dataset on vascular plant distribution covering five centuries of knowledge in France: Results of a collaborative project coordinated by the Federation of the National Botanical Conservatories*» is the outcome of a collaboration between 11 Conservatoires botaniques nationaux (CBN) and their Federation (FCBN): (a) Conservatoire Botanique National Alpin, Domaine de Charance 05000 Gap, France (b) Conservatoire Botanique National de Bailleul, Hameau des Haendries 59270 Bailleul, France (c) Conservatoire Botanique National du Bassin Parisien, Muséum national d'Histoire naturelle, 61, rue Buffon 75005 Paris, France (d) Conservatoire National Botanique de Brest, 52, allée du Bot 29200 Brest, France (e) Conservatoire National Botanique de Corse, Office de l'environnement de la Corse, 14, avenue Jean Nicoli 20250 Corte, France (f) Conservatoire Botanique National de Franche-Comté, Maison de l'environnement de Franche-Comté, 7, rue Voirin

25000 Besançon, France (g) Conservatoire Botanique National de Mascarin, 2, rue du Père Georges

Les colimaçons 97436 Saint-Leu, Ile-de-La-Réunion, France (h) Conservatoire Botanique National du Massif Central, Le Bourg 43230 Chavaniac-Lafayette, France (i) Conservatoire Botanique National méditerranéen de Porquerolles, 34, avenue Gambetta 83400 Hyères, France (j) Conservatoire Botanique National des Pyrénées et de Midi Pyrénées, Vallon de Salut - BP 315- 65203 Bagnères-de-Bigorre Cedex, France (k) Conservatoire Botanique National Sud-Atlantique, Domaine de Certes Graveyron 33980 Audenge, France

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French Ministry of Ecology and the network of the CBN

Methods

Data collection

Primary data are collected by both professional (from CBN and other organisations) and volunteer. As data originate from various sources (field inventories, scientific literature and herbaria), this task involves different trades such as botanists and archivists. Data are entered into CBN databases and then follow a validation process. To insure dataset homogeneity, data records are extracted from CBN databases and provided to the national system in a simplified format that is compatible with the SINP format (edited by MNHN). This format is also based on the Data Specification on Species distribution, produced by the INSPIRE Thematic Working Group *Species distribution* (<http://inspire.ec.europa.eu/>).

For each observation, key variables are recorded, such as a unique code for the record, valid scientific name of the taxon and its identifier in the French national taxonomic repository (TAXREF). Additional details including observation and data transmission dates, the collector name, the source basis of record name and geospatial information, including municipality name and code, and the square code of the national grid, are also provided. The grid system used for species inventories in France is defined by the Muséum National d'Histoire Naturelle: this is a grid composed of cells of 10km by 10km. Information about municipalities are collected from the Insee national repository. When available, additional information is collected such as bibliographic and herbarium references or primary source of the data record.

The evolution of the dataset is described in the Database history section.

Once standardized, data are checked for consistency before being incorporated into the Postgres/Postgis national database by using Talend Open Studio for Data Integration. At the end of the process, data are posted on the FCBN geoportal.

Sampling description: Most records originate from field inventories (88.7%), with other records identified in scientific literature (11%) and in herbaria (0.2%). The protocols for collection vary over time and between collection sites, but also in response to other projects launched. However, in this first version, SIFlore does not include information on the data collection procedures. It is expected that a simplified description of the different protocols used by each CBN will be provided in the near future.

Nevertheless, according to Vallet et al. (2012), it is possible to assess survey completeness of regional floristic inventories despite heterogeneous sources and protocols, through the use of the Jackknife 1, a non-parametric estimator. This estimator

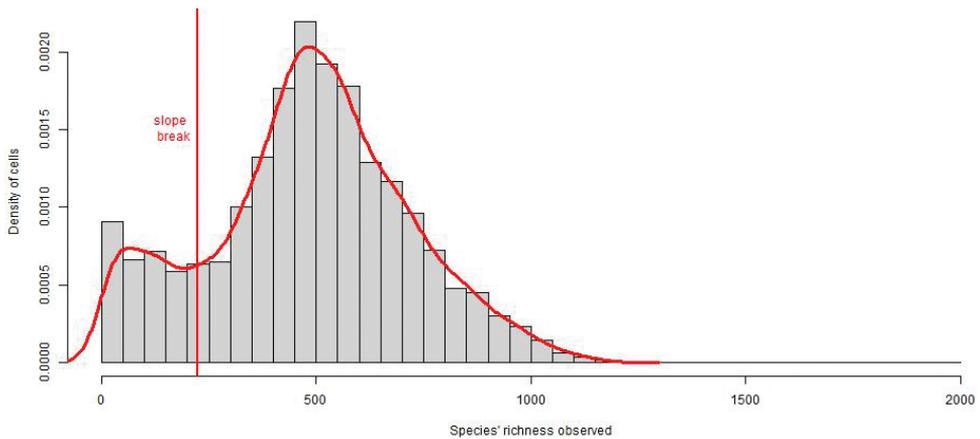


Figure 3. Density of cells by richness of observed species: looking at the distribution within the dataset, it appears that cells with less than 250 distinct species recorded are over-represented.

was calculated for each 10km by 10km cell of the French map, aiming to mitigate sampling bias as effectively as possible. Thus, occurrences were all generalized to the rank of species (including all infraspecies into this one rank) and only recent data were taken in account (from 1990). Cells with less than 250 species were excluded from the analyses, as they were considered as undersampled and therefore over represented (Figure 3). The resulting map (Figure 4) should allow users to interpret their results appropriately.

It has to be noted that the completeness of La Reunion Island survey could not be assured in this work. Indeed, as mentioned above, in 2012, at the time of working on the 1st version of SIFlore, there had been a lack of La Reunion taxa in the French national taxonomic referential for fauna, flora and fungi, TAXREF V5. As the analysis only takes into account the species which correspond across the two taxonomic guidelines (ITR and TAXREF v5), all of the La Reunion cells had been undersampled, according to Jackknife calculation requirements.

Quality control description: Quality control is implemented at different levels, under different responsibilities, throughout the data collection and validation process. Following digitalization, the dataset is first checked by regional data administrators, in order to ensure compliance with the survey protocols. The records are individually reviewed according to specified criteria, including the accuracy of the scientific name and the correctness of the geographical position entered, according to known chorology.

At the national level, a second step is carried out to ensure conformity of the data to the national standards, before compilation. Non-compliant data are rejected and an audit report is sent to the data provider. FCBN is currently working on an additional quality control step in order to ensure global coherence and to provide a relevance score for the distribution map of each species.

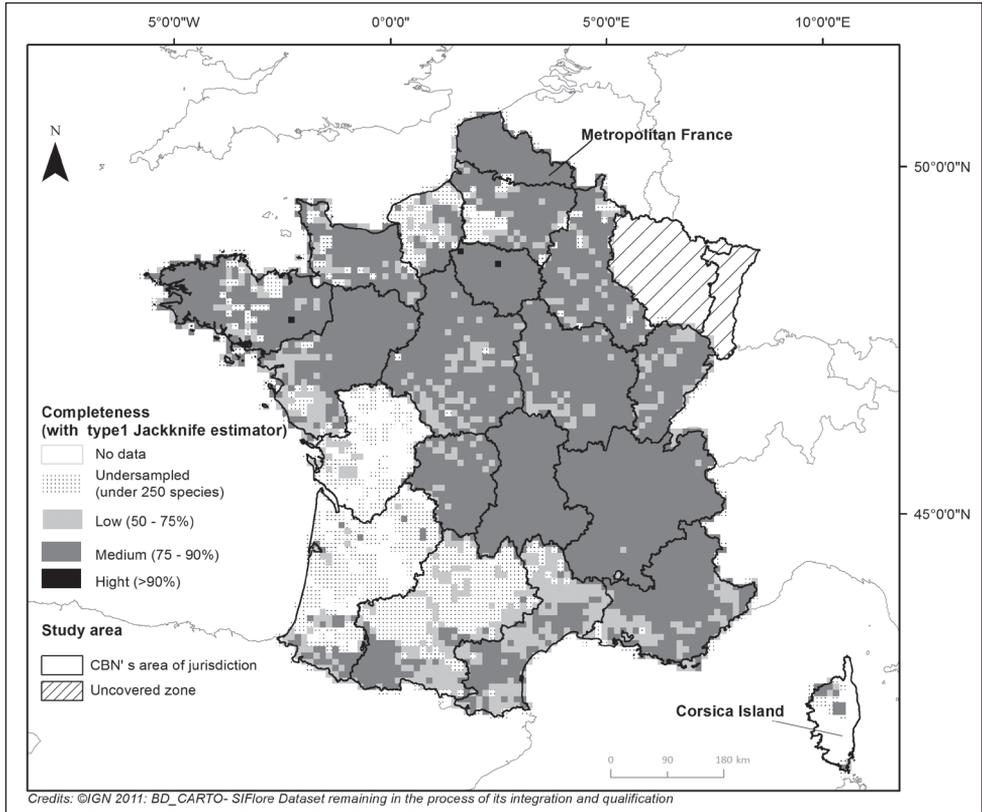


Figure 4. Dataset completeness for Metropolitan France according to the Jackknife 1 estimator (data from 1990 to 2013). The number of records in each cell was used as an estimator of the sampling effort. The ratio between the observed and estimated richness of species measures the completeness of inventory in each surveyed cell (Vallet et al. 2012).

Dataset

Dataset history

In 1975, the Botanical Conservatory of Brest was created, with the support of the Ministry of Environment. This was the first establishment in the world entirely devoted to flora conservation. In 1988, the label “conservatoire botanique national” was legally recognized in France. There are currently eleven national botanical conservatories (CBN) in France.

As they are mandated to share their expertise to the national and local authorities, CBN have built knowledge databases in which information is structured to allow data sharing.

CBN have operational and managerial autonomy. Consequently, their databases differ in terms of structural design and the information contained. Nevertheless, there is an urgent need to provide information on flora distribution at the national level

and, in particular, to define more clearly the flora conservation priorities. Furthermore, FCBN is involved in establishing the IUCN Red List of Threatened Flora at the national level, and in evaluating the conservation status of natural habitats and wild flora, according to the *Council Directive 92/43/EEC of 21 May 1992 on the conservation of natural habitats and of wild fauna and flora*. For these reasons, it was decided to pool all CBN flora records and also to apply a subsidiarity relationship between the FCBN and CBN. This means that data must only be handled by national botanical conservatories, and that the federation may only facilitate networking and ensure data aggregation and management, without altering the records in any way.

In 2010, a working group was created to implement this project. It includes botanists and data managers from across the CBN, and project facilitators. Due to the heterogeneity of the CBN databases, data cannot easily and quickly be aggregated unless determining a database exchange standard. As such, a standardized format was proposed and, in 2011, 10 taxa were selected for a first trial run. Based on this pilot, the data standard was refined. In January 2013, the flora regional dataset aggregation was officially launched. Data were transmitted through various channels under the scenarios prepared by the working group. Data were then compiled and integrated into a Postgresql/Postgis database using an extract, transform and load system (ETL). In May 2013, 18 million data records were aggregated. In January 2014, an additional 3 million records were integrated. Meanwhile, a geoportal was developed to respond to the needs of the CBN and their partners for improving their understanding of flora distribution, as well as allowing the CBN to share its expertise with the public. The portal was finally published on the FCBN's website in February 2014.

Dataset description

The SIFlore dataset is a custom-made SQL view of the global database hosted by the FCBN. Only tracheophyta data are shown. In the current version of the database, the key information provided for each record includes: unique identifier of the data record in SIFlore, identifier that points to the data in the original database file, source institution and database identifier, scientific name, valid identifier in the French national taxonomic referential (TAXREF), taxon rank, location of sighting (grid cell and municipality code), date that the flora was sighted and name of the data collector.

Dataset preview

Object name: SIFlore, a dataset of geographical distribution of vascular plants covering five centuries of knowledge in France: Results of a collaborative project coordinated by the Federation of the National Botanical Conservatories

Character encoding: UTF-8

Format name: Darwin Core Archive Format

Format version: 1.0

Distribution: <http://www.gbif.org/dataset/75956ee6-1a2b-4fa3-b3e8-ccda64ce6c2d>

Publication date of data: 2014-02-10

Language: French

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Metadata language: English

Date of metadata creation: 2014-06-26

Hierarchy level: Dataset

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Supplementary material I

Numerical appendix

Authors: Anaïs Just, Johan Gourvil, Jérôme Millet, Vincent Boulet, Thomas Milon, Isabelle Mandon, Bruno Dutrève

Data type: dataset

Explanation note: A shapefile representing the dataset completeness (based on the Jack-knife 1, a non-parametric estimator) on a grid of 10 km by 10 km cells. The number of records in each cell was used as an estimator of the sampling effort. The ratio between the observed and estimated richness of species measures the completeness of the inventory in each surveyed cell (Vallet et al. 2012).

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Dataset of MIGRAME Project (Global Change, Altitudinal Range Shift and Colonization of Degraded Habitats in Mediterranean Mountains)

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Resource citation: iEcolab, University of Granada-Andalusian Institute for Earth System Research (2015) Dataset of Global Change, altitudinal range shift and colonization of degraded habitats in Mediterranean mountains (MIGRAME). 3839 data records. Contributed by University of Granada, OBSNEV, Pérez-Luque AJ, Navarro-González I, Zamora R, Benito BM, Pérez-Pérez R, Bonet FJ, Matías L, Ruiz-Puche R, Suzart F, Moreno-Llorca R, Rodríguez-Infante J. Online at <http://www.gbif.es/ipt/resource.do?r=migrame> and <http://obsnev.es/noticia.html?id=7841>, version 1.0 (last updated on 2015-05-13). Resource ID: GBIF Key: <http://www.gbif.org/dataset/6c6a9003-ecea-4f3a-9f2f-414107da65c1>

Abstract

In this data paper, we describe the dataset of the Global Change, Altitudinal Range Shift and Colonization of Degraded Habitats in Mediterranean Mountains (MIGRAME) project, which aims to assess the capacity of altitudinal migration and colonization of marginal habitats by *Quercus pyrenaica* Willd. for-

ests in Sierra Nevada (southern Spain) considering two global-change drivers: temperature increase and land-use changes. The dataset includes information of the forest structure (diameter size, tree height, and abundance) of the *Quercus pyrenaica* ecosystem in Sierra Nevada obtained from 199 transects sampled at the treeline ecotone, mature forest, and marginal habitats (abandoned cropland and pine plantations). A total of 3839 occurrence records were collected and 5751 measurements recorded. The dataset is included in the Sierra Nevada Global-Change Observatory (OBSNEV), a long-term research project designed to compile socio-ecological information on the major ecosystem types in order to identify the impacts of global change in this mountain range.

Keywords

Quercus pyrenaica forests, altitudinal migration, colonization of abandoned croplands, global change, Sierra Nevada (Spain), occurrence data, measurement data

Project details

Project title

Global Change, altitudinal range shift and colonization of degraded habitats in Mediterranean mountains (MIGRAME)

Personnel

Regino Jesús Zamora Rodríguez (Principal Investigator, University of Granada)

Funding

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Rationale

Currently, there is strong scientific evidence of the effects of global change on natural systems (Parmesan 2006, Rosenzweig et al. 2008, García et al. 2014, O'Connor et al. 2015). Some ecological processes are being altered due to the changing climate, such as species distribution (Thuiller et al. 2005, Lenoir et al. 2008), phenology (Parmesan and Yohe 2003, Gordo and Sanz 2010, Wolkovich et al. 2014), ecological interactions (Hughes 2000, Suttle et al. 2007); among others. Land-use changes and climate change are the most important drivers of biodiversity shifts (Sala et al. 2000).

One of the most obvious biotic responses from global warming are the latitudinal and altitudinal shifts of species and communities (Allen and Breshears 1998, Jump and Peñuelas 2005, Lenoir et al. 2008). Species tend to expand into new areas that are becoming favourable, and retract from those that turn hostile. In consideration of two main drivers of global change (climatic warming and land abandonment), an understanding of the dynamics of altitudinal migration and colonization of marginal habitats is critical in order to develop effective forest-management strategies.

The project Global Change, altitudinal range shift, and colonization of degraded habitats in Mediterranean mountains (MIGRAME) was designed to assess the capacity of altitudinal migration and colonization of marginal habitats by a Mediterranean forest ecosystem (Zamora et al. 2013, Benito et al. 2013). This assessment considers two global change drivers: temperature increase and land-use changes. In so doing, this project analyzes the pattern of altitudinal migration and colonization of marginal habitats by a vulnerable ecosystem in a Mediterranean mountain region, which represents the rear edge of their distribution: forests of *Quercus pyrenaica* Willd.

The Mediterranean region has shown broad climate shifts in the past (Luterbacher et al. 2006) and is potentially vulnerable to forthcoming climatic changes (Pacifci et al. 2015), being considered a key region in future climate-change projections (Giorgi 2006, Giorgi and Lionello 2008). Concomitantly, land-use changes are considered a major driver of vegetation change (McGill 2015). This is especially relevant in Mediterranean region, which has undergone intense anthropic activities for millennia (Pardilla et al. 2010) shaping the current landscape (Valbuena-Carabaña et al. 2010).

In this context, Mediterranean ecosystems are considered natural laboratories in which to study global change, due to their high sensitivity to global-change drivers (Matesanz and Valladares 2014, Doblas-Miranda et al. 2015).

Study area descriptions/descriptor

The target ecosystem of the project encompasses the Pyrenean oak forests (*Quercus pyrenaica* Willd.) of Sierra Nevada.

Sierra Nevada is a high-mountain range located in southern Spain (37°N, 3°W) with altitudes of between 860 m and 3482 m a.s.l. The climate is Mediterranean, characterized by cold winters and hot summers, with pronounced summer drought (July-August). The Sierra Nevada mountain range hosts a high number of endemic plant species (c. 80) (Lorite et al. 2007) for a total of 2,100 species of vascular plants (25% and 20% of Spanish and European flora, respectively), and thus it is considered one of the most important biodiversity hotspots in the Mediterranean region (Blanca et al. 1998). This mountain area has 27 habitat types (listed in the European Union Habitat Directive) harbouring 31 animal species (20 birds, 5 mammals, 4 invertebrates, 2 amphibians and reptiles) and 20 plant species listed in the Annex I and II of EU Habitat and Bird Directives. Sierra Nevada has several types of legal protection:

Biosphere Reserve MAB Committee UNESCO; Special Protection Area and Site of Community Importance (Natura 2000 network); and National Park. There are 61 municipalities with more than 90,000 inhabitants. The main economic activities are agriculture, tourism, beekeeping, mining, and skiing (Bonet et al. 2010).

For a description of the Pyrenean oak forests in Sierra Nevada, see *Study extent description* section.

Design description

The specific aims of the MIGRAME project are:

- To analyse the relevance of altitudinal migration at the leading edge (high elevation) of the range distribution of Pyrenean oak formation.
- To analyse the importance of the recolonization process of marginal habitats (abandoned croplands and pine plantations) close to Pyrenean oak formation.

Derived from the two global-change drivers, we have considered two main hypothesis (Figure 1):

Altitudinal migration hypothesis

Several studies have pointed out a trend towards higher temperatures and lower precipitation for the Mediterranean area (Giorgi and Lionello 2008, García-Ruiz et al. 2011). Climate projections forecast an increase of +4.8 °C at the end of the 21st century (Benito et al. 2011) for Sierra Nevada. In this context, shifts in the altitudinal (and latitudinal) distribution of species and communities are expected (Thuiller et al. 2008, Gottfried et al. 2012).

We hypothesised that the range shift of *Q. pyrenaica* in Sierra Nevada is changing as a consequence of recent changes to temperature, and we would expect an upward expansion (Figure 1a).

Marginal habitat colonization hypothesis

In Mediterranean area, cropland abandonment has been widespread during the second half of the last century (Valbuena-Carabaña et al. 2010, Pías et al. 2014). Land-use change models predict an increase in this trend in the future (Rounsevell et al. 2006). In fact, land abandonment is considered one of the most powerful global-change drivers in developed countries (Escribano-Avila et al. 2012).

We hypothesised that the land-use changes in high mountain (e.g. abandonment of croplands, management of pine plantations) should facilitate the native forest regeneration, and a process of colonization of marginal habitat (abandoned cropland, pine plantations) will occur (Figure 1b).

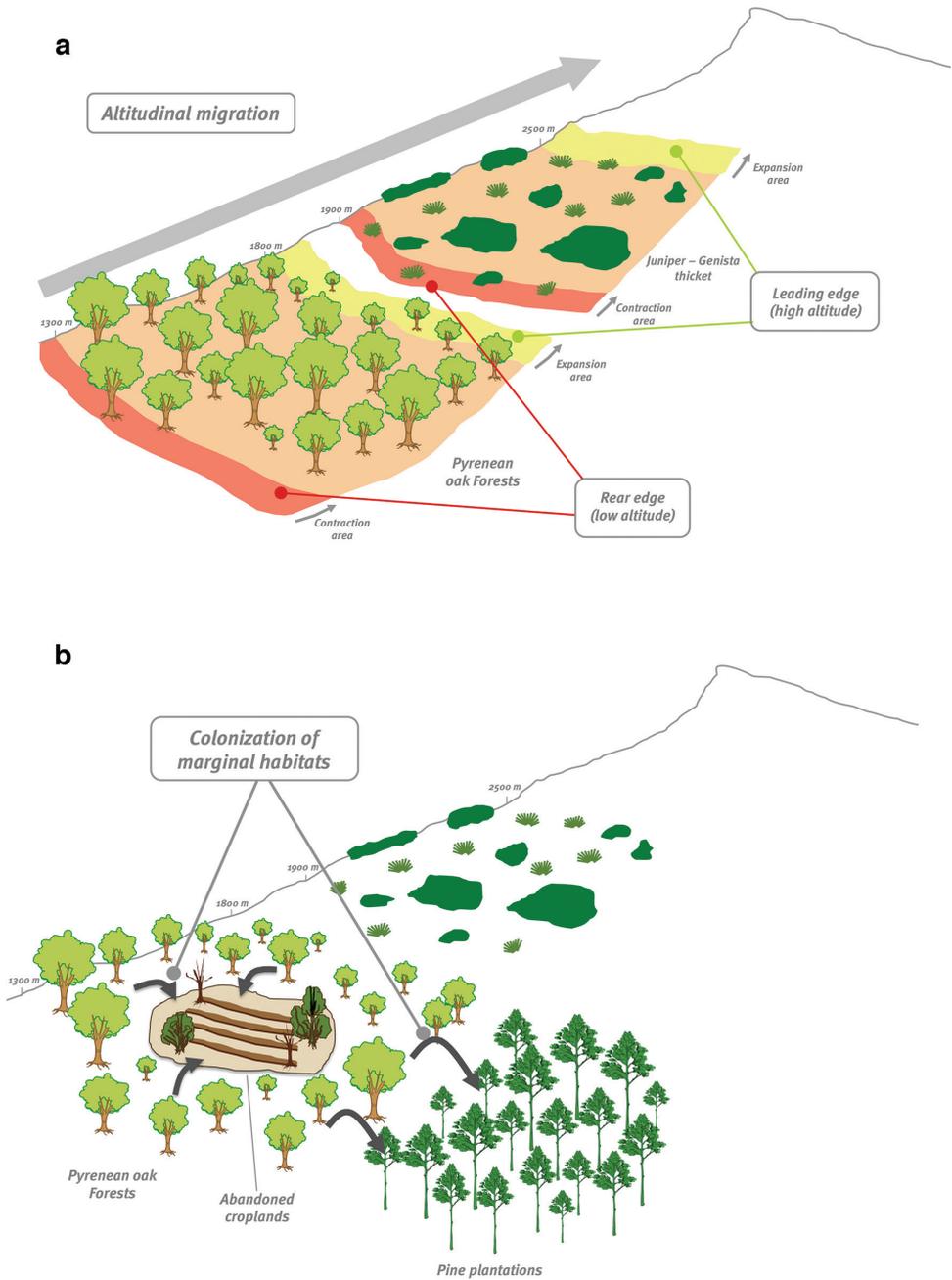


Figure I. Schematic representation of the two main hypothesis of the project: altitudinal migration (a) and colonization of marginal areas (b) of *Q. pyrenaica* forests.

Overall, focusing on changes will occur in altitudinal migration and/or colonization of marginal habitats, we examine the following questions: Are altitudinal changes in Pyrenean oak forests associated with recent climate changes? Are they more consistent with changes in land use, or are they consistent with both global-change drivers?

Data published through GBIF

<http://www.gbif.es/ipt/resource.do?r=migrame>

Taxonomic coverage

This dataset includes records of the phylum Magnoliophyta (3823 records, 99.58%) and marginally Pinophyta (16 records, below 1% of total records). Most of the records included in this dataset belong to the class Magnoliopsida (99.58%). There are 5 orders represented in the dataset, with Fagales (98.98%) being the most important order. The other 4 orders (Rosales, Cupressales, Sapindales and Pinales) represent only 1.02% of the records. In this collection, 5 families are represented: Fagaceae, Rosaceae, Cupressaceae, Pinaceae, and Sapindaceae. The most represented taxa are *Quercus pyrenaica* Willd. and *Quercus ilex* L. (81.74 and 17.24%, respectively). Of the six taxa included on the dataset, three are considered threatened (Table 1).

Taxonomic ranks

Kingdom: Plantae

Phylum: Magnoliophyta, Pinophyta

Class: Magnoliopsida (Dicotyledones), Pinopsida

Table 1. Conservation status and threats of the species included in the dataset.

Scientific Name	Andalusian Red List ¹	IUCN ²	Threat ³
<i>Acer opalus</i> subsp. <i>granatense</i> (Boiss.) Font Quer & Rothm.	NT	VU	1,2,3
<i>Quercus pyrenaica</i> Willd.	NT	LR-cd	1,2,4,5,6
<i>Sorbus aria</i> Wimm.	NT	VU	1,2,3,7

¹ 2005 Red List of vascular flora of Andalusia (Cabezudo et al. 2005). ² IUCN category in Sierra Nevada (Blanca et al. 1998, Blanca et al. 2001, IUCN 2001, Lorite et al. 2007). ³ Threats against the species (Herrera et al. 2000, Prados et al. 2000, Vivero et al. 2000, Marañón et al. 2004, Cabezudo et al. 2005, Gómez-Aparicio et al. 2005, Gómez-Aparicio et al. 2008). 1: regeneration; 2: fire; 3: overgrazing; 4: inappropriate forestry practices; 5: changes in agriculture and agricultural practices; 6: erosion; 7: demography. VU: Vulnerable; NT: Near threatened; LR-nt: LR-cd: Lower Risk-Conservation Dependent.

Order: Fagales, Pinales, Cupressales, Sapindales, Rosales

Family: Fagaceae, Pinaceae, Cupressaceae, Sapindaceae, Rosaceae

Genus: *Quercus*, *Pinus*, *Juniperus*, *Acer*, *Sorbus*

Species: *Quercus pyrenaica*, *Pinus sylvestris*, *Juniperus communis*, *Acer opalus* subsp. *granatense*, *Sorbus aria*, *Quercus ilex*

Spatial coverage

General spatial coverage

Quercus pyrenaica forests

The Pyrenean oak (*Quercus pyrenaica* Willd.) forests extend through south-western France and the Iberian Peninsula (Franco 1990) (Figure 2a) reaching its southern limit in north of Morocco. In the Iberian Peninsula these forests live under meso-submediterranean and mesotemperate areas and subhumid, humid and hyperhumid ombroclimate (Rivas-Martínez et al. 2002) living on siliceous soils, or soils poor in basic ions (Vilches de la Serna 2014). *Q. pyrenaica* requires between 650 and 1200 mm of annual precipitation and a summer minimal precipitation between 100 and 200 mm (Martínez-Parras and Molero-Mesa 1982, García and Jiménez 2009), summer rainfall being a key factor in the distribution of the species (Gavilán et al. 2007, Río et al. 2007).

The forests dominated by *Q. pyrenaica* constitute an ecosystem included in the Annex I of the Habitat Directive (habitat code 9230: *Quercus pyrenaica* oak woods and *Quercus robur* and *Quercus pyrenaica* oak woods from Iberian northwestern). The conservation status of this habitat is not well known (EIONET 2014), partly due to lack of detailed ecological studies (García and Jiménez 2009).

This species reaches its southernmost European limit at Sierra Nevada mountains, where eight oak patches (2400 Has) have been identified (Figure 2b), ranging between 1100 and 2000 m a.s.l. and generally associated to major river valleys. Sierra Nevada is considered a glacial refugia for deciduous *Quercus* species during glaciation (Brewer et al. 2002, Olalde et al. 2002, Rodríguez-Sánchez et al. 2010) and these populations are considered as a rear edge of the habitat distribution, which is important in determining habitat responses to expected climate change (Hampe and Petit 2005).

These forests, like other vegetation types, have undergone intense human pressure (wood cutting, grazing, etc.) which has reduced their distribution area and in some cases has altered their floristic pattern (Gavilán et al. 2000, Gavilán et al. 2007).

Q. pyrenaica is considered as vulnerable in southern Spain (Vivero et al. 2000). The populations of Pyrenean oak forests at Sierra Nevada are considered relict forests (Melendo and Valle 2000, Vivero et al. 2000), undergoing intensive anthropic use in the last few decades (Camacho-Olmedo et al. 2002, Valbuena-Carabaña et al. 2010). The relict presence of this species in Sierra Nevada is related both to its genetic resil-

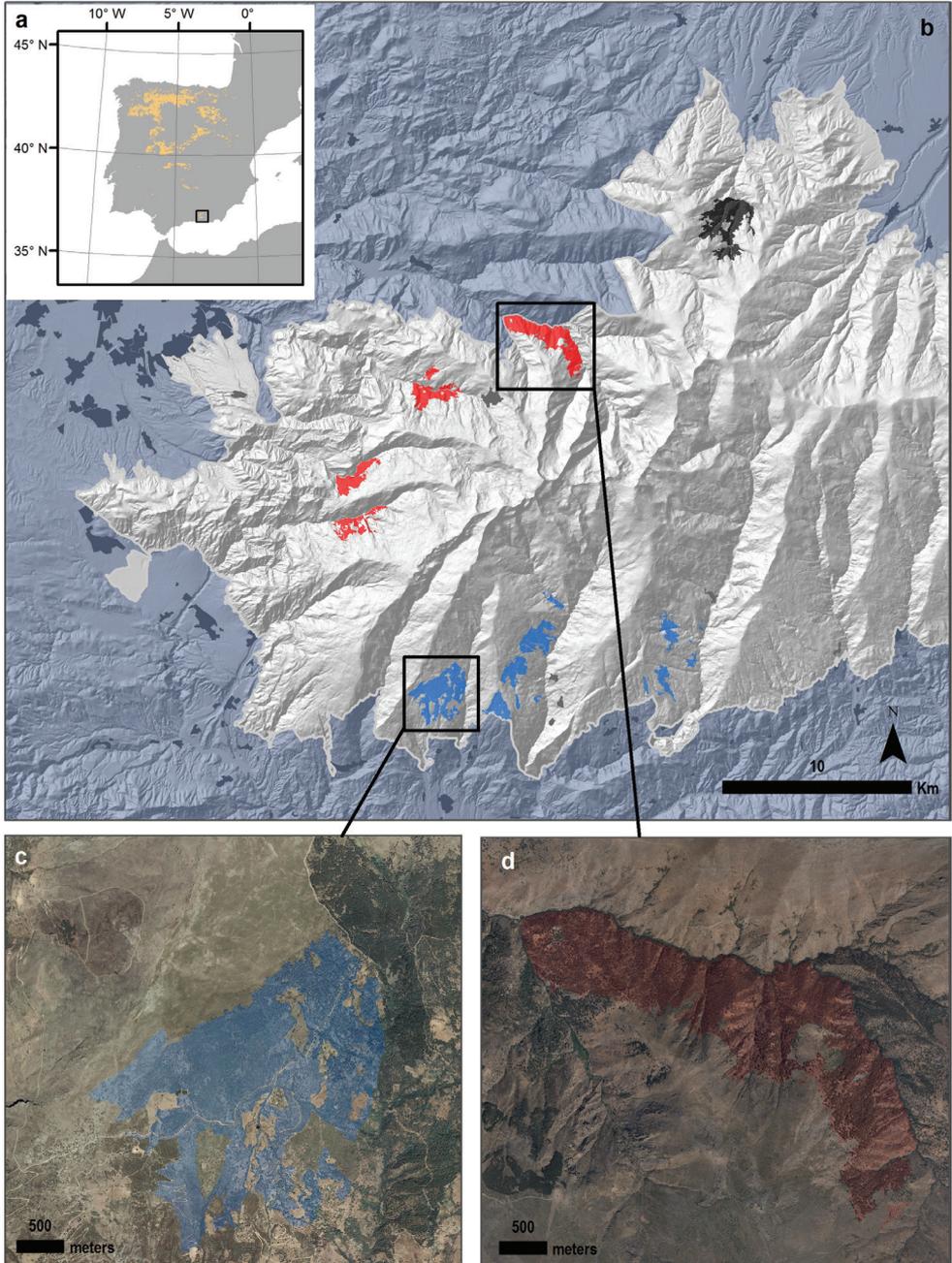


Figure 2. Distribution of *Quercus pyrenaica* forests in Iberian Peninsula (a). Sierra Nevada harbours eight populations of *Q. pyrenaica* clustered into three groups (different colours). We selected two study sites: Robledal de Cañar (c) and Robledal San Juan (d). Colour Orthophotography of 2009 from Regional Ministry of the Environment, Regional Government of Andalusia.

ience as well as to its high intraspecific genetic diversity (Valbuena-Carabaña and Gil 2013). However, they are also expected to suffer the impact of climate change, due to their climate requirements (wet summers). Thus, simulations of the climate change effects on this habitat forecast a reduction in suitable habitats for Sierra Nevada (Benito et al. 2011).

Coordinates

36°56'13.2"N and 37°8'9.6"N Latitude; 3°26'16.8"W and 3°20'16.8"W Longitude

Temporal coverage

2012–2014

Collection name

Dataset of MIGRAME Project (Global Change, Altitudinal Range Shift and Colonization of Degraded Habitats in Mediterranean Mountains)

Collection identifier

<http://www.gbif.es/ipt/resource.do?r=migrame>

Methods

Study extent description

The MIGRAME dataset covers the Pyrenean oak forests (see *Spatial coverage* section) in Sierra Nevada mountain range (see *Study area descriptions* section).

Sampling description

We sampled two localities of the Pyrenean oak forests in Sierra Nevada: Robledal de Cañar and Robledal de San Juan. We selected those two sites based on previous works (Pérez-Luque 2011, Pérez-Luque et al. 2013) that clustered the populations

of *Q. pyrenaica* forests based on their plant species composition and environmental features. The Robledal de Cañar site (Figure 2c) (1366–1935 m a.s.l., 37°57'28.04"N, 3°25'57.1"W; Cañar, Granada, SE Spain) was located in the Alpujarras Region on the southern slopes of Sierra Nevada. The Robledal de San Juan (Figure 2d) (1189–1899 m a.s.l., 37°7'29.63"N, 3°21'54.60"W; Güejar-Sierra, Granada, SE Spain) site was located in the northern slopes of Sierra Nevada.

The sampling design was determined by the hypothesis of the project (see Project Design description section).

Altitudinal migration design

To test our hypothesis of altitudinal migration, we sampled a total of 104 transects (Table 2) distributed along an altitudinal gradient at the two sites. We sampled two transects (at least 10 m apart) every 25 m of elevation from forest limit to treeline ecotone at both study sites. At each locality, we performed three replicates of this design (Figure 3a).

Habitat colonization design

To test the hypothesis of *colonization of marginal habitats*, we laid out transects in two types of marginal habitats: *abandoned agricultural areas* and *pine plantations* (Figure 3b). A total of 64 transects were located within the marginal habitat and on the edge between marginal habitat and Pyrenean oak forest. The number of transects inside the marginal habitat was determined by the size of the marginal habitat (Table 3).

Forest samplings

In addition to the above surveys, we conducted a survey inside *Q. pyrenaica* forests. A total of 31 transects were distributed at the two sites.

Table 2. Transect number of the *Altitudinal migration* design.

Locality	Altitudinal gradient	Transects ¹		
		R1	R2	R3
Robledal de Cañar	1900–2150	12	20	20
Robledal de San Juan	1775–2000	18	18	16

¹ For each replicate (R1 to R3) the number of transects is shown.

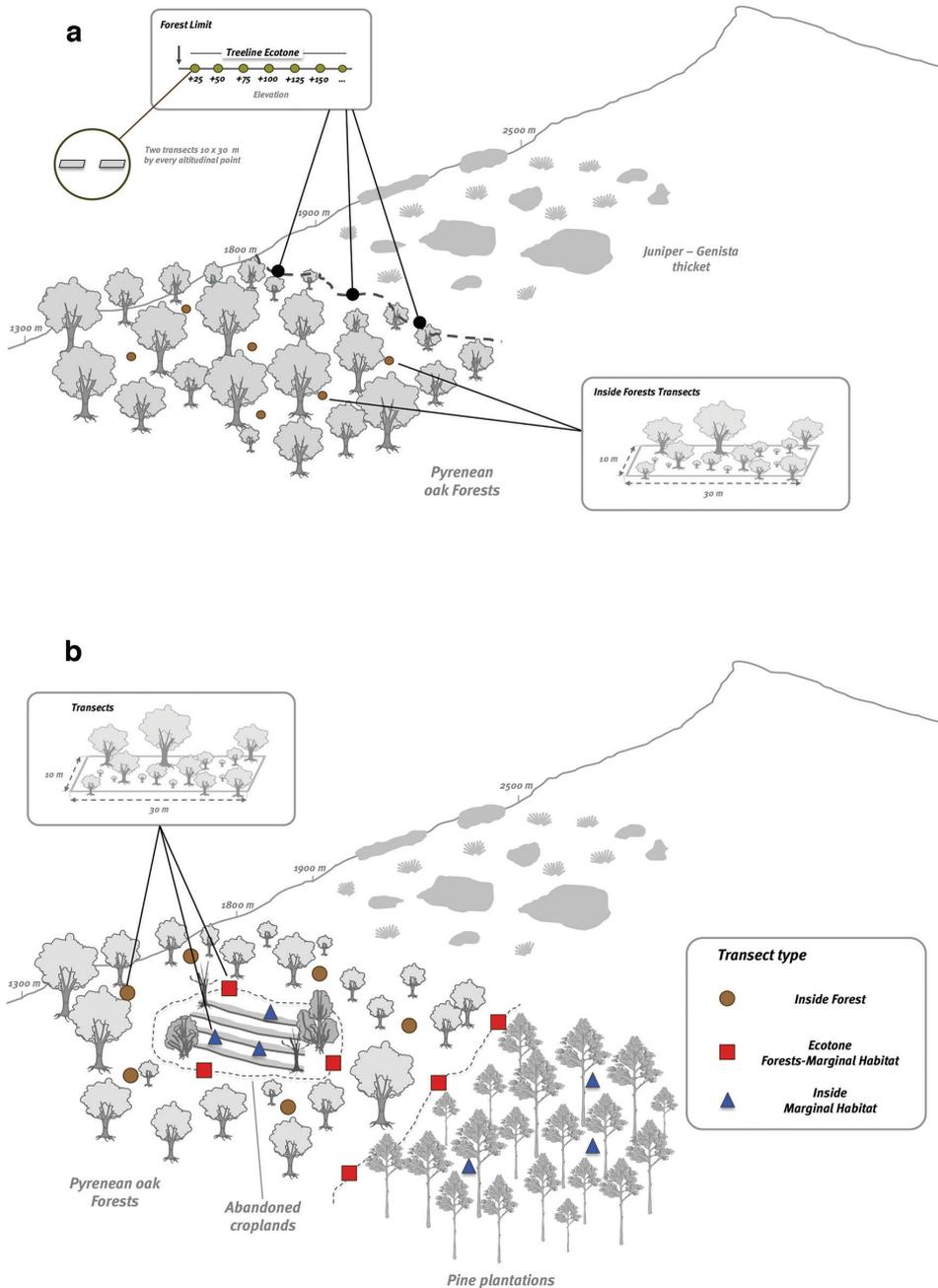


Figure 3. Sampling Design. **a** Altitudinal migration hypothesis. At each study site, from the forest edge to treeline ecotone, we sampled each 25 m of elevation **b** Colonization of marginal habitat hypothesis. Transects were located on three habitat types: Forests (brown circles), Forest Edges (red squares) and Inside Marginal Habitats (blue triangles).

Table 3. Transects number of the *Colonization of marginal habitat* design.

Locality	Marginal habitat	Replicate	Surface (ha)	Transects	
				Inside	Edge
Robledal de Cañar	Abandoned Cropland	R1	3.29	6	3
		R2	5.80	9	3
		R3	1.55	3	3
	Pine plantation		80.70	6	6
Robledal de San Juan	Abandoned Cropland	R1	3.46	6	3
		R2	10.36	13	3

Data collection

We sampled a total of 199 linear transects of 30 m × 10 m (Suppl. material 1). Within each transect, all tree species were recorded and the species identity was recorded. Diameter size and tree height were measured for all individuals. Field data were recorded using handheld PDAs. A customized application (app) (Figure 4) was built to facilitate both data collection and storage (Pérez-Pérez et al. 2013 – <http://obsnev.es/noticia.html?id=4513>). The data were automatically integrated into an information system using this application.

Method step description

All data were stored in a relational database (PostgreSQL) and added to the Information System of Sierra Nevada Global-Change Observatory (Figure 4) (<http://obsnev.es/linaria.html> – Pérez-Pérez et al. 2012; Free access upon registration). Taxonomic and spatial validations were made on this database (see *Quality-control description*). A custom-made SQL view of the database was performed to gather occurrence data and other variables associated with some occurrence data (diameter size and tree height of each individual).

The occurrence and measurement data were accommodated to fulfil the Darwin Core Standard (Wieczorek et al. 2009, Wieczorek et al. 2012). We used Darwin Core Archive Validator tool (<http://tools.gbif.org/dwca-validator/>) to check whether the dataset met Darwin Core specifications. The Integrated Publishing Toolkit (IPT v2.0.5) (Robertson et al. 2014) of the Spanish node of the Global Biodiversity Information Facility (GBIF) (<http://www.gbif.es/ipt>) was used both to upload the Darwin Core Archive and to fill out the metadata.

The Darwin Core elements for the occurrence data included in the dataset were: occurrenceId, modified, language, institutionCode, collectionCode, basisOfRecord, catalogNumber, recordedBy, eventDate, day, month, year, continent, country, countryCode, stateProvince, county, locality, minimumElevationInMeters, maximumEle-

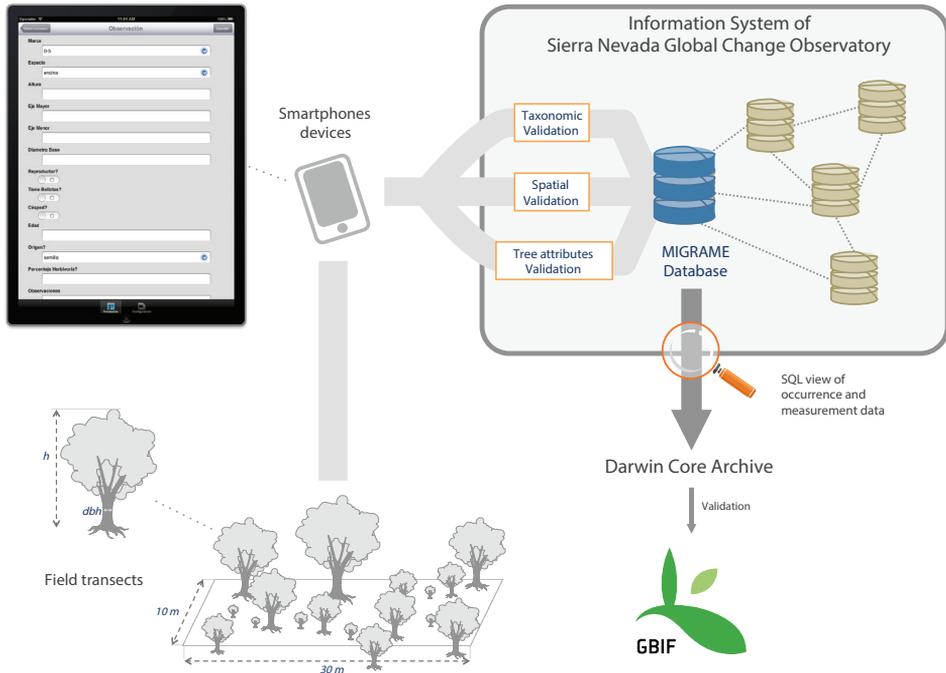


Figure 4. Diagram of integration of the dataset within Information System of Sierra Nevada Global Change Observatory (<http://obsnev.es/linaria.html>). Field data were recorded with Smartphone devices (see Pérez-Pérez et al. 2013). After a validation process (see Quality Control section) the occurrence and measurement data were accommodated to Darwin Core Archive and integrated into GBIF.

vationInMeters, decimalLongitude, decimalLatitude, coordinateUncertaintyInMeters, geodeticDatum, scientificName, kingdom, phylum, class, order, family, genus, specificEpithet, infraspecificEpithet, scientificNameAuthorship.

For the measurement data, the Darwin Core elements included were: occurrenceID, measurementID, measurementType, measurementValue, measurementAccuracy, measurementUnit, measurementDeterminedDate, measurementDeterminedBy, measurementMethod.

Quality control description

Transects coordinates were recorded with a handheld Garmin eTrex Vista Global Positioning System (GPS, ± 5 m accuracy, Garmin (2007)) (WGS84 Datum). We also used colour digital orthophotographs provided by the Andalusian Cartography Institute and GIS (ArcGIS 9.2; ESRI, Redlands, California, USA) to verify the geographical coordinates of each sampling plot (Chapman and Wiczorek 2006).

The specimens were taxonomically identified using Flora iberica (Castroviejo 1986–2005). The scientific names were checked with databases of International Plant Names Index (IPNI 2013) and Catalogue of Life/Species 2000 (Roskov et al. 2015). We also used the R package *taxize* (Chamberlain and Szöcs 2013, Chamberlain et al. 2014) to verify the taxonomical classification.

We also performed validation procedures (Chapman 2005a, 2005b) (geographic coordinate format, coordinates within country/provincial boundaries, absence of ASCII anomalous characters in the dataset) with DARWIN_TEST (v3.2) software (Ortega-Maqueda and Pando 2008).

Dataset description

Object name: Darwin Core Archive Dataset of MIGRAME Project (Global Change, Altitudinal Range Shift and Colonization of Degraded Habitats in Mediterranean Mountains)

Character encoding: UTF-8

Format name: Darwin Core Archive format

Format version: 1.0

Distribution: <http://www.gbif.es/ipt/resource.do?r=migrame>

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Supplementary material I

Table S1

Authors: Antonio Jesús Pérez-Luque, Regino Zamora, Francisco Javier Bonet, Ramón Pérez-Pérez

Data type: Table

Explanation note: Information about transects of the project. Elevation in m a.s.l..

Type: *AM* = Altitudinal migration; *FO* = Forest; *MH* = Marginal Habitat. Subtype: *AC-e*: Abandoned Cropland: edge; *AC-i*: Abandoned Cropland: inside; *Pp-e*: Pine plantations: edge; *Pp-i*: Pine plantations: inside; *TE*: Treeline Ecotone. Locality: *CA* = Robledal de Cáñar; *SJ* = Robledal de San Juan.

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Dendrochilum hampelii (Coelogyninae, Epidendroideae, Orchidaceae) traded as ‘Big Pink’ is a new species, not a hybrid: evidence from nrITS, *matK* and *ycf1* sequence data

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Abstract

In 2013, an unidentified species of *Dendrochilum* appeared in cultivation under the commercial trade name ‘Big Pink’. Using sequences of the nuclear ribosomal ITS1-5.8S-ITS2 region and of the plastid *matK* and *ycf1* genes, we examined the phylogenetic relationships between ‘Big Pink’ and six other species of the phenetically defined *Dendrochilum* subgen. *Platyclinis* sect. *Eurybrachium*. Separate and combined analyses (using Bayesian, Maximum Likelihood and Parsimony inference) showed consistent placement of the unidentified species within a statistically well supported clade. Furthermore, the multi-copy nrITS marker showed clear distinct peaks. Thus, we found no evidence that ‘Big Pink’ could be a hybrid. Against this background, and further supported by species-specific mutations in (at least) nrITS and *ycf1*, we formally describe ‘Big Pink’ as a new species under the name *Dendrochilum hampelii*. Morphologically, it is most similar to *D. propinquum*, but it differs in a number of characters. Of the two cultivated individuals available for our study, one was of unrecorded provenance. The other allegedly originated from the Philippines. Observations of the species occurring in the wild in the Philippines in the northern provinces of Bukidnon and Misamis Oriental on the island of Mindanao confirmed this.

Keywords

Dendrochilum hampelii, Molecular Phylogenetics, Orchids, the Philippines

Introduction

The largely Malesian genus *Dendrochilum* Blume (Blume 1825–1827: 398–399; published 1825) accommodates ca. 275 species—most of them described based on field inventories in the periods ca. 1900–1940 and ca. 1985–2000 (Pedersen 2007a). However, since the turn of the millennium, most new species of *Dendrochilum* have been described based on cultivated material of unrecorded provenance (cf. Pedersen 2011). Following the publication of protologues based on cultivated material, four of these species have been located in the wild (Cootes 2011). This is the case for *D. coccineum* H.A.Pedersen & Gravend. (Pedersen et al. 2004), *D. croceum* H.A.Pedersen (Pedersen 2005), *D. quinquecallosum* H.A.Pedersen (Pedersen 2007b) and *D. undulatum* H.A.Pedersen (Pedersen 2007b). The discovery of *D. coccineum* in the Philippines confirmed a phylogeny-based hypothesis put forward by Pedersen et al. (2004). Similar phylogenetic inference of *D. warrenii* H.A.Pedersen & Gravend. (Pedersen et al. 2004) as probably originating from the Philippines and/or Sulawesi (Pedersen et al. 2004) is still awaiting confirmation.

The formal description of new species of unknown natural distribution has undoubtedly served to stimulate the (partly successful) search for these species in the wild, thus demonstrating the relevancy of this practice—not least in a conservation context. Nevertheless, describing new species based on material in commercial trade also involves a few problems. Thus, Vermeulen et al. (2014) raised some issues of moral concern, and Pedersen (2011) emphasized that care should be taken not to accidentally describe artificial hybrids as new species. Until recently, this risk was negligible in connection with *Dendrochilum* since not a single *Dendrochilum* hybrid had been registered (cf. Pedersen 2011). However, now there are two *Dendrochilum* artificial hybrids registered in *The International Orchid Register* (<http://www.apps.rhs.org.uk/horticulturaldatabase/orchidregister/orchidregister.asp>; accessed on 13 February 2015), originating from Bornean parental species. This demonstrates that human assisted hybridization between different species of *Dendrochilum* is indeed possible—for which reason we must consider the possibility that seemingly undescribed species suddenly appearing in cultivation could in reality be artificial hybrids.

Since chloroplast DNA is usually maternally inherited and nuclear DNA is biparentally inherited in orchids, incongruences between nuclear and plastid gene trees might indicate past events of hybridization. For example, by comparing phylogenies based on cpDNA and nrDNA, Barkman and Simpson (2002) inferred a natural hybrid origin of *D. acuíferum* Carr whereas Gravendeel et al. (2004) detected natural hybrids within the more distantly related genus *Pleione* D. Don. Further evidence for hybridization could potentially come from significant within-individual variation in multi-copy DNA markers.

This paper reports our study of an unidentified *Dendrochilum* (trade name: ‘Big Pink’) that appeared in cultivation in 2013. A live plant presented to the Hortus botanicus in Leiden carried a tag indicating a Philippinese provenance. However, as the plant came from a commercial nursery that trades much material of unknown geographic origin, we felt this provenance was in need of verification.

Synanthous inflorescences in combination with an entire rostellum, presence of stelidia and an apical wing on the column place the study plant in the phenetically defined subgenus *Platyclinis* Engl. as circumscribed by Pedersen et al. (1997). Within this subgenus, a firmly attached entire labellum and a stout and straight column with stelidia but without a foot place the plant in the phenetically defined section *Eurybrachium* Carr ex J.J.Wood, H.A.Pedersen & J.B.Comber (Pedersen et al. 1997). However, the morphology of ‘Big Pink’ does not match any previously described species in section *Eurybrachium*—implying that it should be formally described as a new species, provided it is not either an artificial or natural hybrid.

Altogether, we decided to examine ‘Big Pink’ in a molecular phylogenetic framework—and to describe it as a new species, if the results of the phylogenetic study could reject the possibility of ‘Big Pink’ being a hybrid.

Methods

Plant sampling and DNA extraction

The possible hybrid status of ‘Big Pink’ was tested using a molecular phylogenetic approach based on three markers, namely the biparentally inherited multi-copy nuclear ribosomal internal transcribed spacer (nrITS), and the maternally inherited plastid *matK* and *ycf1* genes. The ingroup consisted of ‘Big Pink’ and six other species belonging to *Dendrochilum* subgen. *Platyclinis* sect. *Eurybrachium* (cf. Pedersen et al. 1997), see Table 1.

A live plant of ‘Big Pink’ was available from the Hortus botanicus in Leiden, whereas the remaining *Dendrochilum* plants sampled for this study were reared in the Botanical Garden, Natural History Museum of Denmark. For information on vouchers, see Table 1. *Thunia alba* Rchb.f. was chosen as outgroup, based on the placement of the genus *Thunia* as sister to *Dendrochilum* using sequences from nrITS, *matK*, *trnL-F*, and *rbcl* (Goldman et al. 2001, Gravendeel et al. 2001, van den Berg et al. 2005).

Total genomic DNA was obtained from 50 mg of silica dried or fresh leaf tissue. In the case of ‘Big Pink’, the tissue was mechanically reduced to dry powder using liquid nitrogen; for all other taxa, it was ground in Lysing Matrix A tubes (MP Biomedicals) and extracted using the DNeasy Plant Mini Kit (Qiagen) following the manufacturer’s protocol.

Amplification and Sanger sequencing

The ITS1-5.8S-ITS2 region of the nuclear ribosomal internal transcribed spacer (nrITS) was amplified using primers 17SE (ACGAATTCATGGTCCGGTGAAGT-GTTC) and 26SE (TAGAATCCCCGGTTCGCTCGCCGTTAC), as described by Sun et al. (1994). Subsequently, a M13 universal sequencing primer was added to the

Table 1. List of species sampled for our DNA-based phylogenetic analysis with voucher data. All species in the table belong to the phenetically defined *Dendrochilum* subgen. *Platyclinis* sect. *Eurybrachium*. Abbreviations of herbaria: C=University of Copenhagen, Copenhagen, Denmark; K=Royal Botanic Gardens Kew, United Kingdom; L=Naturalis Biodiversity Center, Leiden, The Netherlands; N=Nanjing University, Nanjing, China.

Species Voucher	NCBI GenBank accession numbers		
	nrITS	matK	ycf1
<i>Dendrochilum apoense</i> T.Hashim. <i>cult. Hort. Bot. Hafn. s.n.</i> (C!)	KT334200	KT334206	KT334213
<i>Dendrochilum auriculare</i> Ames <i>cult. Hort. Bot. Hafn. P2012.5172</i> (C!)	KT334201	KT334207	KT334214
<i>Dendrochilum coccineum</i> H.A.Pedersen & Gravend. <i>cult. Richard C. Warren, Warren EQ 3060</i> (C!)	AY534923	KT334208	KT334215
<i>Dendrochilum convallariiforme</i> Schauer <i>cult. Hort. Bot. Hafn. P2012.5177</i> (C!)	KT334202	KT334209	KT334216
* <i>Dendrochilum hampelii</i> Sulisty et al. <i>cult. Hort. bot. Leiden 20130654</i> (L! [WAG0116920])	KT334203	KT334210	KT334217
<i>Dendrochilum septemnervium</i> H.A.Pedersen <i>cult. Hort. Bot. Hafn. P2012.5195</i> (C!)	KT334204	KT334211	KT334218
<i>Dendrochilum tortile</i> H.A.Pedersen <i>cult. Hort. Bot. Hafn. P2012.5200</i> (C!)	KT334205	KT334212	KT334219
<i>Thunia alba</i> (Lindl.) Rchb.f. Nepal, <i>Chase 589</i> (K!)	AY008466	AY121731	-
<i>Thunia alba</i> (Lindl.) Rchb.f. China, <i>B. Hou EThuA</i> (N!)	-	-	KF361675

*Trade name: 'Big Pink'

5' end of the forward (TGTA AACGACGGCCAGT) and reverse (CAGGAAACAGCTATGAC) primers to improve Sanger sequencing efficiency. Each PCR reaction consisted of 25 µl, containing the template DNA, CorallLoad PCR buffer (Qiagen), dNTPs, Taq DNA Polymerase (Qiagen), and both primers. The PCR reactions were carried out using a MyCycler Thermal Cycler (Bio-Rad) or a C1000 Touch Thermal Cycler (Bio-Rad). The thermal cycling protocol began with 5 min initial denaturation at 95 °C followed by 35 amplification cycles, each with 30 sec denaturation at 95 °C, 30 sec annealing at 50 °C, and 1 min extension at 72 °C, which were concluded by a 7 min final extension at 72 °C.

The primers for the amplification of the chloroplast *matK* region were also used by Gravendeel et al. (2001), and specified as follows: 19F (CGTTCTGACCAT-ATTGCACTATG) and 881R (TMTTCATCAGAATAAGAGT), 731F (TCTG-GAGTCTTTCTTGAGCGA) and 2R (AACTAGTCGGATGGAGTAG). The PCR mix for the amplification of *matK* followed that of nrITS, but with additional BSA. The thermal cycling protocol for *matK* PCR began with 5 min initial denaturation at 94 °C followed by 28 amplification cycles, each with 30 sec denaturation at 94 °C, 30 sec annealing at 49 °C, 1 min extension at 72 °C, and ended with a 7 min final extension at 72 °C.

The 3' end portion of the chloroplast *ycf1* region was amplified using primers newly designed in this study. The design was based on the *ycf1* sequences data set of Neubig et al. (2008) available on NCBI GenBank (<http://www.ncbi.nlm.nih.gov/GenBank>), specifically from the species of subfamily Epidendroideae. The sequences were aligned using Geneious 5.6.7 (Kearse et al. 2012), and conserved regions were identified to be used as annealing sites. The *ycf1* sequences produced in this study had a complete marker size of approximately 1.5 kb. The *ycf1* region was amplified using a Hot start PCR protocol with primers d147F (TGCAGCRAATTYATTTATGAGTC) and intR2 (GATTTGATTGGGATGATCCAAGG), d557F (TCAAGAGATCAAACCATKCAATCA) and 1560R (CTCTACGACGTCTGGGAGATAG). Each PCR reaction consisted of 25 µl, containing DNA template, Phire Hot Start II DNA Polymerase and Phire buffer (ThermoScientific), dNTPs, BSA, and both primers. The cycling condition started with 30 sec initial denaturation at 98 °C and followed by 30 cycles of 5 sec denaturation at 98 °C, 5 sec annealing at 65.5 °C, and 10 sec extension at 72 °C, concluded with a 1 min final extension at 72 °C.

Sanger sequencing of the amplification products was performed at Baseclear (<http://www.baseclear.com/>), using an ABI 3730xl sequencer (Applied Biosystems). All new sequences are deposited in NCBI GenBank (Table 1). All sequences of *T. alba* were obtained from NCBI GenBank.

Phylogenetic analyses

Raw Sanger sequencing results in the form of AB1 files were edited and contigged using Sequencher 5.3 sequence analysis software (<http://www.genecodes.com>). The ends of all data sets were trimmed to avoid character misinterpretation. Ambiguous bases were replaced with "N" in the data matrix. The sequences were aligned using Geneious multiple sequence alignment in Geneious 5.6.7 (Kearse et al. 2012) with subsequent manual adjustments. Missing data were replaced with "?".

Phylogenetic analyses were carried out by means of Maximum Parsimony and Maximum Likelihood using PAUP* and Bayesian methods using the software Bayesian Evolutionary Analysis and Sampling of Trees (BEAST ver. 1.8.0; Drummond et al. 2012). Both PAUP* and the BEAST program were used to analyze the nrITS, the combined plastid *matK* + *ycf1*, and the combined nrITS + *matK* + *ycf1* data matrices. For the Bayesian analysis, the substitution and clock model was set as unlinked, and the chosen nucleotide substitution model was General Time Reversible (GTR), plus Gamma with 10 categories. The best fit substitution model for each partition was determined using the Find Model web tool (<http://www.hiv.lanl.gov/content/sequence/findmodel/findmodel.html>). A lognormal relaxed clock model was used for each partition, and the chosen tree prior was the Yule speciation process (Gernhard 2008). Tree samplings were generated through Markov Chain Monte Carlo (MCMC), with the number of generations set to 20,000,000 and a tree sampling for every 1000 generations. Three consecutive replicates were done to assess the consistency of the method. The three consistent replicates

were then combined into a single matrix using LogCombiner c1.8.0 (<http://beast.bio.ed.ac.uk/logcombiner>) and used to search for the best probable tree using the program TreeAnnotator ver. 1.8.0 (<http://beast.bio.ed.ac.uk/TreeAnnotator>) with a 20% burnin value to avoid the reduction of posterior probability (PP) values, and visualized using FigTree ver. 1.4.2 (<http://tree.bio.ed.ac.uk/software/figtree/>).

Results

The nrITS sequence alignment contained 854 positions with a mean ungapped length of 834 bp. Included in the alignment were the nrITS1 (236 positions), 5.8S RNA (166 positions), and nrITS2 (253 positions) regions. In total, the number of variable sites for the included positions was 164 (19.2%), of which 39 were potentially phylogenetically informative. Mean pairwise distances within the ingroup varied from 0.2–6.9%. There were six synapomorphic indels, with a size ranging from 1–5 bp. All the sequences included in the nrITS matrix were complete except for *T. alba*, which lacked 110 characters.

The *matK* matrix was characterized by a fairly high number of missing data, mostly due to amplification failures. Samples lacking approximately half (800 bp) of the entire *matK* sequence included *D. apoense* T.Hashim., *D. septemnergium* H.A.Pedersen and *D. tortile* H.A.Pedersen. The *matK* alignment consisted of 1,783 positions, with a mean ungapped length of approximately 1,769 bp. The alignment contained the least variable sites out of the three alignments, 91 sites (5.1%) with 5 potentially phylogenetically informative sites. Mean pairwise distances within the ingroup ranged from 0.8–71.1%. There was a synapomorphic indel of 1 bp.

The *ycf1* alignment consisted of 1,297 positions with mean ungapped length of 1065 bp. The number of variable sites was similar to that of nrITS, 244 (18.8%). Out of these positions, 30 were phylogenetically informative. There was one synapomorphic indel with a size of 9 bp. Mean pairwise distances within the ingroup varied from 10–33.5%. Amplification failures for *D. septemnergium* resulted in almost half of the desired *ycf1* marker missing for this species.

The phylogenetic trees based on the combined *matK* + *ycf1* matrix obtained by all three methods yielded overall stronger branch support relative to that of nrITS (Fig. 1A). The internal nodes gained high (PP = 0.97–1.0) support values, and the preceding replicates showed consistent topologies as well as well-supported clades. Clades presented by the *matK* + *ycf1* tree were highly congruent with the nrITS tree, and with higher support value.

No hard incongruence was present between the nrITS and the plastid phylogenetic trees obtained by all three methods. The combined nrITS + *matK* + *ycf1* matrix yielded a single tree with highly consistent topology and strong support values; the same clades as those in the separate nrITS and *matK* + *ycf1* analyses were identified (Fig. 1B). In all our trees, ‘Big Pink’ was positioned as a sister to *D. tortile* and *D. septemnergium*, which were very closely related, in terms of relative branch length (Fig. 1).

Analysis of the nrITS sequence alignment revealed a species-specific mutation of ‘Big Pink’ at position 567 (Fig. 2). Electropherograms of the ITS sequences of ‘Big Pink’ and its three closest relatives among the study species showed clear, distinct signals for positions included in the alignment, including the ‘Big Pink’ species-specific mutation site (Fig. 2).

Discussion

Nuclear sequence variation found was largely in agreement with previous studies in Coelogyinae (Gravendeel et al. 2001). In general, sequence divergence of nrITS between different species of *Dendrochilum* is known to vary between 0.2–20% (Pedersen et al. 2004; Sulistyono, unpublished data). Additionally, the nrITS sequence obtained from *D. hampelii* is not likely to be a paralogous locus since branch lengths are similar to the sequences of other *bona fide* species analyzed. The position of ‘Big Pink’ was in agreement with preliminary analyses based on larger sampling (Sulistyono, unpublished data), as well as with the analyses based on different sequences. We found no evidence suggesting that the morphologically distinctive ‘Big Pink’ could be an artificial hybrid rather than a new wild species. Firstly, the separate phylogenetic analyses of nuclear and plastid markers proved highly congruent. Secondly, the electropherogram of the nrITS sequence of ‘Big Pink’ showed distinct single peaks with no indication of any heterozygosity of the specimen examined.

Genetically, ‘Big Pink’ possessed a number of automorphic mutations compared to the other species included in our small phylogenetic study. These unique mutations were found in nrITS and *ycf1*, whereas one in *matK* is in need of verification due to the alignment being characterized by a fairly high number of missing data. Morphologically, ‘Big Pink’ is most similar to *D. propinquum* Ames. Unfortunately, no material was available of *D. propinquum* for DNA sequencing for this study. However, ‘Big Pink’ has much larger flowers (approximately twice the size of those of *D. propinquum*), its flowers have petals that are 1.4–1.5 times as broad as the sepals (0.8–1.1 times in *D. propinquum*), its labellum is broadly cordate (broadly elliptic to ovate in *D. propinquum*), and the stamens of its column are acute (obtuse in *D. propinquum*). Against this background, we describe ‘Big Pink’ as a new species below.

Contrary to the studies of Wannatorp et al. (2002) and Pedersen et al. (2004), the taxon sampling underlying the phylogenetic analyses in this study was too small to allow for any inference of a probable geographic origin of ‘Big Pink’. However, in a preliminary study based on systematically and geographically much broader sampling of *Dendrochilum* s.l., individual phylogenetic analyses using sequences from nrITS, plastid *matK*, and *ycf1* have all indicated ‘Big Pink’ to be nested within a clade nearly exclusively consisting of Philippine endemics (Sulistyono, unpublished data). In subsequent field surveys by the second author, a total of 12 plants were observed in February 2014 in the northern provinces of Bukidnon and Misamis Oriental on the island of Mindanao at high elevation, a few of which were flowering. In March 2015, only 4

individuals were observed *in situ* in the wild by the second and third author, and none were flowering. These observations confirm that *D. hampelii* is indeed a Philippine, almost certainly endemic species. It is conjectured to have entered cultivation in Europe through the many domestic markets in Southeast Asia that sell orchid species. For these markets, wild plants are harvested but traded as ‘cultivated’ to circumvent CITES legislation. All Coelogyninae are listed on Appendix 2. Despite this legal protection, illegal trade is continuing at international orchid shows and by web based orders from buyers of specific species or nursery owners hoping to incorporate desirable wild traits into new hybrids (Hinsley et al. 2015).

Taxonomic treatment

Based on these results, it is determined that “Big Pink” is a new species in need of recognition. Formally naming the species is relevant for horticulture and *ex situ* conservation, because the name provides an unambiguous way to refer to the species. The morphology of ‘Big Pink’ was described using terminology of the vocabulary and list of individual absolute terms in Stearn (1983), if relevant standardized according to the Orchidaceae glossary in Pedersen et al. (2011).

Dendrochilum hampelii Sulistyo, Gravend., R.Boos & Cootes, sp. nov.

urn:lsid:ipni.org:names:77150223-1

Figs 3, 4

Type. Sine loco et anno, *Perry 490* (holotype L!).

Diagnosis. This new species is similar to *D. propinquum* Ames, but is distinguished by its larger flowers with petals proportionally broader (1.4–1.5×) than the sepals, a broadly cordate labellum (6.8–8.0 × 7.2–7.6 mm) and acute stelia.

Medium-sized, tufted epiphytic herb. *Roots* appearing from the rhizome, ca. 2.7 mm in diameter. *Pseudobulbs* tightly clustered on a short rhizome, fusiform, 3.5–5.0 cm long, 0.5–1.4 cm in diameter, longitudinally striated when dry, 1-leaved, initially covered by ca. 3 imperfectly to nearly perfectly tubular, rounded to acute cataphylls that soon disintegrate into persistent fibers. *Leaves* convolute, dorsiventrally flattened, petiolate; petiole channeled, 3.0–4.5 cm long; lamina (ob)lanceolate, obtuse, 13.0–20.0 × 3.7–5 cm, subcoriaceous, with 7–8 distinct (and many indistinct) nerves. *Inflorescence* synanthous, racemose; peduncle suberect, arched, slender, somewhat flattened, 18.0–21.2 cm long, sparsely and finely setose; rachis pendent with distichously alternating flowers (but the rachis axis twisted so as to produce a cylindrical inflorescence), many-flowered with internodes of 3–7 mm, somewhat furrowed, 20.0–27.5 cm long, sparsely and finely setose, basally with 1 appressed non-floriferous bract; flowering starting from the proximal part of the rachis. *Floral bracts* glumaceous, broadly lanceolate to (ovate-)oblong when flattened, obtuse to acute, 4.0–9.5 × 2.2–4.3 mm, entire,

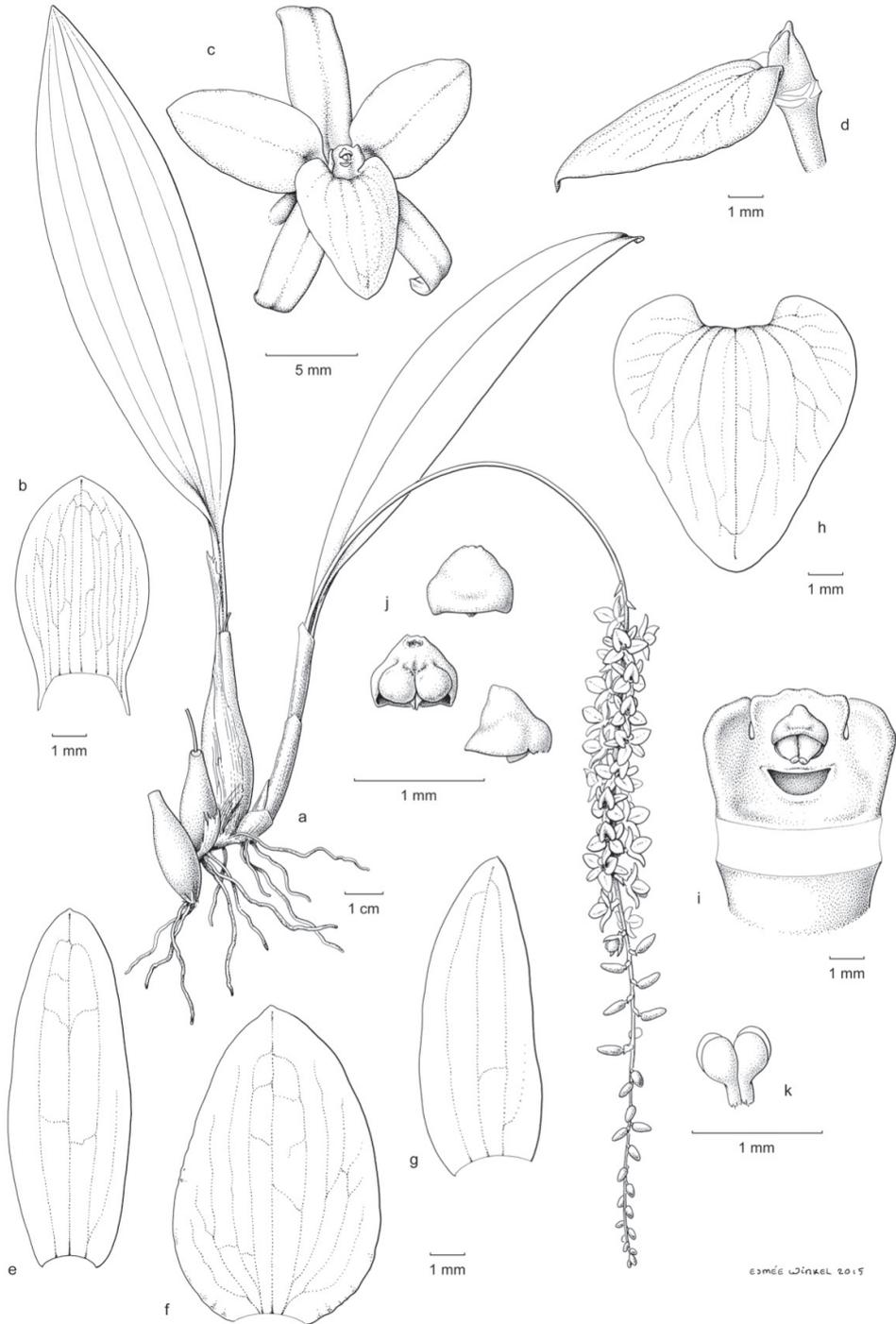


Figure 3. *Dendrochilum hampelii*: **a** habit **b** floral bract **c** flower **d** flower (sepals and petals removed) **e** dorsal sepal **f** petal **g** lateral sepal **h** labellum **i** column, front view **j** anther **k** pollinia. Drawing by Esmée Winkel based on *Hort. bot. Leiden* 20130654 (L! [spirit no. WAG0116920]).

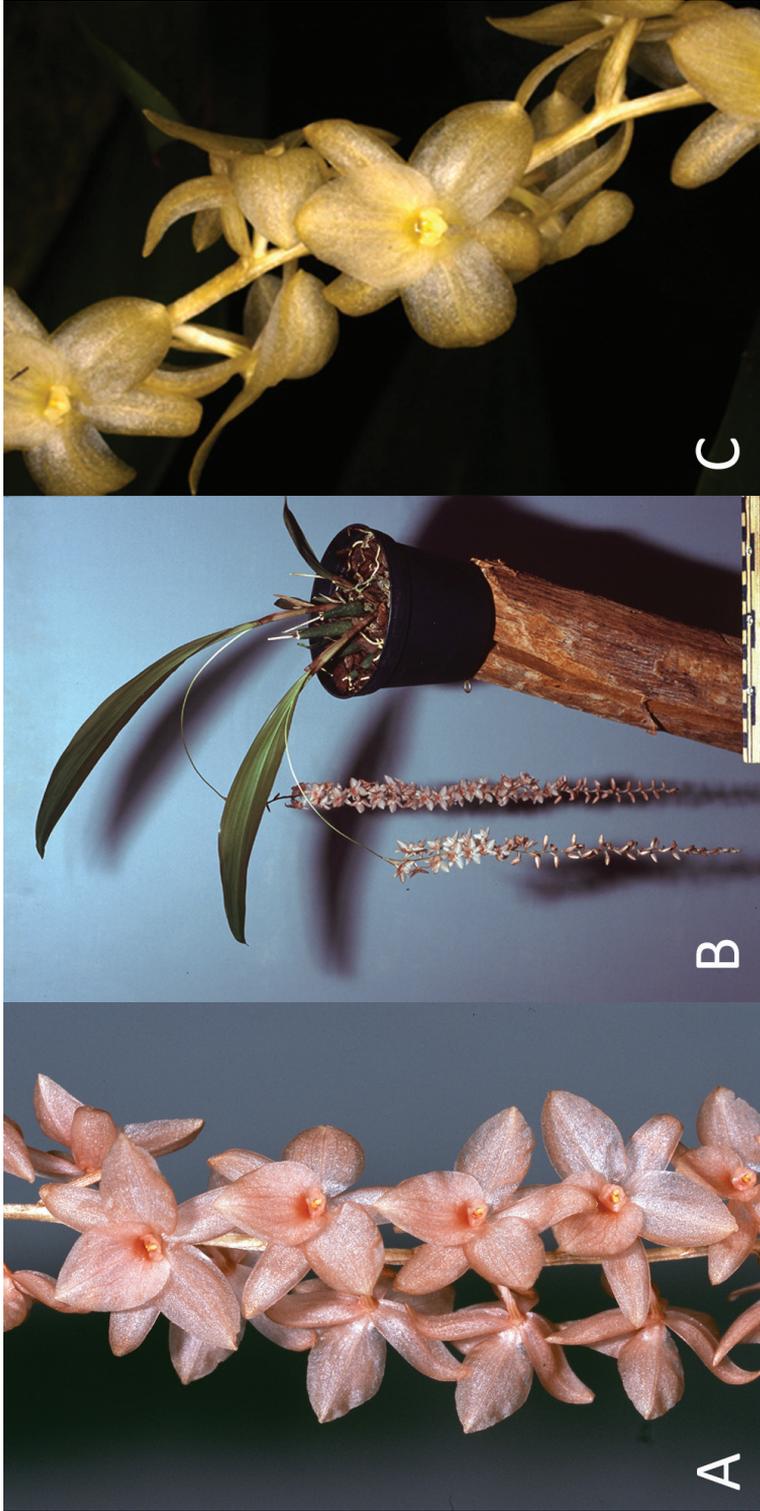


Figure 4. *Dendrochilum hampelii*: **A** portion of inflorescence of cultivated pinkish salmon-coloured form **B** habit. Photographs by Lubbert Westra of *Hort. bot. Leiden 20130654* (L! [spirit no. WAG0116920]) **C** portion of inflorescence of pale yellow-colored form of a plant growing in the wild in the Philippines in the Misamis Oriental province of the island of Mindanao. Photograph by James Cootes.

9- to 19-nerved from the base, finely setose on the dorsal side. *Flowers* non-resupinate, pinkish salmon-coloured (Fig. 4A–B) or pale yellow (Fig. 4C) with yellow anther. *Sepals* recurved with revolute margins, entire, obtuse to rounded, minutely mucronate, glabrous, 3- to 5-veined from the base; dorsal sepal lanceolate-oblong, 8.7–11.0 × 3.5–3.7 mm when flattened; lateral sepals ovate-oblong, slightly oblique, 8.1–10.0 × 3.7–4.0 mm when flattened. *Petals* recurved with flat margins, broadly (ovate-)elliptic, often with a subbasal fold in either side, rounded to acute, 8.4–11.1 × 5.4–5.7 mm, 1.4–1.5 times as wide as the sepals, entire, glabrous, 3- to 5-veined from the base. *Labellum* firmly attached, sessile, describing a right to obtuse angle to the column, flat, broadly cordate with entire margins, acute to short-acuminate, 6.8–8.0 × 7.2–7.6 mm, without ornaments, glabrous and smooth, 5- to 7-veined from the base. *Column* suberect, straight, semiterete, 1.7–2.1 mm long, smooth, distally prolonged into a truncate to obscurely 3-lobed wing that distinctly exceeds the anther; stelia appearing from the distal part of column proper, erect, falcately triangular-oblong, acute, subequal to the apical wing; anther circular to transversely elliptic in upper view, rounded in front, lobed at the back, with a small wart on top; pollinia 4, ellipsoid, devoid of caudicles; rostellum slightly protruding, flat, semicircular; fertile stigma part crescent-shaped, concave. *Ovary* (including pedicel) subterete, slightly longitudinally furrowed, twisted through 180°, distally incurved, 3.8–4.5 mm long, glabrous. *Fruit* not seen.

Additional material examined. PHILIPPINES? *Sine loco et anno, sine coll./cult. Hort. bot. Leiden 20130654* (L! [spirit no. WAG0116920]).

Etymology. The specific epithet honours Georg Hampel, who was one of the first to provide us with study material of the newly described species.

Distribution and ecology. The species occurs in the wild in the Philippines in the northern provinces of Bukidnon and Misamis Oriental on the island of Mindanao (Fig. 4C). It grows as an epiphyte at elevations approximately 1,200 m above sea level among mosses on the trunks and branches of trees. Fresh flowers of plants observed in the wild were pale yellow whereas fresh flowers of the cultivated plants studied were pinkish salmon-coloured. We do not consider this reason to describe them as a different variety or forma as color dimorphism is known to occur in other Coelogyninae as well (Gravendeel 2000).

Reproductive biology. The live plant in Leiden flowered in mid-December. Attempts to pollinate flowers of *D. hampelii* were made using pollinia from the same flower and pollinia from a different flower in the same inflorescence. None of these efforts led to fruit formation. This indicates that *D. hampelii* is probably self-incompatible, as previously demonstrated for *D. longibracteatum* Pfitzer (Pedersen 1995), although it should be noted that experimental pollination was severely challenged by the small size of the stigmatic cavity.

Conservation status. Although the species occurs in cultivation we as yet know very little about the distribution and abundance of *D. hampelii* in the wild. As such, we recommend the species to be considered for the Data Deficient category of the IUCN Red List of Threatened Species (IUCN 2012).

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A new subspecies of *Seseli gummiferum* (Apiaceae) from Ilgaz Mountain National Park, northern Turkey

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Abstract

A new subspecies *Seseli gummiferum* Pall. ex Sm. subsp. *ilgazense* A.Duran, Ö.Çetin & M.Öztürk, **subsp. nov.** (Apiaceae) is described from Kastamonu province, Turkey. It was collected from the open *Pinus sylvestris* L. and *Abies nordmanniana* (Steven) É.Spach. mixed forest in the northern Anatolian region. An endemic apparently confined to the Ilgaz Mountain National Park, the new taxon is closely related to *Seseli gummiferum* subsp. *gummiferum*. Diagnostic morphological characters for closely similar taxa are discussed, and a key to the subspecies of *Seseli gummiferum* is presented. ITS (Internal Transcribed Spacer) region of the nuclear ribosomal DNA of closely related *Seseli* L. taxa and *Pimpinella* is used to construct phylogenetic tree by using BioEdit and Seaview Programme.

Keywords

New taxon, *Seseli gummiferum*, Turkey, Umbelliferae

Introduction

The Apiaceae comprise approximately 450 genera and 3700 species worldwide (Pimenov and Leonov 1993). However, the distribution of species among the genera vary, with almost half of the genera monotypic and 26% consisting of only two or three species. Sixty percent of the species in the family assign to just a few genera, which genera encompass over 20 species have been noted as polyphyletic (Spalik et al. 2004). Asian countries with the greatest biodiversity for the Apiaceae include China,

Asian Turkey, Iran, Asian Russia, and Kazakhstan, with the most species given for the Chinese flora (677 species in 108 genera) (Pimenov and Leonov 2004). Turkey, with a considerably smaller geographic area, is second only to China in its diversity for the Apiaceae, with 450 species in 109 genera. There are four endemic genera in Turkey, with 140 species among 42 genera. This suggests that the Asiatic region in Turkey has the highest known species-level diversity for the Apiaceae in Asia, if not in the world (Pimenov and Leonov 2004).

Seseli L. is one of the largest genera in the Apiaceae with 125 to 140 taxa ascribed to the genus worldwide. Represented by both intraspecific and interspecific diversity, *Seseli* is distributed in Europe, Asia, Africa, North America and Australia (Pimenov and Leonov 2004). The first revision of *Seseli* in Turkey was made by Hedge and Lamond (1972), who recognized 10 infrageneric taxa. *Seseli gummiferum* subsp. *gummiferum* was reported as a new record from Turkey (Duman 2000). After that *Seseli ramosissimum* replaced with *Seseli hartvigii* by Parolly (Parolly and Nordt 2001). Latest revision of *Seseli* in Turkey was made by Doğan Güner and Duman (2013). So the total number of these taxa is 13 now.

Material and methods

In 2008, during a field trip in the Black Sea region of Turkey, an unusual specimen of *Seseli* was collected by the authors. Study of the descriptions in Hedge and Lamond (1972), Davis et al. (1988), Duman (2000), Ball (1968), Rechinger (1987), Parolly and Nordt (2001), Shishkin (1950), Özhatay et al. (2009), Doğan Güner and Duman (2013) as well as comparison with herbarium material in GAZI, HUB, KNYA and ANK revealed that the specimens indeed represented a new taxon. In particular, the new taxon was compared with the closely similar taxa *Seseli gummiferum* Pall. ex Sm. subsp. *gummiferum* and *S. corymbosum* Boiss. & Heldr. In the morphological description below, each numerical value is the average of ten measurements from different specimens. The abbreviations of the authors of plant names were checked from Brummitt and Powell (1992).

DNA isolation: Total DNA was obtained from 50–75 mg leaf and fruit from six different individuals. DNAs are isolated with CTAB method and after concentrations were determined by Nanodrop. Sample DNAs were diluted 25 ng/μl. Stock DNAs were kept at -86 °C.

ITS amplifications: ITS region of studied taxa were amplified using ITS4 (5' TCC TCC GCT TAT TGA TAT GC 3') and ITS5 (5' GGA AGG AGA AGT CGT AAC AAG 3') primers. PCR condition is 95 °C for 5 min initial denaturation, 35 cycles of 94 °C for 30 s denaturation, 50 °C for 30 s annealing, and 72 °C for 1 min extension, 72 °C for 10 min final extension.

Data collection and cluster of phylogenetic analysis: PCR products were visualised by agarose gel. The amplified fragments were sequenced using the same primers used for amplification. ITS sequences of the taxa were aligned via Bioedit and were used to construct phylogenetic trees by using Seaview.

Taxonomic treatment

Seseli gummiferum gummiferum Pall. ex Sm., *Exot. Bot.* [Smith] ii, 121 (1807).

Replaced synonym: *Bubon rigidus* Spreng., *Syst. Veg.* (ed. 16) [Sprengel] 1: 900 1825 [1824], nom. illeg., non *Bubon rigidus* (Waldst. & Kit.) Spreng. *Pl. Min. Cogn. Pug.* 2: 53. 1815. Type: [London] Cult. in Oxford Bot. Garden and Hort. Lady Hume.

Seseli gummiferum crithmifolium (Boiss.) P.H.Davis, *Notes Roy Bot. Gard. Edinb.* 21: 120 (1953).

Basionym: *Seseli crithmifolium* Boiss., *Fl. Orient.* [Boissier] 2: 962 (1872). Type: Greece, Insulae maris Aegaei, *Tournefort* 324 (holotype P, photo!, E!).

Seseli gummiferum ilgazense A.Duran, Ö.Çetin & M.Öztürk, *subsp. nov.*

urn:lsid:ipni.org:names:77150275-1

Figs 1–6

Affinis *S. gummiferum* Pall. ex Sm. *subsp. gummiferum* sed *umbellis centralibus radiis* 13–21 (*nec* 25–30), *bracteis* 2–7 (*nec plerumque* 8–15), *umbellis lateralibus radiis* 7–13 (*nec* 15–20), *ovariis glabris* (*nec cum pilis*), *fructibus glabris* (*nec cum pilis*) *differt.*

Type. TURKEY. A4 Kastamonu: Ilgaz Mountain Natural Park, Kastamonu road, from Çatören village to Büyük Hacet Hill, 6 km, in open *Pinus sylvestris* L. and *Abies nordmanniana* (Stev.) Spach. mixed forest, serpentine stony slopes, 41°06'344"N, 33°48'628"E, 1465 m, 22 August 2008, A.Duran 8135, Ö.Çetin & M.Öztürk (holotype KNYA! isotypes ANK!, GAZI!, HUB!).

Description. Plants monocarpic, 15–30 cm tall; rootstock thickened, cylindrical, oblong, ± vertical, 8–15 mm diameter; stems 3 to 5, terete, finely ridged, mostly glabrous, sparsely puberulent above, with a developed fibrous collar 2.5–7 cm; stems mostly branching from the base, below and rarely at the middle part, green to purplish green. Basal leaves ovate to oblong-ovate, 2-pinnate, 6–20 × 3–10 cm, glabrous; ultimate segments lanceolate, linear-oblong, 5–15 × 0.5–1.5 mm, acute to acuminate; sheaths developed, distinctly widened at base, upper sheath surface sulcate, margin membranous; cauline leaves similar to basal leaves, partly reduced, amplexicaule, middle and upper portions of the stem leafless. Flowers hermaphroditic; the central umbel stout, 7–11 cm diam., equal to or longer than lateral umbels, rarely shorter, with 13 to 21 rays, 1.8–5.5 cm long, puberulent above, unequal, each central umbel with by 2 to 7 bracts; bracts lanceolate, rarely widened at base, 10–17 mm long, margin ± membranous, sometimes bifid to trifid, glabrous or puberulent; umbellules 9–15 mm diam, each comprising



Figure 1. *Seseli gummiferum* subsp. *ilgazense* A.Duran, Ö.Çetin & M.Öztürk, subsp. nov.

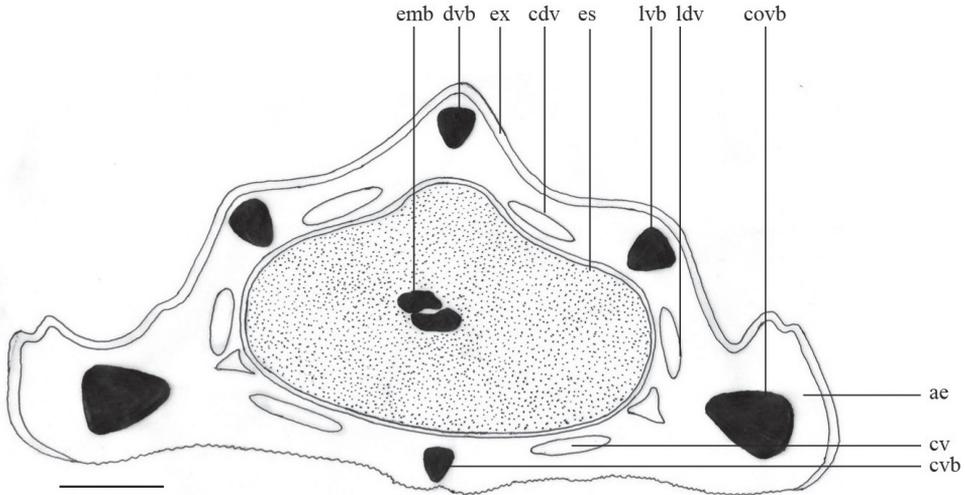


Figure 2. Cross section of fruit: emb = embriyo; dvb = dorsal vascular bundle; ex = exocarp; cdv = central dorsal vittae; es = endosperm; lvb = lateral vascular bundle; ldv = lateral dorsal vittae; ae = aerenchyma; cv = commissural vittae; cvb = carophore vascular bundle; covb = commissural vascular bundle. Scale bar = 0.2 mm.

55 to 70 flowers; bracteoles 15–20, connate at base, 5–8 mm long, linear-lanceolate, acuminate, entire or bifid to trifid, green to partly purple, margin distinctly membranous, especially ciliate at apex, out side glabrous to puberulent; lateral umbels 3.5–6 cm diam. with 7 to 13 rays, 1–3.5 cm long, with bracts or without. Flowers subsesile, glabrous, sepals ±purplish, broadly lanceolate, glabrous, persistent, ca. 1 mm; petals white, glabrous with deflexed apex; filament white, anther clearly purple; ovary glabrous. Fruit oblong-elliptic, 3.5–4 × 1.5–2 mm, glabrous, with 5 ribs prominent, obtuse; stylopodium short-conical; styles deflexed in fruit, distinctly purple.

Distribution and IUCN red list category. The new subspecies is known only from the type locality, with specimens collected only from Ilgaz Mountain National Park (Kastamonu province) in Turkey, where the species seems to be very rare. This area is ca. 1.5 km², and mature individuals of the type population number approximately 125. The location is very close to the road side and near forest management. The population is going to be negatively affected from cars, trucks and people in the future. The habitat of this subspecies is clearly under threat of destruction, and therefore, the taxon should be considered Critically Endangered (CR), according to IUCN Red List Criteria (IUCN 2001).

Habitat and ecology. This new subspecies grows at 1450–1470 m with *Lapsana communis* L., *Abies nordmanniana* (Stev.) Spaach, *Centaurea drabifolia* Sm., *Erysimum thyrsoideum* Boiss., *Pteridium aquilinum* (L.) Kuhn, *Sorbus umbellata* (Desf.) Fritsch, *Valeriana alliariifolia* Adams, *Eryngium giganteum* M.Bieb., *Bupleurum falcatum* L. subsp. *persicum* (Boiss.) Koso-Pol., *Salvia verticillata* L., *Teucrium chamaedrys* L., *Dactylis glomerata* L., *Asyneuma rigidum* (Willd.) Grossh. subsp. *rigidum*.

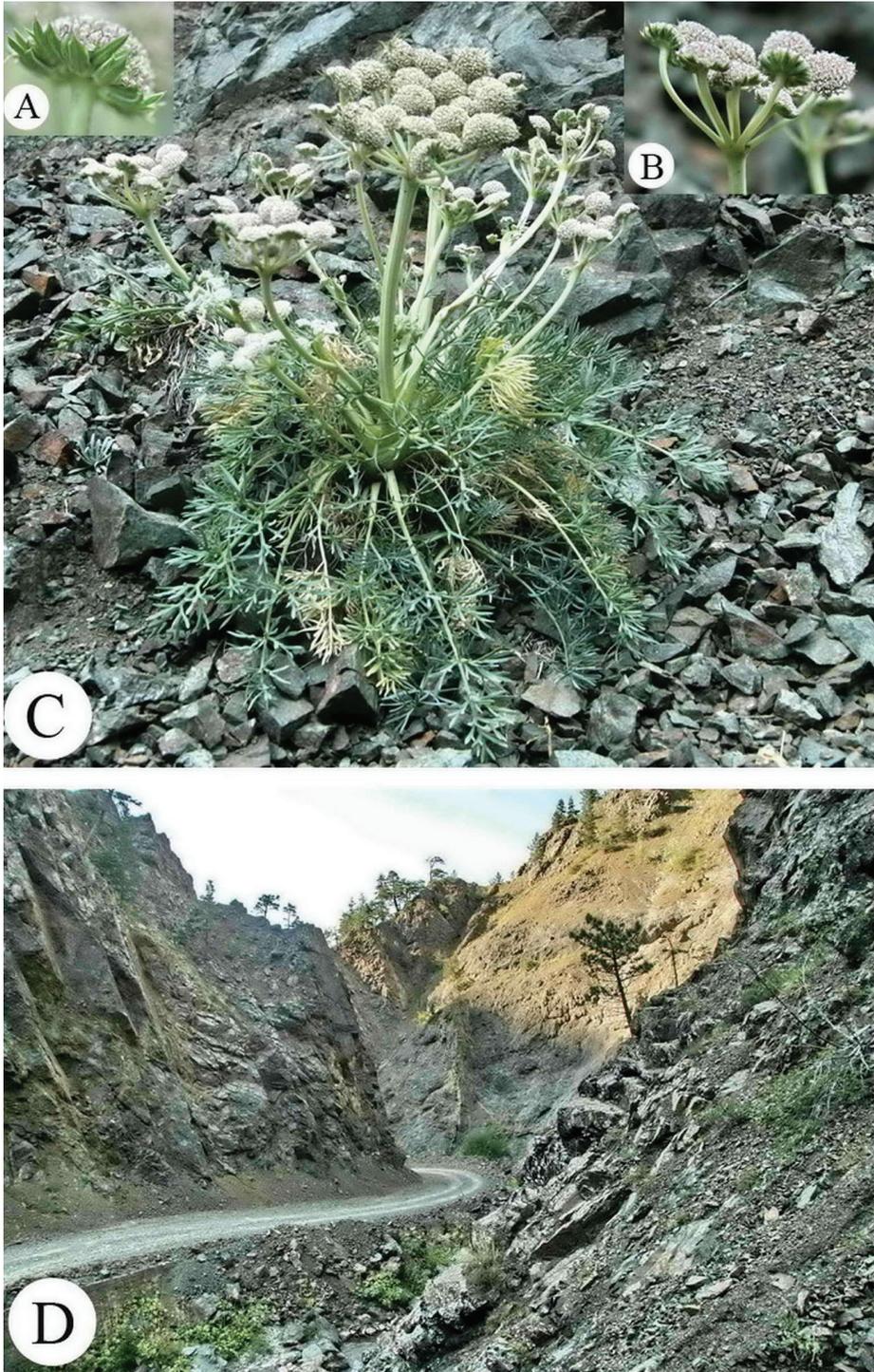


Figure 3. *Seseli gummiferum* subsp. *ilgazense*. **A** trifid and entire bracteoles **B** lateral umbel **C** general aspects **D** habitat and general view of type locality. Photo by A.Duran.



Figure 4. Comparison of *Seseli gummiferum* fruits. *S. corymbosum* fruits. **A** general view **B** surface details. *S. corymbosum*: **C** general view **D** surface details. *S. gummiferum* subsp. *ilgazense*: **E** general view **F** surface details.

Discussion and conclusion. Turkey is the most complex country in the Middle East with regard to geographic structure and landforms. It's comprised of comparatively narrow and long, variously oriented mountain chains, separated by deep valleys and also high- and medium-elevational plateaus. The geological composition and physical direction, exposure and altitude of these mountains are here largely influential not only upon the diversity of vegetation, but also on the richness of the flora (Zohary 1973). Ilgaz Mountain, which is situated in a transitional zone in central and North of Anatolia and is generally composed of serpentine, schist and volcanic rocks. The mountain is orogenically interesting, with the quite active north Anatolian fault found along the southern slopes of Ilgaz Mountain (Kuter 2008). One of the more important reasons for protecting the Ilgaz Mountain is the richness and endemism of its flora. Approximately 100 endemic plants occur within the boundaries of the National Park and the type localities of 19 endemic taxa are found on Ilgaz Mountain. *Delphinium ilgazense*

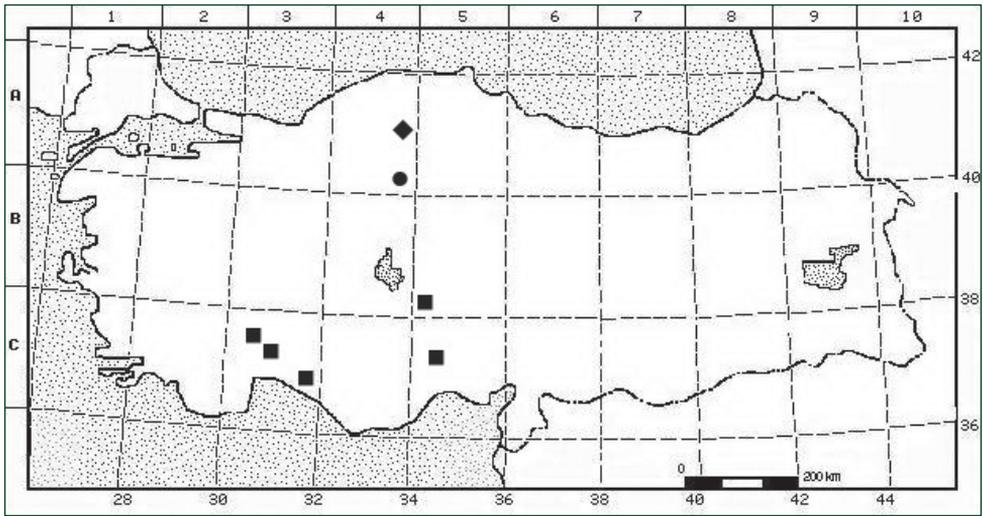


Figure 5. Distribution of *Seseli gummiferum* subsp. *ilgazense* (◆), *S. gummiferum* subsp. *gummiferum* (●) and *S. corymbosum* (■) in Turkey.

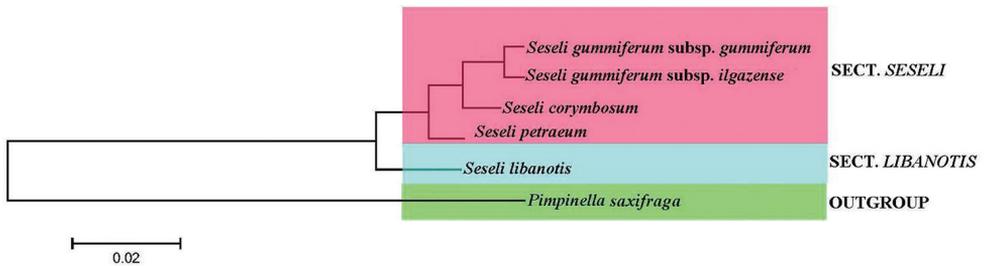


Figure 6. The neighbour joining tree generated using nrITS DNA sequences of some *Seseli* taxa and *Pimpinella saxifraga*.

P.H.Davis, *Arabis abietina* Bornmüller, *Draba anatolica* A.Duran & Dinç, *Astragalus nabelekii* Czechtz, *Heracleum paphlagonicum* Czechtz, *Hieracium macrogonum* (Zahn) P.D.Sell & C.West and *H. tuberculatum* Freyn, *Festuca ilgazensis* Markgr.-Dann. are all noteworthy endemic taxa confined to the national park (Davis 1965–1985, Davis et al. 1988, Duman 2000, Duran et al. 2008).

Seseli gummiferum subsp. *ilgazense* is closely related to two other subspecies found in Turkey. *S. gummiferum* subsp. *gummiferum* is distributed in Crimea, Central Anatolia (Shishkin 1950, Ball 1968, Duman 2000). The new subspecies differs from *S. gummiferum* subsp. *gummiferum*, based on its glabrous fruits (not with indument), fewer central umbels, with 13 to 21 rays (not 25 to 30), fewer lateral umbels, with seven to 13 rays (not 15 to 20), as well as the bracteoles 15 to 20 (not 11 to 16) (Hedge and Lamond 1972, Duman 2000).

Seseli gummiferum subsp. *ilgazense* also differs from *S. gummiferum* subsp. *crithmifolium* (DC.) P.H.Davis, which is distributed in west and east Crete, Folegandros, Sikinos,

Amargos, Karpathos, Saria and neighbouring islands in Aegean Sea. The new taxon is not so broadly distributed, endemic and found only in northern Anatolia (Ilgaz Mountain). *Seseli gummiferum* subsp. *crithmifolium* principally differs from subsp. *ilgazense* by its puberulent fruits, the central umbels with 20–45 rays, and the oblong leaf segments (6–) 10–30 × 2–5 mm (Ball 1968, Hedge and Lamond 1972).

Key to closely related *Seseli gummiferum* subspecies

- 1 Fruit glabrous; the central umbel 13 to 21 rays; lateral umbels with 7 to 13 rays **subsp. *ilgazense***
- Fruit with hairs; the central umbel 22 to 70 rays; lateral umbels with 13 to 47 rays
- 2 Basal leaves glabrous **subsp. *crithmifolium***
- Basal leaves puberulent or finely pubescent **subsp. *gummiferum***

Since Morison's (1672), *Plantarum umbelliferarum*, fruit morphology and anatomy have been regarded as essential to the taxonomy of Apiaceae (Drude 1898, Constance 1971, Spalik et al. 2001). Details of the fruits have been traditionally viewed as rich sources of taxonomic characters, exhibiting some, but not excessive variation in features such as fruit shape, the degree and direction of mericarp compression, modifications of the pericarp ribs (e.g. wings or spines), and the shape of mericarp commissural faces. Thus, most traditional classifications of Apiaceae have relied almost exclusively on fruit characters (Plunkett and Downie 1999, Pimenov et al. 2004). *Seseli gummiferum* subsp. *ilgazense* has some distinctive characteristics in terms of carpological features. Mericarps of *Seseli gummiferum* subsp. *ilgazense* have five large vascular bundles situated beneath the each rib. Large vittae present in mesocarp layer adjacent to the endocarp. There are also two large vittae in the commissure. Differing from *Seseli gummiferum* subsp. *gummiferum*, the new subspecies does not have short secretory ducts around vascular bundles. In addition, the vittae around the endocarp are always large and elliptical. The endosperm is round shaped. Commissure width is approximately equal to mericarp width.

Diagnostic characters of *Seseli gummiferum* subsp. *ilgazense* with the three related taxa are provided in Table 1.

Five *Seseli* taxa and *Pimpinella* were evaluated in the phylogenetic analysis. PCR amplification with ITS 4/ITS 5 primers generated bands ranging from 595 to 665 bp. Alignment of the ITS sequences was done using Bioedit. Neighbour-Joining (NJ) tree were constructed using Seaview programme (Figure 6). According to NJ analyses, the taxa of *Pimpinella* placed in first clade. This species was used as outgroup. The second clade includes *Seseli libanotis*, which is found in Section *Libanotis*. *Seseli libanotis* is separated from *S. gummiferum* and *S. petraeum* by having highly wide leaf segment. The second clade includes *Seseli petraeum*, *S. corymbosum*, *S. gummiferum* in sect. *Seseli*. *Seseli petraeum* is close to *Seseli gummiferum*. It mainly differs from *S. gummiferum*

Table 1. Diagnostic characters of *Seseli gummiferum* subsp. *ilgazense*, *S. gummiferum* subsp. *gummiferum*, *S. gummiferum* subsp. *crithmifolium* and *S. corymbosum*.

Characters	subsp. <i>ilgazense</i>	subsp. <i>gummiferum</i>	subsp. <i>crithmifolium</i>	<i>S. corymbosum</i>
Stems per plant	3 to 5	1 to 4	solitary	solitary
Stem branching	mostly below, rarely in middle portion	below the middle	above the middle	above the middle
Central umbel rays	13 to 21	25 to 30	22 to 45	30 to 70
Lateral umbel rays	7 to 13	15 to 20	17 to 35	13 to 47
Bracts	2 to 7	mostly 8 to 15	mostly absent, rarely up to 2	0 to 1
Bracteoles	15 to 20	11 to 16	19 to 26	19 to 23
Petals	glabrous	glabrous	pubescent	pubescent
Ovary	glabrous	pubescent	puberulent	pubescent
Fruit	glabrous	pubescent	pubescent	pubescent

because it has free bracteol from base and main umbel shorter than lateral umbels. *Seseli corymbosum* (Boiss. & Heldr.) P.H.Davis which only occurs in South Anatolia, is readily distinguished from *S. gummiferum*, by its solitary stem branching above, bracts either lacking or one below the central umbel, more numerous bracteoles, 19 to 23, larger central umbels with 30 to 70 rays and the lateral umbels with 13 to 47 rays, and finally by the pubescent petals and fruits (Hedge and Lamond 1972). Although *Seseli gummiferum* subsp. *ilgazense* is closely related to *S. gummiferum* subsp. *gummiferum*, this taxa is treated as different subspecies.

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Appendix

Representative specimens examined (*which used for DNA samples): – *Seseli corymbosum*: Turkey, C3 Antalya: Akseki, Pınarbası village, S of Gidefi Mountain, *A.Duran* 2970 (GAZI); Akseki, Gidefi Mountain, *A.Duran* 1847 (GAZI); C5 Niğde; Ulukışla, between Alihoca-Maden villages, *A.Duran* 6078* (KNYA). – *S. gummiferum* subsp. *gummiferum*: Turkey, A4 Ankara: Hasanoğlu, İdris Mountain, above Adilahmet village, *M.Koyuncu* 16348 (GAZI); Hasanoğlu, İdris Mountain, 1500–1600 m., 14.09.2002, *E.Doğan* 1650* (GAZI). – *S. gummiferum* subsp. *critmifolium*: Greece, Dodecanese, Karpathos, side of Kali Limni, 10 m, 21.07.1950, *Davis* 18010 (E). – *Seseli petraeum*: Turkey, Trabzon, between Araklı-Bayburt, 27.07.2002, *A.Duran* 6059* (KNYA). – *Seseli libanotis*: Turkey, Erzurum, between İspir-Ovit, 1700 m, 18.08.2013, *A.Duran* 9778* (KNYA).

Reinstatement of the Loyalty Islands Sandalwood, *Santalum austrocaledonicum* var. *glabrum* (Santalaceae), in New Caledonia

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Abstract

Sandalwoods encompass 19 species restricted to southeast Asia and the Pacific. The species *Santalum austrocaledonicum* Vieill. (Santalaceae) is endemic to New Caledonia (Grande-Terre, Isle of Pines, Loyalty Islands) and Vanuatu, where several varieties are recognized. The Loyalty Islands sandalwood variety is here reinstated as *Santalum austrocaledonicum* var. *glabrum* Hürl. emend. Butaud & P.Firmenich, mut. char. It was previously considered a synonym of the type variety; however, new morphological and genetic studies confirmed its distinctiveness. The key for New Caledonian varieties of *Santalum austrocaledonicum* has been updated and a short description of its essential oil composition and organoleptic quality is given.

Keywords

Santalum austrocaledonicum, Santalaceae, Loyalty Islands, New Caledonia, essential oil

Introduction

Sandalwoods are shrubs or small trees well known for the essential oil extracted from their fragrant heartwood and used in perfumery. They belong to the genus *Santalum* (Santalaceae) comprising 19 species restricted to southeast Asia and the Pacific (Harbaugh and Baldwin 2007, Harbaugh 2007, Harbaugh et al. 2010). The most sought-after species is the Indian sandalwood, *Santalum album* L.

Santalum austrocaledonicum Vieill. is the only native sandalwood in New Caledonia and Vanuatu (Guillaumin 1925, Hallé 1988, Harbaugh and Baldwin 2007), and is endemic to these archipelagoes. It has been heavily harvested for the past 150 years (Shineberg 1967) and its wood is still exploited for the fragrance industry as its essential oil can be considered as a substitute for Indian sandalwood oil (Braun et al. 2005).

The most recent taxonomical work on *S. austrocaledonicum* was carried out by Hallé (1988) who recognized three botanical varieties based on specimens from New Caledonia in Paris (P) herbarium:

- *S. austrocaledonicum* Vieill. var. *austrocaledonicum* from Grande-Terre (main island of New Caledonia), Isle of Pines, Loyalty Islands and Vanuatu;
- *S. austrocaledonicum* var. *pilosulum* N.Hallé in the vicinity of Nouméa on the southwest coast of Grande-Terre;
- *S. austrocaledonicum* var. *minutum* N.Hallé from the northwest coast of Grande-Terre.

Since that revision, several studies have shown the great morphological variations of var. *austrocaledonicum* in New Caledonia and Vanuatu which are linked to geographical distribution (Quemin 1988, Nasi 1995, Chauvin and Ehrhart 1998, Bottin 2006, Bouvet et al. 2005, Bottin et al. 2007). The main differences in New Caledonia can be summarized as follows:

- Loyalty Islands: large seeds (L = 8–11 mm, D = 7–10 mm), short and wide juvenile leaves (L = 30–52 mm, W = 8–15 mm);
- Isle of Pines: medium-sized seeds (L = 8–10 mm, D = 6–9 mm), long and narrow juvenile leaves (L = 25–76 mm, W = 2–10 mm);
- Grande-Terre: small seeds (L = 6–9 mm, D = 5–7 mm), long and very narrow juvenile leaves (L = 52–70 mm, W = 2–4 mm).

No comprehensive study of the variation of these characters is available in Vanuatu due to lack of herbarium specimens from most of sandalwood populations there.

For this reason, Nasi (1994) intended to describe the Loyalty endemic sandalwood under the variety *loyaltensis* but his manuscript was never published.

More recently, molecular studies of New Caledonian sandalwood showed strong genetic differentiation between islands and led to the recognition of two evolutionarily significant units, i.e. Grande-Terre and Isle of Pines for the first, and Loyalty Islands for the second (Bottin et al. 2005, 2007).

The New Caledonian sandalwood is subject to exploitation through harvesting and is grown in plantations to satisfy the increasing international demand of sandalwood essential oil. However, its taxonomy appears to be in need of revision to more precisely describe the variability of this New Caledonian biodiversity hotspot species (Myers et al. 2000) and to contribute to the sustainable management of this natural resource.

A first step of this revision is presented here, with the recognition of an endemic sandalwood variety from the Loyalty Islands based on morphological and molecular studies as well as examination of living plants and herbarium specimens.

Nomenclature

The New Caledonian sandalwood, *Santalum austrocaledonicum*, was described by Vieillard (1861) from samples collected on the hills of Arama, in the Northern extremity of Grande-Terre (*E. Vieillard 1090*, holotype P00645808). Later, it was confirmed that this species was also present on the Isle of Pines, Loyalty Islands and Vanuatu (Guillaumin 1925, 1970, Virot 1950).

In 1964, Hürlimann described a new variety based on a sample collected on the island of Maré in the Loyalty Islands (Stauffer and Hürlimann 1964), *Santalum austrocaledonicum* var. *glabrum* Hürl. characterized by glabrous flowers, differing from the type variety (*Santalum austrocaledonicum* Vieill. var. *austrocaledonicum*) represented erroneously by samples gathered around Nouméa (Ouen Toro, Anse Vata, Baie de l'Orphelinat) which have villous flowers.

In 1988, the revision of the New Caledonian *Santalum* by Hallé recognized the three varieties mentioned in the introduction. Hallé reduced var. *glabrum* of Hürlimann to synonymy under the type (autonym) variety, considering it superfluous due to confusion by Hürlimann on what was really the type of the species. Indeed, the latter described var. *glabrum* in comparison with what is now recognized as var. *pilosulum*, this one differing morphologically from var. *austrocaledonicum*. The true var. *austrocaledonicum* and var. *glabrum* are in fact identical relative to the morphological differences pointed out by Hürlimann in his diagnosis.

As the native Loyalty Islands sandalwoods are quite homogeneous, only one variety is to be recognized for the entire Loyalty archipelago, which is the one of Hürlimann. Thus, to reinstate the varietal name *glabrum* for the endemic Loyalty sandalwood, its description must be amended to distinguish it from the true type specimen.

Systematics

***Santalum austrocaledonicum* var. *glabrum* Hürl. emend. Butaud & P.Firmenich, mut. char.**

S. austrocaledonicum var. *glabrum* Hürl., Mém. Mus. Hist. Nat., ser. B, Bot. 15(1): 15 (1964).

Type. New Caledonia, Loyalty Islands, Maré, près de Rawa, arbre, 8 m, en fleurs et en fruits, forêt mésophile, 17 July 1951, *M.G. Baumann-Bodenheim 14762* (holotype: P scan!; isotype: Z scan!).

Diagnosis. *Santalum austrocaledonicum* var. *glabrum* is most similar to var. *austrocaledonicum* in its glabrous inflorescence and leaves wider than 1.5 cm, which differentiates them from the other New Caledonian *S. austrocaledonicum* varieties. *Santalum austrocaledonicum* var. *glabrum* differs from *S. austrocaledonicum* var. *austrocaledonicum* by the seed size, which is more than 7.5 mm wide for the former and less than 7.5 mm for the latter.

Description. Shrub to small tree 2–10 m tall, trunk up to 30 cm dbh; bark rough, grey to reddish-brown, longitudinally fissured; heartwood fragrant, yellowish to brownish. **Leaves** glabrous; petiole canaliculate, 7–13 mm long; blades of the mature leaves 3.5–6.0 (–6.6) × (1.6–) 2.0–3.5 (–4.1) cm, usually elliptic or rarely obovate, apex obtuse to acute or apiculate, base acute, secondary veins mostly 7–9 pairs. **Inflorescences** glabrous, in axillary or terminal panicles, usually trichotomous and several times branched, with 10–40 flowers; peduncles 10–38 mm long. **Flowers** bisexual with outer surface of petal greenish and glabrous; pedicels 1.5–2 mm long. **Petals** 4, narrowly triangular, 2.5–3.0 × 1.5–2.0 mm, inner surface white when opening turning brownish later; petal internal margin glabrous. **Stamens** 4, surrounded by long hairs at the base; the outer ones reaching the anther apex, the inner ones reflexed in the cup-shaped disk; anthers 1.5–2.7 × 0.8–1.0 mm. **Disk** concave, more than 2 mm deep; disk lobes fleshy and erected between petals, 1.3–1.4 × 0.8–0.9 mm. **Ovary** unilocular, conic, acute, 1.1–1.7 × 0.6 mm; style free, 4 mm long; stigma 3 or 4 lobed. **Fruit** a globose fleshy drupe, 15–21 × 12–15 mm when fresh, topped by the petal scars 3–5 mm diameter, green turning red to deep purple and black at maturity. **Seed** globose, with a hard endocarp (8.5–) 9.0–11.5 × 7.5–10.0 (–10.5) mm.

Phenology. Flowering and fruiting probably occurring throughout the year but with some peaks; herbarium samples provide the following data: flowers from December to August, fruits from January to August.

Distribution. New Caledonia, endemic to Loyalty Islands; known only from Ouvéa, Lifou and Maré islands (Figure 1). Not recorded on the smaller islands of Beautemps-Beaupré, Tiga and Walpole.

Habitat and biology. This variety is restricted to the calcareous soils of uplifted atolls between 5 and 80 m elevation and is closely linked with traditional agriculture which consists of shifting cultivation. Regeneration by seeds occurs mainly in the open cultivated areas and young fallow lands. Loyalty sandalwood is therefore characteristic of fallows, shrublands and secondary forests, and rarely occurs in mature forests. It is also commonly found along roads and close to villages in open areas where it is generally protected and managed by inhabitants. The surrounding vegetation is often composed of trees and shrubs, such as *Acacia spirorbis* Labill., *Acalypha* spp., *Acronychia laevis* J.R.Forst. & G.Forst., *Dodonaea viscosa* (L.) Jacq., *Elattostachys apetala* (Labill.) Radlk., *Glochidion billardierei* Baill., *Melochia odorata* L.f., *Morinda citrifolia* L., *Pandanus macrocarpus* (Brongn.) Solms, *Podonophelium homei* (Seem.) Radlk., *Polyscias bracteata* (R.Vig.) Lowry subsp. *bracteata*., *Psidium guajava* L., and *Schinus terebenthifolius* Raddi. Loyalty sandalwood is a hemiparasitic tree like all *Santalum* species; its pollination is insect-mediated whereas its fleshy fruits are dispersed mainly by doves and pigeons (Bottin et al. 2005).

Conservation status. Using the categories and criteria of IUCN (2001), we propose for *S. austrocaledonicum* var. *glabrum* the IUCN Red List Category Vulnerable (VU): B (1+2) ab (iii,v). Its population size is estimated at more than 10,000 mature individuals (excluding criteria C and D) with an extent of occurrence around 8,000 km² and an area of occupancy around 1,000 km². Criteria A can not be used due to

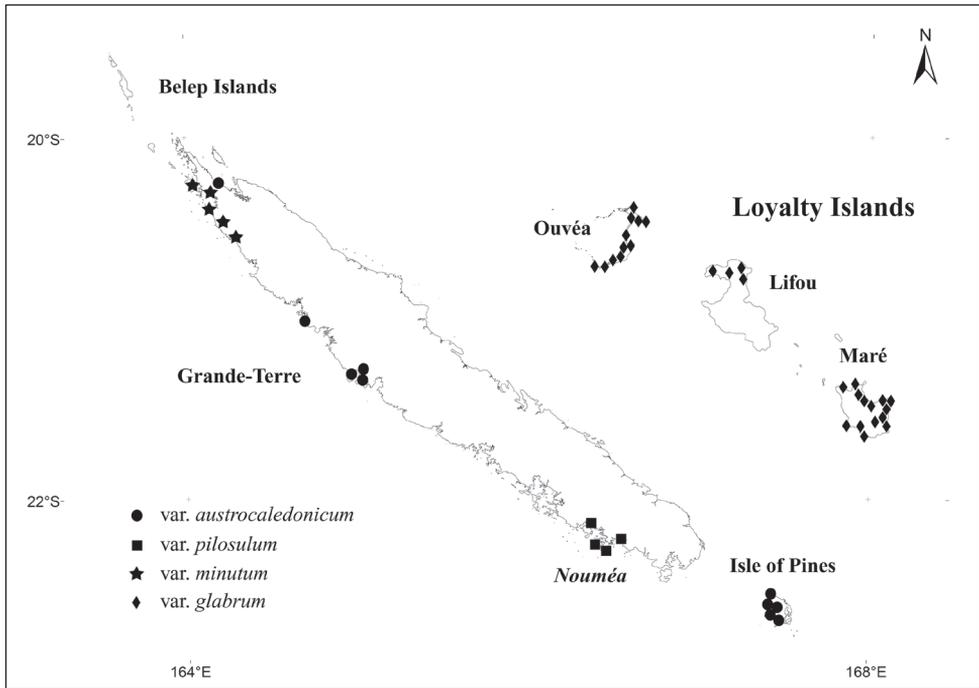


Figure 1. Distribution map of New Caledonian varieties of *Santalum austrocaledonicum* based on the specimens examined.

lack of knowledge of generation length and magnitude of population size reduction. Three locations (one per island) can be distinguished without any fragmentation. A continuing decline is observed and projected in terms of habitat quality and number of mature individuals due to harvest, competition with invasive plant species (*Schinus terebinthifolius* Raddi, *Pluchea odorata* (L.) Cass., *Lantana camara* L.), hybridization with other *S. austrocaledonicum* varieties used in plantations, and changes in the traditional agricultural system (less cultivated fields, short fallows...). Indeed, despite provincial regulations establishing quota and exploitability criteria, illegal logging is still occurring (Butaud et al. 2013) whereas hybridization is suspected due to sandalwood interspecific crossability (Tamla et al. 2012).

Common names. The common names recorded for *S. austrocaledonicum* var. *glabrum* are “tapakae” (pers. obs. 2014) or “tapakai” (Lenormand 1968) on Lifou, “wekesi” (Lormée et al. 2011) on Maré and “wahata” (Ozanne-Rivierre 1984) on Ouvéa.

Discussion. *Santalum austrocaledonicum* var. *glabrum* is the sole native sandalwood in the Loyalty Islands. Nevertheless, two other varieties have been introduced for plantation purposes, mainly in Maré and Lifou: var. *pilosulum* from Ouen Toro in Nouméa, and var. *austrocaledonicum* from Isle of Pines. These plantations can be considered a risk for the Loyalty variety because of hybridization and subsequent introgression. Plantations with exotic varieties should be discouraged to preserve the



Figure 2. Flowers of *Santalum austrocaledonicum* var. *glabrum* on Ouvéa atoll in January 2015 (specimen Butaud 3414).



Figure 3. Fruit of *Santalum austrocaledonicum* var. *glabrum* on Ouvéa atoll in January 2015 (specimen Butaud 3414).

Loyalty sandalwood's morphological, genetic, silvicultural and chemical specificities (Bottin 2006, Bottin et al. 2007, Butaud et al. 2013, Ehrhart 1998). On the other hand, the sustainable exploitation of natural stands of Loyalty Islands sandalwood is becoming increasingly difficult with the lack of regeneration and the increasing international demand for sandalwood essential oil. Well-managed plantations with variety *glabrum* could be promoted to preserve the natural stands, to develop the Loyalty sandalwood sector, and to increase the production of heartwood and essential oil (Butaud 2011, Butaud et al. 2013).

The taxonomy of *S. austrocaledonicum* still needs to be further investigated. Indeed, the study of herbarium samples of var. *austrocaledonicum* and previous molecular and morphometric studies (Bottin 2006, Bouvet et al. 2005) showed significant variability. It is expected that future work supported by increased surveys and sampling of northern Grande-Terre sandalwood could reveal one or two new varieties, including one on Isle of Pines (taxon previously described as *Santalum homei* Seem.). Moreover, two new endemic varieties of *S. austrocaledonicum* are expected based on the recent study of Millet et al. (2012) on the genetic structure of Vanuatu sandalwood, one for the northern islands and one for the southern islands.

Key to New Caledonian varieties of *Santalum austrocaledonicum*

(adapted from Hallé 1988)

- 1 Inflorescence peduncles, rachis segments and outer surface of petals sparsely to densely hairy..... **var. pilosulum**
- Inflorescence peduncles, rachis segments, outer surface of petals and petal internal margins glabrous..... **2**
- 2 Leaf blade usually less than 3.5×1.5 cm; petiole less than 7 mm; blade adaxial surface glaucous and bluish in color; interstaminal disk lobes very narrow (W/L = $1/3$ – $1/4$) **var. minutum**
- Leaf blade usually more than 3.5×1.5 cm; petiole more than 7 mm; blade adaxial surface not glaucous and bluish in color; interstaminal disk lobes wide (W/L = $1/2$) **3**
- 3 Seed usually more than 9×7.5 mm; globose (L/D < 1.2) **var. glabrum**
- Seed usually less than 9.5×7.5 mm; ovoid (L/D > 1.2) **var. austrocaledonicum**

Essential oil quality

Essential oil of *Santalum austrocaledonicum* was previously assessed for its composition and organoleptic properties, and was considered as a possible substitute for Indian sandalwood oil (*Santalum album*) but also as a promising new raw material for the fra-

Table 1. Main constituents of Loyalty Islands sandalwood (var. *glabrum*) essential oil compared to ISO standards for *S. album* oil.

Essential oil	(Z)- α -santalol (%)	(Z)- β -santalol (%)	(E)-lanceol (%)
ISO Standard 3518 : 2002 (<i>S. album</i>)	41 to 55	16 to 24	-
New Caledonia Braun et al. (2005)	38.2	18.2	9.1
Loyalty Oil 1	44.3	19.4	14.1
Loyalty Oil 2	47.4	21.3	8.5

grance industry (Braun et al. 2005). These evaluations were performed on essential oils resulting from mixtures of sandalwood varieties *glabrum* (Loyalty islands), *pilosulum* (surroundings of Nouméa) and *austrocaledonicum* (Isle of Pines), leaving unknown the quality of each individual variety.

To investigate the quality of Loyalty Islands sandalwood essential oil (var. *glabrum*), two samples were analyzed for their main sesquiterpenoids but also for their organoleptic properties:

- Loyalty Oil 1 (EI1) obtained in 2015 from Distillerie de Boulouparis (New Caledonia) with Ouvéa sandalwood,
- Loyalty Oil 2 (EI2) obtained in 2002 from Michel Point and processed by Koop Cuada distillery with Maré and Lifou sandalwoods.

The gas-chromatography was performed on an apolar column (HP-1, 10 m x 0.1 mm, film 0.1 μ m, 50° (1') to 280° (2') at 50°/min., vector gas: hydrogen). Its results are given in Table 1 (C. Vial and S.A. Firmenich, pers. comm. 2015).

The organoleptic evaluation showed that the Loyalty essential oil is lighter and less milky than the Indian sandalwood; the former has also a character less woody but more animal and masculine (P.-A. Blanc and S.A. Firmenich, pers. comm. 2015).

These findings are in accordance with Braun et al. (2005), especially for the organoleptic evaluation. Moreover, the composition of both Loyalty essential oils meets the ISO Standard for Indian sandalwood, which was not the case for the samples of the previous study. Thus, *Santalum austrocaledonicum* var. *glabrum* or Loyalty sandalwood constitutes a true substitute for Indian sandalwood in the perfume industry.

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Appendix

Specimens examined

Santalum austrocaledonicum var. *glabrum* Hürl.: New Caledonia, Loyalty Islands.

Ouvéa. Lékine, 15 May 1976, *D. Bourret 815* (NOU); Lekiny, bord de route goudronnée, 24 January 2015, *J.-F. Butaud 3414* (NOU); Lekiny, bord de route goudronnée, 24 January 2015, *J.-F. Butaud 3415* (NOU); Lekiny, bord de route goudronnée, 24 January 2015, *J.-F. Butaud 3416* (NOU); Mouli, bord de route goudronnée, 24 January 2015, *J.-F. Butaud 3417* (NOU); Hnyimehe, route menant à la salle omnisport, 24 January 2015, *J.-F. Butaud 3421* (NOU); Hwaadrila, piste carrossable menant au Cap St Hilaire, 25 January 2015, *J.-F. Butaud 3422* (NOU); St Joseph, 14 August 1925, *A.U. Däniker 2546* (P scan, Z n.v.); Saint-Paul, 10 m, forêt, February 1980, *H.S. MacKee 37848* leg. *Douheret* (NOU, P scan); Nimaha, 29 April 1987, *H.S. MacKee 43516* leg. *Cherrier* (NOU, P scan, Z n.v.); Nimaha, 29 April 1987, *H.S. MacKee 43517* leg. *Cherrier* (P scan); Hanawa, forêt dense littorale, 29 April 1987, *H.S. MacKee 43520* leg. *Cherrier* (P scan); Hanawa, forêt dense littorale, 30 April 1987, *H.S. MacKee 43526* leg. *Cherrier* (NOU, P scan); Pointe de Mouli, 30 April 1987, *H.S. MacKee 43527* leg. *Cherrier* (NOU, P scan); Wakat, 30 April 1987, *H.S. MacKee 43530* leg. *Cherrier* (NOU, P scan); Wakat, 30 April 1987, *H.S. MacKee 43532* leg. *Cherrier* (NOU, P scan); Gossanat, forêt, 11 May 1987, *H.S. MacKee 43545* leg. *Ongat* (NOU, P scan); Gossanat, forêt, 11 May 1987, *H.S. MacKee 43546* leg. *Ongat* (NOU, P scan););

- Teouta, 11 May 1987, *H.S. MacKee 43547* leg. *Ongat* (NOU, P scan); Teouta, 11 May 1987, *H.S. MacKee 43548* leg. *Ongat* (P scan); Ogniat, en lisière d'une cocoteraie, 11 May 1987, *H.S. MacKee 43549* leg. *Ongat* (P scan); Ogniat, en lisière d'une cocoteraie, 11 May 1987, *H.S. MacKee 43550* leg. *Ongat* (P scan); Takedji, 11 May 1987, *H.S. MacKee 43551* leg. *Ongat* (NOU, P scan); Takedji, 11 May 1987, *H.S. MacKee 43552* leg. *Ongat* (NOU, P scan); 19 July 1984, *P. Morat 7782* (NOU).
- Lifou. July 1869, *B. Balansa 1692b* (P scan); 1928, *C. Bergeret 106* (P scan); Mutschaweng, 30 m, lisière de forêt, 18 February 1974, *H.S. MacKee 28169* (P scan, Z n.v.); Natchaom, 5 June 1987, *H.S. MacKee 43577* leg. *Wapae* (P scan); Natchaom, 5 June 1987, *H.S. MacKee 43578* leg. *Wapae* (P scan); Natchaom, 5 June 1987, *H.S. MacKee 43579* leg. *Wapae* (P scan); Ouanaham, 3 August 1987, *H.S. MacKee 43638* leg. *Case* (NOU, P scan); Hunete, 4 August 1987, *H.S. MacKee 43639* leg. *Case* (P scan); Hunete, dans un jardin, 4 August 1987, *H.S. MacKee 43640* leg. *Case* (NOU, P scan); Hunete, 4 August 1987, *H.S. MacKee 43641* leg. *Case* (NOU, P scan); March 1979, *J.-M. Veillon 3920* leg. *Lespès* (NOU); March 1979, *J.-M. Veillon 3921* leg. *Lespès* (NOU, P scan).
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Santalum austrocaledonicum Vieill. var. *austrocaledonicum*:

New Caledonia, Grande-Terre. Arama, collines près de la mer, 1855–60, *E. Vieillard 1090* (holotype: P scan; isotypes: P [2] scan, K p.p. scan); Arama, collines près de la mer, 1855–60, *E. Vieillard 1090bis* (P scan; K p.p. scan); Vavouto, 26 September 2007, *J. Munzinger 4518* (NOU); Presqu'île de Pindai, propriété Kuhn, 2 July 1987, *J.M. Veillon 6422* (NOU, P scan); Presqu'île de Népoui, Pindai, 100 m, 18 November 1987, *J.M. Veillon 6574* (NOU, P scan); Presqu'île de Pindai, 100 m, 1 April 1988, *J.M. Veillon 6794* (NOU, P scan); Poya, forêt de Nekoro, 5 m, 28 September 1988, *J.M. Veillon 6917* (NOU); Poya, station de Mueo, propriété Johnston entre 10–20 m, 6 May 1998, *J.M. Veillon 8106* (NOU); Poya, station de Mueo, propriété Johnston entre 10–20 m, 6 May 1998, *J.M. Veillon 8107* (NOU, P scan).

New Caledonia, Isle of Pines. 1852, *Home s.n.* (BM scan); 1853, *MacGillivray 818b* (K scan); Kuto, 1 February 1980, *H.S. MacKee 37852* leg. *Douheret* (NOU, P scan); Kuto, 9 February 1980, *H.S. MacKee 37853* leg. *Douheret* (NOU, P scan); Kuto, 1 February 1980, *H.S. MacKee 37872* leg. *Sevenet* (NOU, P scan); Kuto, 1 February 1980, *H.S. MacKee 37873* leg. *Sevenet* (NOU, P scan); Plateau, 25 February 1980, *H.S. MacKee 37874* leg. *Sevenet* (NOU, P scan); Ouro, 7 October 1987, *H.S. MacKee 43738* leg. *Quemin* (NOU, P scan); Ouro, 9 October 1987, *H.S. MacKee 43739* leg. *Quemin* (NOU, P scan); Kuto, 9 October 1987, *H.S. MacKee 43740* leg. *Quemin* (NOU, P scan); Ouameo, 8 October 1987, *H.S. MacKee 43741* leg. *Quemin* (NOU, P scan); Oupotoue, Gadji, 8 October 1987, *H.S. MacKee 43742* leg. *Quemin* (NOU, P scan).

Santalum austrocaledonicum var. *pilosulum* N.Hallé: New Caledonia, Grande-Terre. Nouméa, Ouen Toro, 50 m, forêt côtière sur pente caillouteuse schisteuse 29 December 1971, *H.S. MacKee 24766* (holotype: P scan); Mont Dore, Ilot Pêcheur, 27 January 2015, *G. Gâteblé 708* (IAC); Paita, Stand de Tir, 27 January 2015, *G. Gâteblé 709* (IAC); Ouen Toro, March–April 1983, *Herbier Convention 10* (NOU); Ouen Toro, 12 February 1979, *M. Hoff 184* (NOU); Nouméa, île Nou, 5 February 1978, *H.S. MacKee 34688* (NOU, P scan); Plantule provenance Ouen Toro, Port-Laguerre, Paita, 1 October 1982, *H.S. MacKee 40837* (NOU, P scan); Nouméa, Ouen Toro, 50 m, 26 June 1987, *H.S. MacKee 43600* (NOU, P scan); Plantule provenance Ouen Toro, Port-Laguerre, Paita, 17 August 1987, *H.S. MacKee 43657* (NOU, P scan); Ouen Toro hill at S End of Noumea, 50 m, 31 January 1982, *G. MacPherson 4558* (NOU, P scan); Nouméa, Anse Vata, SW-Hang des Mt Ouen Toro, 100 m, 22 February 1964, *H.U. Stauffer 5701* (NOU, P scan, Z n.v.); Nouméa, Anse Vata, SW-Hang des Mt Ouen Toro, 100 m, 22 February 1964, *H.U. Stauffer 5702* (NOU, P scan, Z n.v.); Areal der IFO, Anse Vata, Nouméa, 11 March 1964, *H.U. Stauffer 5792* (NOU, P scan, Z n.v.); IFO, Anse Vata, 6 January 1965, *J.M. Veillon 18* (NOU, P scan); Nouméa, Colline du Ouen Toro, 1 April 1969, *J.M. Veillon 1934* (NOU, P scan).

Santalum austrocaledonicum var. *minutum* N.Hallé: New Caledonia, Grande-Terre. Montagne de Poum, pic 272, versant Est, 50 m, arbuste 3m, 25 March 1982,

J.M. Veillon 4852 (holotype: P n.v.; isotype NOU scan); Arama, collines près de la mer, 1855-60, *E. Vieillard 1090ter* (P scan); Koumac, Camp militaire, SMA, 8 August 1994, *A. Dessert 2* (NOU); Koumac, Babouillat, 14 June 2014, *G. Gâteblé 518* (IAC); Entrée de Koumac, terrain du SMA, 16 December 1994, *T. Jaffré 3257* (NOU, P scan); Au pied de la Tiebaghi 18 October 1970, *M. Schmid 3465* (NOU); Montagne de Poum, 25 March 1982, *B. Suprin 1744* (NOU); Montagne de Poum, 9 June 1982, *B. Suprin 1948* (NOU); Koumac, Camp militaire, SMA, 9 August 1994, *B. Suprin 2435* (NOU).

Corrigenda: A revision of infrageneric classification in *Astelia* Banks & Sol. ex R.Br. (Asteliaceae)

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In Birch (2015), *Astelia banksii* A.Cunn. was incorrectly stated as present in New Caledonia within the “Included species and distribution” section for *Astelia* sect. *Isoneuron* Skotts. (page 112). The correct distribution of *Astelia banksii* A.Cunn. is New Zealand. The *Astelia* sect. *Isoneuron* Skotts. “Included species and distribution” section should read: Included species and distribution. New Caledonia: *A. neocaledonica* Schltr. New Zealand: *A. banksii* A.Cunn.

Additionally, the designation of the *A. microsperma* Colenso *pro parte* type was incorrectly stated (page 113) as being made by Skottsberg on page 81 (1934). This type designation was made by Skottsberg on page 87 (1934). The designation of the *A. microsperma* type should correctly read:

Astelia microsperma Colenso *pro parte*, Trans. & Proc. New Zealand Inst. 17: 251. 1885 (description of fruit only). Type: NEW ZEALAND. North Island. Seventy-mile Bush, between Norsewood and Dannevirke, County of Waipawa. 1884, *W. Colenso s.n.* (Lectotype: K [000524879, digital image!], fruiting material in packet, designated by Skottsberg, 1934, 87).

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