Phylogeny of Cladonia uncialis (Cladoniaceae, Lecanoromycetes) and its allies

Soili STENROOS, Raquel PINO-BODAS, Diana WECKMAN and Teuvo AHTI

Abstract: The species from Cladonia section Unciales are characterized by the absence of squamules and soredia on the corticate podetia and the presence of usnic acid. Different subspecies, varieties and forms have been distinguished in the type species C. uncialis. In this study, a molecular phylogeny of Cladonia uncialis and members of the traditionally recognized section Unciales, along with additional potentially allied species, was constructed. DNA sequences from three gene loci, namely ITS rDNA, IGS rDNA and β -tubulin, were analyzed using Maximum Parsimony, Maximum Likelihood, and Bayesian methods. Eleven species were analyzed for the first time using DNA sequence data. Cladonia uncialis subsp. uncialis and subsp. biuncialis were recognized as distinct taxa. The recognition of C. pseudostellata as a species was not supported by the analyses, but it represents a hypothamnolic acid chemotype, which is reported here as new to Europe (Scotland). The presence of subsp. biuncialis in North America (Newfoundland) was substantiated. The subsp. uncialis usually lacks squamatic acid, but in the eastern United States a morph referred to as subsp. uncialis does normally contain that acid. However, this morph did not attain taxonomic recognition based on phylogenetic analyses. All the other taxa formerly included in sect. Unciales turned out to belong to other groups of Cladonia, mainly Amaurocraeae, Borya, Divaricatae, and Perviae. The formerly recognized genus Cladina (reindeer lichens) is non-monophyletic, consisting of three groups within Cladonia, making the concept Cladina even nomenclaturally useless. Alternative topology tests rejected the monophyly of C. pseudostellata, section Unciales and Cladina.

Key words: β-tubulin, Cladina, Cladonia pseudostellata, Cladonia uncialis subsp. biuncialis, IGS rDNA, infrageneric taxonomy, ITS rDNA, lichens

Accepted for publication 17 April 2015

Introduction

The formerly recognized *Cladonia* section *Unciales* (Delise) G. Merr. (e.g. Vainio 1887: 235; Ahti 2000; note the corrected author citation; the combination by Merrill 1908: 109 has been overlooked) included species typically defined by characters such as the soon evanescent primary thallus, the absence of podetial squamules and soredia, the presence of a more or less distinct cortex and the cortical substance usnic acid. This acid gives a visible yellowish tint to these species, depending on its concentration. There are over 40 *Cladonia* species in the world with these features (Ahti 2000).

The status of the section Unciales as a whole has been discussed by a few authors, including Nylander (1866), Vainio (1880, 1897), Mattick (1938, 1940, 1951), Dahl (1952) and Aasamaa (1961). Vainio (1897: 98) attempted a preliminary subdivision of the Unciales and distinguished three major lineages: Cladonia divaricata, C. peltasta, and the rest of the group. Choisy (1928) claimed that, against common belief, C. uncialis (L.) F. H. Wigg. and C. amaurocraea were not closely related. In Mattick's (1951) final scheme, the Unciales were placed as a subsection under the section Perviae. Ahti (1973) recognized the so-called C. boryi group within the Unciales, including the species that develop needle crystals (presumably triterpenoids) on the tips of podetia. Finally, Stenroos et al. (2002) presented the first comprehensive phylogeny of the genus Cladonia, based on DNA sequences.

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Unciales was resolved as a non-monophyletic group, but recognized in the strict sense, many species being placed into other, provisionally recognized and informally named groups. The following species from the Unciales were transferred to other groups of Cladonia: C. capitellata, C. peltastica and C. perforata were placed in the Supergroup Perviae, and C. subchordalis in the Supergroup Cladonia. The Supergroup Crustaceae included most of the taxa of the former section Unciales, but they were placed in several Groups: Group Amaurocraeae, Group Divaricatae, and Group Unciales. Group Unciales was divided into two Subgroups: Subgroup Borya, which included the taxa that Ahti (1973) assembled in the C. boryi group, and Subgroup Unciales, including our current target species Cladonia uncialis.

Cladonia uncialis itself is morphologically and chemically variable. Typically, its podetia are continuously corticate, yellowish, moderately branched, erect, brown-tipped and spine-like, with a well-developed and fairly smooth cortex (or sometimes with a slightly rough surface). These characters distinguish it from the reindeer lichens (former *Cladina*), which are its common associates in thick lichen mats on forest floors.

Vainio (1922) distinguished by morphology as many as six forms of C. uncialis in Finland. Kärenlampi (1964) and Kärenlampi & Pelkonen (1971) examined in detail its various morphological characters, such as the number of branches, the coverage of the podetial surface by algal cells, and the production of conidiomata and apothecia. As a result, two varieties of C. uncialis were distinguished, namely var. uncialis and var. dicraea (Ach.) Räsänen (author citation corrected here). The former variety was characterized by a polytomic branching pattern, a relatively low coverage of algal cells, and its common production of conidiomata and apothecia. The latter variety was described as mainly dichotomous, with a higher coverage of algal cells, and rare production of conidiomata and apothecia. Brodo & Ahti (1996) distinguished several morphotypes among C. uncialis s. lat. These morphs were based on branching patterns, surface structure, and chemical composition.

Today, the two morphotypes mentioned above are better known as subsp. *uncialis* and subsp. biuncialis (Hoffm.) M. Choisy (e.g. Ahti & Stenroos 2013). The subspecies concept was also suggested by Hawksworth (1973), who studied the variability of C. uncialis in Britain and introduced the combination C. uncialis subsp. dicraea (Ach.) D. Hawksw. Ahti (1978) noted that subsp. *biuncialis* is an older name at subspecies level. However, the taxonomic treatment of the subsp. biuncialis has varied. In addition to being distinguished as a subspecies, variety or form (originally as a species, C. biuncialis Hoffm.), it has often not been given any formal status. A chemotype of C. uncialis s. lat. containing hypothamnolic acid was found in Japan. Asahina described it as a different species, C. pseudostellata. However, Brodo & Ahti (1996) considered C. pseudostellata as synonymous with C. uncialis s. lat., since they did not find any correlation between the presence of hypothamnolic acid and morphology. To date, the taxonomic status of C. uncialis and its postulated segregates has not been resolved.

The goals of the present study therefore are: 1) to clarify the status of *Cladonia uncialis* s. lat. and test if its segregates can be distinguished and possibly warrant a species status, and 2) try to resolve the relationships of the members formerly referred to section *Unciales*.

Material and Methods

Taxon sampling

In the present study, 74 samples from 32 species of section Unciales (Ahti 2000) were included (Table 1). Our work emphasizes the circumscription of Cladonia uncialis s. lat. Therefore we included 14 specimens of C. uncialis subsp. uncialis, 11 specimens of C. uncialis subsp. biuncialis, and six specimens of C. pseudostellata. Specimens of other Cladonia groups, representing all the major clades outlined in the previous phylogeny of the genus (Stenroos et al. 2002), were included in this study: eight specimens of Cladina, three of Cocciferae, six of Divaricatae, three of Miniatae, three of Perviae, and five of Cladonia (Table 1). The taxa related to Unciales members (sensu Stenroos et al. 2002) were selected. Cladonia furcata was used to root the tree. The collections studied are deposited in the herbarium H (Botanical Museum, University of Helsinki).

			GenBa	nk accession	numbers	01
Taxon	Voucher specimen	Code	ITS rDNA	IGS rDNA	β-tubulin	
C. ahtii S. Stenroos	Brazil, Paraná, Ahti & Eliasaro 57582 (H)	AT727	AF453275	KR019426	AF458486	
C. albofuscescens Vain.	Brazil, Minas Gerais, Stenroos 5019 (TUR)	SATU5	AF455242	KR019427	_	
C. albofuscescens Vain.	Brazil, Minas Gerais, Stenroos 4946 (TUR)	SATU9	AF455241	KR019428	AF458548	
C. amaurocraea (Flörke) Schaer.	Finland, Stenroos 5172 (TUR)	LK23	AF455245	KR019429	AF458549	P
C. amaurocraea (Flörke) Schaer.	Finland, Stenroos 5159 (TUR)	LK7	AF455244	KR019430	_	þ
C. amaurocraea (Flörke) Schaer.	Greenland, Narsaq, Högnabba 871 (H)	DW16	KR019406	KR019501	KR019522	/lo
C. arbuscula (Wallr.) Flot.	Canada, Nova Scotia, Ahti 57095 (H)	LK36	AF458292	KR019431	AF458577	ğ
C. arbuscula (Wallr.) Flot.	USA, Alaska, Aleutian Islands, Talbot & Schofield s.n. (H)	DW27	KR019410	KR019505	KR019523	Ë
C. atlantica A. Evans	USA, Massachusetts, Ahti 56853 (H)	LK42	AF457884	KR019432	AF458561	y c
C. bahiana Ahti	Brazil: Minas Gerais, Splett 968 (H)	AT715	AF456403	KR019433	_	Ĭ
<i>C. bahiana</i> Ahti	Brazil, Bahia, <i>Stocker</i> s.n. (H)	AT716	AF456402	KR019434	_	ß
C. borealis S. Stenroos	Finland, Stenroos 5157 (TUR)	LK4	AF454434	KR019445	AF458504	aa
<i>C. borvi</i> Tuck	USA. New York. Stenroos 5742 (H)	DW6	KR019388	KR019446	_	tor
<i>C. borvi</i> Tuck	Canada, Newfoundland, Ahti & Scott 56962 (H)	LK50	AF457907	KR019447	_	iia
C bory Tuck	Canada, Nova Scotia, <i>Ahti</i> 57176 (H)	LK6	AF457906	KR019448	_	n 1
<i>C. candelabrum</i> (Bory) Nyl.	Madagascar, Baranow & Szlachetko (H)	CL106	KR019384	KR019449	KR019531	nc
C candelabrum (Bory) Nyl	France, Réunion, Room 40493 (H)	DW21	KR019385	KR019450	KR019532	ia
<i>C</i> capitellata (Hook f & Taylor) C Bab	New Zealand, Stenroos 6023 (H)	CL73	KR019386	KR019451	KR019533	lis-
C caroliniana Tuck	USA South Carolina <i>Ahti</i> 58186 (H)	AT636	AF456408	KR019452	AF458557	
C. cenotea (Ach.) Schaer	Finland Mullus 213 (TUR)	IK61	AF457896	KR019453	AF458567	S
C. consimilis Vain	Brazil Minas Gerais Steproos 5050 (TUB)	SATUI	AF456405	KR019454		en
C. consimilies Vain	Brazil, Minas Gerais, Stenroos 5048 (TUR)	SATU2	AE456400	KR019454		ro
C. delagrani Abbayes	Bhutan Sachting 8408 (H)	1K30	AE458304	KR019455	AF458582	so
C. dilloniana Elörke	Cuba Buch 55700 (H)	CI 312	AI-450504	KR019450	AI-430302	et
C. dimerchaclada Pobbins	USA South Caroling Akti 58180 (TUR)	AT635	AE456407	KR019450	AE458556	al
C. dimorphociada Robbins	Prozil Minos Coroio Stannos 4000 (TUP)	SATUIO	AE457010	KR019439	AE458570	•
C. divaricata INVI.	Brazil, Minas Gerais, Sterross 5052a (TUR)	AT710	AE456401	KK019400	AE458555	
C. fuerence (Hunda) Schwad	LISA Coorrige Abri 59292 (TUD)	AT / 10	AE455220		AE458520	
C. jurcaia (Huds.) Schrad.	DSA, Georgia, Anni 56265 (TUK) Pussia, Kamabatha tamitany, Himalbuant 02082011, 1 (H)	CI 244	KP010280	KR019401	KP010525	
C. kanewskii Oxner	Russia, Kamenatka territory, Himelorani 02002011-1 (H)	CL 244	KR019369	KR019402	KR019555	
C. kanewskii Owner	LISA Alasha Neitlich & Handhach 2160d (II)	UL245	AE456406	KR019405	KK019550	
C. Ranewskii Oxner	Disa, Alaska, Neulich & Hasselbach 21000 (H)	LK32	KP010201	KK019404		
C. aff. kanewskii Oxner	Russia, Buryana, Orbanavichene & Orbanavichus S. n. (H)	DW22	KR019591		KR019557	
C. labraaorica Anti & Brodo	Canada, Quebec, Seppara EI (H)	CL167	KKU19394	KR019465		
C. lepiaophora Anti & Kashiw.	Unite, Usorno, Feuerer 60297 (TUK)	A1507	AF454440	KR019466	AF458506	
C. lopezu S. Stenroos	Brazil, Minas Gerais, Stenroos 5029 (TUR)	A1561	AF453279	KR019467		21
C. medusina (Bory) Nyl.	Madagascar, Baranow & Szlachetko s. n. (H)	CL161	KR019395	KR019468	KR019538	-1

TABLE 1. List of Cladonia specimens used in this study with voucher information and GenBank accession numbers.

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			GenBan	k accession 1	numbers
Taxon	Voucher specimen	Code	ITS rDNA	IGS rDNA	β -tubulin
C. medusina (Bory) Nyl.	Madagascar, Baranow & Szlachetko s. n. (H)	CL162	KR019396	KR019469	KR019539
C. minarum Ahti	Brazil, Minas Gerais, Stenroos 4961 (TUR)	SATU7	AF457909	KR019470	_
C. mitis Sandst.	Finland, Stenroos 5209 (TUR)	AT651	AF457914	KR019471	AF458574
C. mitis Sandst.	Russia, Kamchatka territory, Himelbrant & Stepanchikova s. n. (H)	FH336	KR019392	KR019472	KR019540
C. nipponica Asahina	USA, Alaska, Kodiak Island, Dillman 19 (H)	CL213	KR019397	KR019473	KR019541
C. nipponica Asahina	Russia, Primorskiv Kray, Zhdanov Sikh-3-3 (H)	FH338	KR019393	KR019474	_
C. pachycladodes Vain.	USA, Florida, Rosentreter 16470 (H)	DW18	KR019398	KR019475	KR019542
C. pachyclados (Vain.) Ahti	France, Réunion, Boom 40543 (H)	DW20	KR019399	KR019476	KR019543
C. peltasta Spreng.	France, Réunion, Boom & Boom 40397 (H)	CL104	KR019425	KR019477	_
C. perforata A. Evans	USA, Florida, 1993, Yahr 93/2 (US)	Yahr	AF457903	_	AF458570
C. peziziformis (With.) J. R. Laundon	USA, District of Columbia, Stenroos 5198 (TUR)	AT631	AF455221	KR019478	AF458540
C. pleurota (Flörke) Schaer.	Mexico, Veracruz, Stenroos 5143 (TUR)	AT587	AF454445	KR019479	AF458510
C. pseudostellata Asahina	Japan, Honshu, Ohmura 6000 (H)	FH328	KR019400	KR019480	KR019544
C. pseudostellata Asahina	USA, Alaska, Aleutian Islands, Talbot & Schofield TIG003-X-3 (H)	DW28	KR019411	KR019506	KR019547
C. pseudostellata Asahina	USA, Alaska, Aleutian Islands, Talbot & Schofield ADA122-X-01 (H)	DW5	KR019414	KR019509	KR019548
C. pseudostellata Asahina	USA, Alaska, Aleutian Islands, Talbot & Schofield KML 003-X-1 (H)	FH326	KR019421	KR019516	KR019553
C. pseudostellata Asahina	Great Britain, Scotland, Stenroos 6088 (H)	FH350	KR019423	KR019518	KR019555
C. pseudostellata Asahina	Great Britain, Scotland, Stenroos 6095 (H)	FH347	KR019383	KR019444	KR019530
C. pycnoclada (Pers.) Nyl.	Chile, Prov. Osorno, Feuerer 60257 (TUR)	AT509	AF458297	KR019482	AF458579
C. rugulosa Ahti	Guyana, Stenroos 4831 (TUR)	AT577	AF457894	KR019483	AF458565
C. secundana Nyl.	Guyana, Stenroos 4812b (TUR)	LK74	AF453274	KR019484	AF458485
C. siamea Abbayes	Indonesia, Papua, Miettinen 11620,3 (H)	CL77		KR019485	_
C. solitaria H. Marg.	USA, Hawaii, Palmer et al. 2677 (US)	2677	AF457905		_
C. stenroosiae Ahti	Brazil, Minas Gerais, Stenroos 5013 (TUR)	LK25	AF456409	KR019486	_
C. stereoclada Abbayes	Spain, Canary Islands, Burgaz s.n. (MACB 97913)	3STEREO	KR019556	KR019558	_
C. stereoclada Abbayes	Spain, Canary Islands, Alanko 128470a (H)	CL138	KR019557	KR019559	_
C. stevermarkii Ahti	Guyana, Stenroos 4916 (TUR)	LK89	AF456404	KR019487	_
C. strepsilis (Ach.) Grognot	Finland, Stenroos 5160 (TUR)	AT537	AF457880	KR019488	AF458559
C. stygia (Fr.) Ruoss	Finland, Steproos 5200 (TUR)	AT647	AF458308	KR019489	AF458584
C. subchordalis A. Evans	Chile, Magallanes, Feuerer 60166 (TUR)	AT512	AF455175	KR019490	AF458524
C. subchordalis A. Evans	Chile, Osorno, Feuerer 60406 (TUR)	LK90	AF455174	KR019491	_
C. subreticulata Ahti	Brazil, Minas Gerais, Stenroos 5078 (TUR)	SATU3	AF457904	KR019492	AF458571
C. subsetacea Robbins ex A. Evans	USA, Florida, Rosentreter 16465 (H)	CL141	KR019402	KR019493	
C. subsetacea Robbins ex A. Evans	USA, Florida, Rosentreter 16475 (H)	DW19	KR019403	KR019494	_
C. substellata Vain.	Brazil, Minas Gerais, Stenroos 4964 (TUR)	SATU21	AF457877	KR019495	AF458558

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TABLE 1. Continued

			GenBar	nk accession	numbers	01
Taxon	Voucher specimen	Code	ITS rDNA	IGS rDNA	β-tubulin	
C. subtenuis (Abbayes) Mattick C. subulata (L.) F. H. Wigg. C. terrae-novae Ahti C. uncialis (L.) F. H. Wigg. subsp. uncialis C. uncialis (L.) F. H. Wigg. subsp. uncialis C. uncialis (L.) F. H. Wigg. subsp. uncialis C. uncialis (L.) F. H. Wigg. subsp. uncialis	Canada, Nova Scotia, Ahti 57068 (H) Germany, Thell 9932 (TUR) Canada, Newfoundland, Ahti & Scott 56942(H) Finland, Haikonen 26612 (H) USA, New York, Stenroos 5743 (H) Russia, Leningrad region, Ahti 68342 (H) Russia, Kamchatka territory, Himelbrant & Stepanchikova s.n. (H)	AT571 LK64 AT572 CL204 DW2 DW25 FH332	AF457911 AF455181 — KR019404 KR019407 KR019408 KR019401	KR019496 KR019497 KR019498 KR019499 KR019502 KR019503 KR019481	AF458573 AF458528 AF458580 KR019545	Phyloger
C. uncialis (L.) F. H. Wigg. subsp. uncialis C. uncialis (L.) F. H. Wigg. subsp. uncialis	Canada, Nova Scotia, Ahti 62683 (H) USA, New York, Stenroos 5713 (H) USA, Washington, Droker 24191208-1 (H) USA, New York, Stenroos 5712 (H) Canada, Newfoundland, Stenroos 5701 (H) Canada, Ouchec, Stenroos 5707 (H)	DW26 DW3 DW4 DW7 FH234 FH235 FH237	KR019409 KR019412 KR019413 KR019415 KR019417 KR019418 KR019419	KR019504 KR019507 KR019508 KR019510 KR019512 KR019513 KR019514		ny of Cladonia
C. uncialis (L.) F. H. Wigg, subsp. uncialis C. uncialis subsp. biuncialis (Hoffm.) M. Choisy C. uncialis subsp. biuncialis (Hoffm.) M. Choisy C. uncialis subsp. biuncialis (Hoffm.) M. Choisy	Canada, Newfoundland, Ahti 67881 (H) USA, Washington, Droker 150208-1 (H) USA, Alaska, Aleutian Islands, Talbot AML002-24 (H) Greece, Sipman & Raus 58672 (H) France, Haute-Savoie, Ahti 68190 (H) Finland, Weckman 2 (H)	FH232 FH324 FH349 CL210 DW1 DW10	KR019387 KR019420 KR019422 KR019374 KR019375 KR019376	KR019457 KR019515 KR019517 KR019435 KR019436 KR019437	KR019532 	t uncialis—St
C. uncialis subsp. biuncialis (Hoffm.) M. Choisy C. uncialis subsp. biuncialis (Hoffm.) M. Choisy	Finland, Weckman 3 (H) Iceland, Högnabba 1345 (H) Iceland, Högnabba 1391 (H) Canada, Newfoundland, Ahti et al. 67978 (H) Denmark, Faeroe Islands, Väre L1840 (H) Finland, Ahti 68261a (H)	DW11 DW14 DW15 FH233 FH236 FH325	KR019377 KR019378 KR019379 KR019380 KR019381 KR019382	KR019438 KR019439 KR019440 KR019441 KR019442 KR019443	KR019524 KR019525 KR019526 KR019527 KR019528 KR019529	enroos et al.
C. uncialis subsp. biuncialis (Hoffm.) M. Choisy C. uncialis subsp. biuncialis (Hoffm.) M. Choisy C. vareschii Ahti C. variegata Ahti C. zopfii Vain.	Iceland, <i>Högnabba</i> 1298 (H) Finland, <i>Weckman</i> 1 (H) Guyana, <i>Stenroos</i> 4881 (TUR) Guyana, <i>Stenroos</i> 4922 (TUR) Portugal, Trás-os-Montes, <i>Burgaz</i> s.n. (H)	DW12 DW9 LK85 AT601 FH344	KR019405 KR019416 AF457878 AF455240 KR019424	KR019500 KR019511 KR019519 KR019520 KR019521	KR019546 KR019549 — —	

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Chemical study

The secondary metabolites of all the samples of *C. uncialis* subsp. *uncialis*, *C. uncialis* subsp. *biuncialis*, and *C. pseudostellata* were analyzed using thin-layer chromatography (TLC), in solvents A and B, according to White & James (1985).

DNA extraction, PCR and sequencing

DNA was extracted using DNeasy Blood and Tissue Kit (Qiagen), according to the manufacturer's protocol. The extracted DNA was eluted in 160 µl of elution buffer included in the kit. Several potential loci (including mtSSU, ef1α, mcm7, ITS rDNA, IGS rDNA, β-tubulin and other unpublished markers) were tested in a subset of specimens in order to check the variation and the PCR success of each one. On the basis of the preliminary results, we decided to choose ITS rDNA, IGS rDNA and β -tubulin for the molecular study. The ITS rDNA region was amplified using the primers ITS1F (Gardes & Bruns 1993) and ITS4 (White et al. 1990) or ITS1-LM (Myllys et al. 1999) and ITS2-KL (Lohtander et al. 1998); the IGS rDNA region using IGSf and IGSr (Wirth *et al.* 2008); and the β -tubulin gene using the primer pair Bt3-LM and Bt10-LM (Myllys et al. 2001). The amplification programmes were as follows: 95 °C for 5 min; 5 cycles of 30 s at 95 °C, 30 s at 58 °C, 60 s at 72 °C; 30 cycles of 30 s at 95 °C, 30 s at 56 °C, 60 s at 72°C; 7 min at 72°C for ITS rDNA; 95°C for 5 min; 35 cycles of 30 s at 95 °C, 30 s at 54 °C, 60 s at 72 °C; 10 min at 72 °C for IGS rDNA; 95 °C for 5 min; 5 cycles of 30s at 95 °C, 30s at 55 or 56 °C, 60s at 72 °C; 30 cycles of 30 s at 95 °C, 30 s at 52 or 54 °C, 60 s at 72 °C; 7 min at 72 °C for β -tubulin. PCR was carried out using Ready-To-Go PCR Beads (GE Healthcare), with 25 µl of final volume, 1 µl of each primer at 10 µM concentration, and 4 or 5 µl of DNA. PCR was performed in PTC-200 Thermal Cyclers (MJ Research) and Mastercycler ep gradient S (Eppendorf). PCR products were purified using illustra GFX PCR DNA and Gel Band Purification Kit (GE Healthcare). Sequencing reactions were carried out at Macrogen Inc. (http://www.macrogen.com).

Phylogenetic analyses

The alignments were assembled using MUSCLE (Robert 2004) for each locus separately. The ambiguously aligned regions were manually delimited (13 positions in ITS rDNA and four in IGS rDNA) and excluded from the analyses. Each locus was analyzed by maximum likehood (ML), using RAxML 7.04 (Stamatakis 2006), assuming a GTRGAMMA model. The best ML trees were searched using every fifth bootstrap tree as a starting tree (100 independent searches). The nodal support was assessed with 500 bootstrap pseudoreplicates using the rapid bootstrap option. The β -tubulin locus was analyzed using two partition approaches: 1) considering it as a single subset, 2) considering the introns and each codon position from the coding regions as a different subset (in total eight subsets) and analyzed with the same model. The introns were delimited by comparing Cladonia sequences in

GenBank (AF458533 and AF458550) with our sequences. The topology of β -tubulin trees obtained with both approaches was the same and we decided to use the whole locus as a single subset in the combined analyses. The clades with bootstrap support >75% were examined to assess the congruence among the loci according to the method of Kauff & Lutzoni (2002, 2003). No strongly supported incongruence was detected among the loci, and the different datasets were therefore combined. In the combined matrix, only those samples were included for which the sequences of at least two loci were available, except for C. nipponica FH338, C. siamea CL77 and C. solitaria 2677. Only IGS rDNA or ITS rDNA sequences were obtained for these samples, but they were included because the species are rare and no fresh material was available. The combined dataset was analyzed by maximun parsimony (MP), ML and Bayesian inference.

The MP analysis was performed in PAUP ver. 4.0.b.10 (Swofford 2003) using heuristic searches with 1000 random taxon-addition replicates, and with TBR branch swapping and the MulTrees option. All the characters were treated as equally weighted and gaps were coded as missing data. The clade support was determined by bootstrap analysis, with 1000 replicates, using the heuristic option. The ML analyses were implemented using RAxML 7.04, considering a partition with three subsets: ITS rDNA, IGS rDNA, and β -tubulin, assuming a GTRGAMMA model, and using the same options as for single gene analyses. Bayesian analysis was carried out using MrBayes 3.1.2 (Huelsenbeck & Ronquist 2001). The best-fit evolutionary model for each locus was selected by MrModeltest 2.3 (Nylander 2004) under the AIC criterion. The three models are listed in Table 2. Two simultaneous runs with 10 000 000 generations, each starting with a random tree and employing four simultaneous chains, were executed. Every 1000th tree was saved into a file. The average standard deviation of split frequencies between the runs was below 0.01, indicating convergence of the chains. The first 1 000 000 generations (i.e., the first 1000 trees) were deleted as the 'burn-in' of the chain. Cumulative split frequency plot in AWTY (Nylander et al. 2008) was used to determine when the chains reached the stationary stage. The 50% majority-rule consensus tree was calculated using the 'sumt' command of MrBayes.

Tree topology test

The phylogenetic estimates of the concatenated dataset revealed that *C. pseudostellata* is not monophyletic. In order to dismiss the possibility that this result is an artefact of the phylogenetic analyses, we conducted a Shimodaira-Hasegawa test (SH; Shimodaira & Hasegawa 1999) and used the expected likelihood weight test (ELW; Strimmer & Rambaut 2002). RAxML 7.04 was used to estimate the maximum likelihood tree consistent with the alternative hypotheses (monophyly of *C. pseudostellata*, *Unciales* and *Cladina*). The topological constraints analyses enforced only the monophyly of the taxa under study (*C. pseudostellata*, *Unciales* taxa or

Cladina taxa). The SH and ELW tests were run in TREE-PUZZLE 5.2 (Schmidt *et al.* 2002), using the GTR+I+G model and with four-category approximation to the gamma distribution for substitution rate among sites. The tests were estimated using 1000 replicates under the RELL method.

Genetic distances

The pairwise distances within and between *C. uncialis* subsp. *uncialis* and *C. uncialis* subsp. *biuncialis* were calculated in PAUP*, using the K2P model (Kimura 1980) for each locus separately (ITS rDNA, IGS rDNA and β -tubulin). We applied this model as it was used in Pino-Bodas *et al.* (2013). To compare the genetic variability between *C. uncialis* subsp. *uncialis* and *C. uncialis* subsp. *biuncialis*, the mean nucleotide difference within and between taxa was calculated in DnaSP 5.1 (Librado & Rozas 2009). In addition, the genetic similarity (GD) for each locus was calculated as GD = 1 - (genetic distance between sample pairs). Histograms of genetic distances and genetic similarity within and between taxa were created for each marker (Fig. 3).

Results

combined dataset contained 102 The sequences and 1819 characters. Table 2 summarizes the variation of the sequences. A total of 186 new sequences were generated for the study. The MP analysis yielded a total of 1000 equally parsimonious trees with 2058 steps, CI = 0.5042 and RI = 0.7781. The ML analysis yielded a tree with lnL (log likelihood) =-13871.90, while the Bayesian analyses yielded a consensus tree with $\ln L = -13798 \cdot 10$ (arithmetic mean). All three methods yielded trees with the same topology and only the 50% majority-rule tree from the Bayesian analysis is presented in Fig. 1. The provisional clade names mostly correspond to those presented in Stenroos et al. (2002).

The section *Unciales* is non-monophyletic, and most of the species appear in four groups,

viz. Amaurocraeae, Borya, Divaricatae and species from Unciales. Other section Unciales fall within Perviae (C. candelabrum, C. capitellata, C. dilleniana, C. medusina, C. pachyclados, C. rugulosa, C. siamea and C. subsetacea), and Cladonia (C. subchordalis); C. delavayi is closely related to Impexae. The SH and ELW tests rejected the monophyly of section Unciales with a P-value of <0.01. Furthermore, the former genus Cladina splits into three entities (Cladinae, Impexae, and Tenues), all of which are nested within the genus Cladonia. The ELW test rejected the monophyly of *Cladina* (P = 0.0464) but it was not rejected by the SH test (P = 0.3340). Cladonia uncialis s. lat. appears monophyletic, and can be divided into two well-supported clades.

In all the phylogenetic analyses, C. pseudostellata was resolved as nonmonophyletic (Fig. 1). The specimens of this taxon were clustered in the Cladonia uncialis s. lat. clade. The SH and ELW tests rejected the monophyly of C. pseudostellata with a P-value of <0.01 in both tests.

Cladonia uncialis s. lat. contains usnic acid as a major, constant substance. The presence of squamatic acid did not correlate with any of the clades obtained within *C. uncialis* or its subclades. This compound can be found in subsp. *uncialis* as well as in subsp. *biuncialis* (Fig. 2). The six specimens of *C. pseudostellata* contained usnic and hypothamnolic acids (Fig. 2).

The genetic distances and genetic similarity are shown in Table 3 and Fig. 3. In all the loci, *C. uncialis* subsp. *uncialis* had greater variation in the genetic distances and average nucleotide differences than *C. uncialis* subsp. *biuncialis*. The locus IGS rDNA showed the highest intra- and inter-clade distance values. Fig. 3 shows the similarity in *C. uncialis*

 TABLE 2. Summary of variation in each locus studied in the Cladonia uncialis phylogeny: alignment length in number of bases (positions), number of variable characters, parsimony informative characters and evolutionary models selected by MrModeltest using AIC criterion.

Locus	Positions	Variable sites	Parsimony-informative	Model
β -tubulin	758	199	153	HKY+G
ITS rDNA IGS rDNA	$\frac{647}{414}$	311 223	227 162	SYM+G GTR+G

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FIG. 1. Phylogeny of the section Unciales resulting from the Bayesian analysis of the combined dataset of ITS rDNA, IGS rDNA and β -tubulin. 50% consensus majority tree from the Bayesian analysis. The support values \geq 70% MP bootstrap, \geq 70% ML bootstrap, \geq 0.95 posterior probalility of Bayesian analysis appear on the branches. Branches supported in the three analyses (MP, ML & Bayesian) are indicated with thick lines. Grey rectangles show the species of the section Unciales. Black vertical bars indicate the provisional classification of the species according to Stenroos *et al.* (2002).



FIG. 2. The clade *Cladonia uncialis* s. lat. from the 50% consensus majority tree of the Bayesian analysis based on the concatenated dataset. The different chemotypes and the specimen localities are indicated for each specimen. HTHA = hypothamnolic acid, SQU = squamatic acid, USN = usnic acid.

subsp. *uncialis*, *C. uncialis* subsp. *biuncialis* and between them. In all cases, the similarity was very high (greater than 0.94). The lower values of similarity were obtained in IGS rDNA within *C. uncialis* subsp. *uncialis*, and between *C. uncialis* subsp. *uncialis* and *C. uncialis* subsp. *biuncialis*.

Discussion

Phylogenetic reconstructions have enormously changed the classification in several groups of lichenized fungi. Changes are still taking place, even in *Cladonia*, a conspicuous and fairly well studied genus (for example Ahti 2000; Stenroos *et al.* 2002; Burgaz & Ahti 2009; Ahti & Stenroos 2013). Stenroos *et al.* (2002) distinguished three informal Subdivisions within the genus *Cladonia*. These Subdivisions were further divided into Supergroups, Groups and Subgroups. Some of their Supergroups essentially corresponded with former sections (such as *Cladonia*, *Cocciferae*, *Perviae*, etc.), but in many cases the formal sections were found to be non-monophyletic. Therefore, new groupings were distinguished, but no nomenclaturally accurate names were introduced for them. A new multigene analysis for the *Cladoniaceae* is currently under preparation, and while waiting for the results, we will not formalize any of the used group names here either.

Most *Cladonia* clades (Fig. 1) are well supported (with the exception of *Divaricatae* and *Amaurocraeae*); nonetheless the phylogenetic relationships among them remain unresolved in this study (Fig. 1). A greater number of taxa will be necessary to clarify this question; we confine ourselves here to discussing the taxa compositions.

				Gen	etic vari:	ability			
	I	TS rDN.	A	Ī	GS rDN	, A	c	β-tubulir	
Source of variation	GD	z	GS	GD	z	GS	GD	z	GS
Within C. uncialis ubsp. uncialis	0.00-0.0181 (0.0091)	5.06	0.9818-1 (0.9908)	0.00-0.0532 (0.0224)	5.98	0.9467 - 1 (0.9775)	0.00-0.0158 (0.0059)	3.77	0.9841-1 (0.9945)
Within C. uncialis ubsp. biuncialis	0.00-0.0162 (0.0076)	3.76	0.9837 - 1 (0.9923)	0.00-0.0073 (0.0027)	0.74	0.9926 - 1 (0.9972)	0.00-0.0031 (0.0015)	3.85	0.9968 - 1 (0.9984)
Between subspp mcialis and biuncialis	0.0035 - 0.0217 (0.0149)	6.03	0.9782 - 0.9964 (0.9851)	0.0109 - 0.0493 (0.0244)	5.45	0.9506 - 0.9890 (0.9754)	0.0206-0.0287 (0.0266)	9.85	0.9712 - 0.9793 (0.9733)
GD = ranges of ge	netic distances; N =	= averag	te nucleotide differei	nces; GS = ranges	s of gene	tic similarities. The	mean genetic distar	aces are g	given in brackets.

According to our results, Unciales includes only C. uncialis s. lat. (C. uncialis is the type species of the formal section). The other species earlier assigned to Unciales are nested in other clades, primarily in Borya, Divaricatae and Amaurocraeae. In addition, quite a few species turned out to belong to Perviae, which includes taxa that have open branch axils and are typically without usnic acid. However, species such as C. capitellata, C. dilleniana, and C. vareschii, all with usnic acid, clearly belong to Perviae. In fact, Ahti (2000) already noted that some species from Unciales were morphologically similar to Perviae species but had a different chemical composition.

Borya is characterized by the production of needle-like 'steroid' crystals in the apical parts of the podetia (except for C. solitaria), and a fibrous skeletal tissue in the medulla (Ahti 1973). Altogether 11 species appear in the Borya clade, confirming the species composition of Borya presented by Ahti (2000). There might yet be an additional species in the group. Our C. aff. kanewskii DW22 collected from South Siberia, Russia, morphologically resembles and which C. kanewskii, is probably an undescribed species. However, it is a single specimen and its placement is not clear (only supported in the Bayesian analysis). Other than that, we believe that all of the potential Borya species of Cladonia have now been analyzed.

Divaricatae includes species with a spiny appearance. Usnic acid may be present or absent, without a correlation with morphological characters. We included eight species, the same as in Stenroos et al. (2002). Divaricatae appears basal to the clade consisting of the red-fruited Cocciferae and Miniatae, as well as Amaurocraeae and Perviae. In the phylogenetic analysis presented by Stenroos et al. (2002), this group appeared closely related to Borya, Unciales, and Cladinae. A few more species still await placement (C. crassiuscula, C. ibitipocae, C. spinea, and C. sufflata).

Amaurocraeae is a small, enigmatic group consisting only of C. amaurocraea and the now newly placed C. peltasta. The former species is elongated and slender, and the smoothly corticated podetia are often tipped

TABLE 3. Genetic variability between and within C. uncialis subsp. uncialis and C. uncialis subsp. biuncialis for each locus.



FIG. 3. Histograms illustrating variation in genetic distance and genetic similarity in *Cladonia uncialis* subsp. *uncialis* (\square), *C. uncialis* subsp. *biuncialis* (\square), and between the subspecies (\blacksquare) A, ITS rDNA; B, IGS rDNA; C, β -tubulin.

with scyphi. Cladonia peltasta is also slender, but scyphi are absent and it produces ochraceous apothecia. Both species produce usnic and barbatic acid as secondary metabolites (Huovinen & Ahti 1986a). However, the relationship of C. peltasta with C. amaurocraea is not supported, therefore other relationships cannot be ruled out.

The following species have now been placed using phylogenetic analyses for the first time:

C. candelabrum, C. dilleniana, C. medusina, C. pachyclados, C. siamea, and C. subsetacea belong to Perviae in the present analysis; C. peltasta belongs to Amaurocraeae, and C. kanewskii, C. labradorica and C. pachycladodes belong to Borya.

The increase of taxa in future studies will clarify whether other species of the former and widely delimited section *Unciales* are phylogenetically closely related to C. uncialis or belong to the other segregates of the section. The taxa not yet analyzed are: C. bangii, C. chimantae, C. congesta, C. crassiuscula, C. glabra, C. hokkaidensis, C. ibitipocae, C. papuana, C. recticaulis, C. robusta, C. southlandica, C. spinea, C. sufflata and C. usambarensis.

Taxonomic status of *Cladonia uncialis* s. lat.

The phylogenetic analyses based on three loci showed that Cladonia uncialis s. lat. is monophyletic. It is divided into two wellsupported clades, which correlate with the two previously described subspecies, C. uncialis subsp. uncialis and C. uncialis subsp. biuncialis. In Stenroos et al. (2002), the two subspecies were non-monophyletic. However, the present study is based on an increased sampling of three loci, and therefore our results are more robust. Four specimens originally identified as C. pseudostellata (containing hypothamnolic acid, Fig. 2) were referred to C. uncialis subsp. uncialis, and two specimens to C. uncialis subsp. biuncialis. The monophyly of C. pseudostellata was also rejected by the SH and ELW tests. These results agree with the taxonomic proposal of Brodo & Ahti (1996) that C. pseudostellata is a chemotype of C. uncialis, although this suggestion has not been accepted by all lichenologists (e.g., Kurokawa & Kashiwadani 2006). This chemotype has now also been detected in Scotland, in subsp. *biuncialis*, and is a new record to Europe.

In the present work, we use genetic distances to discuss what the most appropriate taxonomic rank is for C. uncialis subsp. uncialis and C. uncialis subsp. biuncialis. In the genus Cladonia, the genetic distance variation ranges have been studied for 35 species that belong to the Supergroup Cladonia (sensu Stenroos et al. 2002; Pino-Bodas et al. 2013). The average values of the intraspecific genetic distances were 0.0094 for the ITS rDNA and 0.0289 for the IGS rDNA. Our results show that the average genetic distance for IGS rDNA between C. uncialis subsp. uncialis and C. uncialis subsp. biuncialis is lower than the average for *Cladonia*, which could be interpreted as a species including

two subspecies. In the ITS rDNA, the average value of the genetic distances between the two clades was higher than the average found by Pino-Bodas et al. (2013) in Cladonia. However, these authors found monophyletic species with higher values (e.g. C. acuminata, C. cariosa, and C. rei). The β -tubulin gene has not been used in previous barcoding studies with Cladonia, or other closely related genera of lichenized fungi, and therefore no genetic distance values are available for comparison. However, the three loci showed an overlapping of intra- and inter-clade genetic distances (Table 3, Fig. 3) and the genetic similarity among the taxa is very high. Therefore we consider that the subspecies status is the most appropriate one for our taxa. In addition, the genetic distances of ITS rDNA fell inside the intraspecies threshold (0.015-0.017) for the Parmeliaceae (Del-Prado et al. 2010).

The genetic divergence within the clade C. uncialis subsp. uncialis is higher than within the clade C. uncialis subsp. biuncialis for the three loci, particularly in IGS rDNA (Fig. 3, Table 3). This could indicate that the clade C. uncialis subsp. uncialis hides several infraspecific taxa. From a morphological viewpoint, this clade is much more variable than the clade C. uncialis subsp. biuncialis (Fig. 4). A wider sampling is necessary to test this hypothesis. Based on the observations by Ahti (2000) and J. Lendemer (pers. comm.) on the deviating populations of C. uncialis in the eastern United States (well-developed on Long Island, New York, for example; for description, see Hinds & Hinds 2007; Fig. 4F), we expected that the specimens from there would represent a distinct clade. However, though they clustered together, they were not resolved as a distinct group. Therefore, we are not recognizing a taxonomic entity there. These populations need special attention when additional loci are used in future analyses.

As to secondary chemistry, the yellow pigment usnic acid is constantly present in *C. uncialis.* Now that *C. pseudostellata* is included into the species, both subspecies may produce hypothamnolic acid, but as far as is known, only in some coastal areas such



FIG. 4. Morphological variation of Cladonia uncialis s. lat. A, C. uncialis subsp. biuncialis, Finland (photo: V. Haikonen); B, C. uncialis subsp. biuncialis, C. N. Tavares VIII-51, Portugal; C, C. uncialis subsp. uncialis, Finland; D, C. uncialis subsp. biuncialis, T. Ahti 2603, Canada, Newfoundland; E, C. uncialis subsp. uncialis, T. Ahti 67881, Canada, Newfoundland; F, C. uncialis subsp. uncialis, R. C. Harris 56802, USA, New York; G, C. uncialis subsp. uncialis, G. W. Scotter 8097, Canada, Northwest Territories; H, C. uncialis subsp. uncialis, T. Ahti 39182, Canada, British Columbia; I, C. pseudostellata, S. Talbot & W. B. Schofield KML003-X-1, USA, Alaska. Scales = 1cm. In colour online.

Japan, Alaska (especially Aleutian as Islands), and Scotland. In subsp. uncialis, only usnic acid is usually present (Leuckert et al. 1971; Carlin 1981; Huovinen & Ahti 1986a; Burgaz & Ahti 2009; Ahti & Stenroos 2013). However, squamatic acid is sometimes present as well, for example in Finland (Fig. 2). The somewhat deviating morph in eastern North America (Ahti 2000: 343), included here in subsp. uncialis, normally contains squamatic acid. On the other hand, subsp. biuncialis almost always produces squamatic acid. Very rarely, small amounts of barbatic acid are perhaps present (Ahti & Stenroos 2013), but the report might be based on confusion with C. amaurocraea which always contains barbatic acid, looks similar, and grows intermixed with C. uncialis.

There are obvious ecological differences between the two subspecies of Cladonia uncialis. In Europe, subsp. biuncialis is characteristic of oceanic, coastal conditions but extends far inland in the Iberian Peninsula (maps in Burgaz & Ahti 2009: 106) and Central Europe (Austria, Czech Republic, Germany, Poland, Slovakia, Switzerland, not reaching Russia beyond the Baltic Sea coast). Outside Europe it is known only from Newfoundland in eastern Canada (and the adjacent French possession St. Pierre & Miquelon), being absent from the Pacific coast. Subsp. uncialis is more continental, and is the only subspecies present within most of the wide, holarctic range of C. uncialis s. lat. (map in Litterski & Ahti 2004), although absent or rare right on the coast in Europe (e.g. absent from Iceland).

Although the two taxa are often easily identified morphologically, it is not always so. Kärenlampi & Pelkonen (1971) and Ahti & Stenroos (2013) pointed out that there are seemingly intermediate populations in areas where the subspecies meet, especially in southern Sweden and south-western Finland. Some authors (Coppins 1978; Burgaz & Ahti 2009) have paid attention to the inner surface of the podetial wall, which seems to be pulverulent in subsp. *biuncialis* and smooth in subsp. *uncialis*. The reliability of this character has not been tested.

Details of nomenclature and typification of the recognized subspecies

The treatment below includes a new typification and other nomenclatural notes.

Cladonia uncialis subsp. biuncialis (Hoffm.) M. Choisy

Bull. Mens. Soc. Linn. Lyon 20: 9 (Jan 1951).—Cladonia biuncialis Hoffm. Deutschl. Fl. 2: 116 (1796); type: [Germany?], hb. G. F. Hoffmann 8614 (MW-Hoffmann, neotype, designated by Ahti 1978: 9, as 'lectotype', corr. by Ahti 1993: 100).

Cladonia uncinata Hoffm., Deutschl. Fl. 2: 116 (1796); type: drawing in Dillenius, Hist. Musc. t. 16, fig. 21B (1742) (lectotype designated here by T. Ahti); sine loco, hb. Dillenius, Hist. Musc. No. 98.21B (OXF, epitype designated here by T. Ahti).

Baeomyces uncialis var. dicraeus Ach., Methodus: 353 [Jan-Apr 1803).—Cladonia uncialis var. dicraea (Ach.) Räsänen, Meddeland. Soc. Fauna Fl. Fenn. 46: 171 (1921) [not Kärenlampi & Pelkonen 1971: 55].— Cladonia uncialis subsp. dicraea (Ach.) D. Hawksw. in Heywood, Taxonomy and Ecology: 41 (1973); type: Sweden ('Suecia') (H-ACH 1625B = H 950273, lectotype, designated by Kärenlampi & Pelkonen 1971: 55).

Baeomyces aduncus Ach., Methodus: 353 (Jan-Apr 1803), nom. illeg. superfl. for Cladonia uncinata Hoffm.

Cladonia uncialis (L.) F. H. Wigg.

Fl. Holsat.: 90 (29 Mar 1780) subsp. uncialis Lichen uncialis L., Sp. Pl.: 1153 (1 Mai 1753); type (cons.): Sweden, Dalarna, Stora Kopparberg, Rotneby ('Rottneby prope urbem Fahlun Dalekarliae'), C. Stenhammar in Stenhammar, Lich. Suec. Exs., ed. 2, No. 210 (UPS; isotypes H, MIN).

Cladonia pseudostellata Asahina, J. Jap. Bot. 18: 620 (10 Nov 1942); type: Japan, Hokkaido, Kamikawa Dist. (Prov. Ishikari), Mt. Daisetsu, 1937, Y. Asahina 37016 (TNS, lectotype designated by Ahti 1993: 91; isolectotype US-Evans).

Polyphyly of the old genus Cladina

It has already been shown many times that *Cladina* (reindeer lichens) do not warrant a generic status but should be included in *Cladonia* (Hyvönen *et al.* 1995; Stenroos *et al.* 1997, 2002; DePriest *et al.* 1999; Ahti & DePriest 2001). These lichens commonly appeared monophyletic within *Cladonia* (Stenroos *et al.* 2002), but non-monophyly was also demonstrated in some cases (DePriest *et al.* 1999, 2000). Interestingly, as

early as in Choisy (1928), Cladina was treated as non-monophyletic and three different lineages were distinguished. In the present analyses, Cladina is non-monophyletic (but the monophyly of *Cladina* was rejected only by the ELW test) and is divided into three lineages, referred to here as Impexae, Tenues and Cladinae. They all correspond to the former sections defined by Ahti (1984, under genus Cladina; see also Huovinen & Ahti 1986b and Ahti 2000). Guo & Kashiwadani (2004) obtained a similar result based on ITS rDNA. In their analysis, C. uncialis is placed as sister to either the Tenues or Cladinae, depending on the model used. In our analyses, the phylogenetic relationships between Impexae, Tenues and Cladinae remain unresolved (Fig. 1). The proper placing of these clades will therefore have to wait for a broader sampling.

As stated above, we are using the infrageneric group names informally for the time being. The lineages concur with chemical characters in addition to the branching types.

Impexae, represented here by C. pycnoclada and C. terrae-novae, are typically defined by richly branched, curly thalli and the presence of the depside perlatolic acid. The Himalayan C. delavayi is placed surprisingly close to Impexae. Although it was originally placed in Unciales (also in Huovinen & Ahti 1986a), it is not related to any current segregates of former Unciales. A similar result was obtained by Stenroos et al. (2002). This species is, however, different from other Impexae by 4-O-methylcryptochlorophaeic containing and cryptochlorophaeic acids, and having very slender, little branched podetia. In the present analyses, C. delavayi is positioned on a long branch separate from the rest of the Impexae, implying that it is substantially different from the others.

Tenues are represented here by *C. stygia* and *C. subtenuis*. A diagnostic character of *Tenues* was a red pigment in the conidiomata. The inclusion of *C. rangiferina* in this group (Stenroos *et al.* 2002) indicates that the red pigment is not diagnostic after all.

The third lineage of former *Cladinae* includes *C. arbuscula* and *C. mitis*, and is referred to here as *Cladinae*. Stenroos *et al.*

(2002) also showed *Cladinae* (*C. arbuscula* and allies) and *Tenues* (*C. subtenuis* and allies) as separate clades, although as sister to each other, and due to the overall topology the two clades were differently ranked.

Morphologically, *C. arbuscula* (*Cladinae*) as well as *C. stygia* and *C. rangiferina* (*Tenues*) are very similar in branch architecture, although they differ in chemistry and surface structure (Ahti & Stenroos 2013). The traditionally recognized characters, such as branching patterns, presence of cortex, and chemistries may be quite misleading, when related clades are compared. It appears that the former *Unciales* are spread across the sequence-based phylogenetic tree of the genus *Cladonia*.

We thank several people who sent us material or discussed various problems with us: R. Droker, D. Himelbrant, J. Lendemer, and S. Talbot. F. Högnabba worked as an adviser for Diana Weckman's M.Sc. thesis on the subject. This thesis was used as a basis for the present study. The Academy of Finland is cordially acknowledged for financial support to SS (grant 211171). RP-B was funded by a Marie Curie Intra-European Fellowship (PIEF-GA-2013-625653).

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