Standard Paper

Phylogenetic study of the Cladonia cervicornis group (Cladoniaceae, Lecanorales) discloses a new species, Cladonia teuvoana

Raquel Pino-Bodas^{1[,](https://orcid.org/0000-0001-7122-9425)2,3} D. Alberto Herrero⁴ D. André Aptroot⁵ D. Ulrik Søchting⁶ D. Richard Troy McMullin⁷ D and

Ana Rosa Burgaz⁸

¹Departamento de Biología y Geología, Física y Química Inorgánica, Universidad Rey Juan Carlos (URJC), 28933 Móstoles, Spain; ²Instituto de Investigación en Cambio Global (IICG-URJC), Universidad Rey Juan Carlos, 28933 Móstoles, Spain; ³Royal Botanic Gardens, Kew, Richmond, TW9 3DS, UK; ⁴Real Jardín Botánico (CSIC), 28014 Madrid, Spain; ⁵Instituto de Biociências, Universidade Federal de Mato Grosso do Sul, CEP 79070-900, Campo Grande, Mato Grosso do Sul, Brazil; ⁶University of Copenhagen, 2100 Copenhagen, Denmark; ⁷Canadian Museum of Nature, Ottawa, Ontario, K1P 6P4, Canada and ⁸Universidad Complutense de Madrid, 28040, Madrid, Spain

Abstract

The Cladonia cervicornis group comprises lichen-forming fungi characterized by having scyphi with central proliferations. It includes c. 20 species globally. The taxonomy of this group is poorly resolved, with many species not thoroughly disentangled. The focus of this study is the European species in the C. cervicornis group. In order to estimate the phylogenetic relationships of these species, six loci were used: ITS rDNA, IGS rDNA, RPB1, RPB2, ef1α and cox1. Species delimitation methods (ASAP, PTP and GMYC) were used to infer the species boundaries based on four loci, ITS rDNA, IGS rDNA, cox1 and RPB2. A morphological analysis based on multivariate methods was performed to assess the importance of phenotypic differences among the lineages. The phylogenetic reconstructions placed the species of this group in the subclade Cladonia. Five lineages were recovered, corresponding to C. cervicornis, C. macrophyllodes, C. pulvinata, C. verticillata and a new lineage that we describe here, C. teuvoana. Our analyses revealed that Cladonia cineracea, C. stricta and C. trassii are polyphyletic.

Keywords: Lecanoromycetes; lichens; morphology; taxonomy

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Introduction

The genus Cladonia is one of the most speciose genera of macrolichens (Lücking et al. [2017](#page-20-0)), with more than 475 accepted species described (Stenroos et al. [2019\)](#page-21-0). Most of the species are terricolous, growing in open areas that have a certain amount of moisture (Ahti [2000\)](#page-20-0). The genus has a subcosmopolitan distribution. It is notably diverse in the Neotropics $(c. 195$ species), particularly Eastern Brazil, and Australasia-Melanesia with around 40% of species endemic for this region (Ahti & Aptroot [1992;](#page-20-0) Ahti 2000 ; Aptroot *et al.* 2021), while in Europe *c*. 105 species have been reported (Litterski & Ahti [2004\)](#page-20-0). The genus Cladonia is easily recognizable by usually having a dimorphic thallus, consisting of a squamulose or crustaceous primary thallus and a fruticose secondary thallus. However, species identification within this genus can be challenging (Burgaz et al. [2020](#page-20-0); Černajová et al. [2022\)](#page-20-0). Most of the taxonomic characters used to distinguish Cladonia species are associated with the secondary thallus, called podetium (Ahti [2000\)](#page-20-0). Due to the limited number of characters available, distinguishing species based on squamule morphology is often difficult (Burgaz et al. [2020\)](#page-20-0). However, many species

have a dominant primary thallus and rarely develop podetia (Ahti [2000;](#page-20-0) Pino-Bodas et al. [2010](#page-21-0)a, [2012](#page-21-0)). In these cases, morphological characters associated with the primary thallus are indispensable for distinguishing species. The study of secondary metabolites can also be of great use for species circumscription (Huovinen & Ahti [1982](#page-20-0); Culberson [1986](#page-20-0)), since morphologically similar species sometimes contain different secondary metabolites, for example C. subulata (L.) F. H. Wigg. and C. rei Schaer. or C. humilis (With.) J. R. Laundon and C. conista (Nyl.) Robbins (Dolnik et al. [2010](#page-20-0); Pino-Bodas et al. [2010](#page-21-0)b, [2013](#page-21-0)a).

This study focuses on the C. cervicornis (Ach.) Flot. group in Europe. Members of this group are characterized by scyphose podetia with a corticate surface and by having proliferations arising from the centre of the scyphi. There are c. 20 species of Cladonia globally with these features (Ahti [2007](#page-20-0)). The most recent phylogeny of the genus placed them within the clade Cladonia, subclade Cladonia. This clade also includes species of the former sections Cladonia, Helopodium and Unciales, including the type species of the genus, C. subulata (Stenroos et al. [2019](#page-21-0)). Numerous authors have paid attention to the taxonomy of species with central proliferations in different geographical regions (Abbayes [1949;](#page-20-0) Ahti & Marcelli [1995;](#page-20-0) Ahti [1978,](#page-20-0) [1980](#page-20-0), [1983,](#page-20-0) [1998,](#page-20-0) [2007](#page-20-0); van Herk & Aptroot [2003;](#page-21-0) Pino-Bodas et al. [2010](#page-21-0)a; Charnei & Eliasaro [2013](#page-20-0)). However, many taxa are still not well understood (Ahti [2000](#page-20-0), [2007\)](#page-20-0) and phylogenetic studies have shown that some are polyphyletic (Pino-Bodas et al. [2013](#page-21-0)b; Stenroos et al. [2019](#page-21-0)).

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Corresponding author: Raquel Pino-Bodas; Email: raquel.pino@urjc.es

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Nine species in the C. cervicornis group have been previously reported from Europe: C. cervicornis, C. firma (Nyl.) Nyl., C. macrophyllodes Nyl., C. pulvinata (Sandst.) Van Herk & Aptroot, C. stricta (Nyl.) Nyl., C. subcervicornis (Vain.) Kernst., C. trassii Ahti, C. uliginosa (Ahti) Ahti, and C. verticillata (Hoffm.) Schaer. (Ahti & Stenroos [2013\)](#page-20-0). However, phylogenetic studies have shown that C. firma and C. subcervicornis do not belong to this group as they are phylogenetically distant from the rest of the species (Stenroos et al. [2019](#page-21-0)). In addition, there is another species restricted to Macaronesia, C. microphylla Ahti & Aptroot (Ahti & Aptroot [2009](#page-20-0)). Cladonia cervicornis, C. pulvinata and C. verticillata have a wide distribution in Europe (van Herk & Aptroot [2003](#page-21-0); Ahti & Stenroos [2013;](#page-20-0) Burgaz et al. [2020;](#page-20-0) Pino-Bodas et al. [2021](#page-21-0)), while C. stricta, C. trassii and C. uliginosa are primarily distributed in the arctic or arctic-boreal regions of Eurasia and North America, with some outposts in the Alps, although their distribution is not yet well known (Ahti [1998](#page-20-0); Brodo et al. [2001;](#page-20-0) Ahti & Stenroos [2013](#page-20-0); Pino-Bodas et al. [2021\)](#page-21-0). Cladonia macrophyllodes is more widely distributed, but outside arctic regions it is restricted to mountainous areas (Goward & Ahti [1997;](#page-20-0) Ahti & Stenroos [2013;](#page-20-0) Burgaz et al. [2018,](#page-20-0) [2020](#page-20-0)). The distribution patterns of C. cervicornis, C. pulvinata and C. verticillata differ, although in several regions of Europe they often coexist, and morphological discrimination can be difficult (Ahti [1980](#page-20-0); Ahti & Stenroos [2013;](#page-20-0) Søchting [2017;](#page-21-0) Gheza et al. [2018](#page-20-0); Burgaz et al. [2020\)](#page-20-0). Morphological studies by van Herk & Aptroot [\(2003\)](#page-21-0) showed that the coloration and morphology of the primary thallus can be used to distinguish these three taxa. In addition, the presence of psoromic acid allows C. pulvinata to be distinguished from the other two species, which do not synthesize this compound. Cladonia cervicornis is a highly variable species and some authors have indicated the need for further studies to clarify its taxonomy (Ahti & Stenroos [2013](#page-20-0); Burgaz et al. [2020](#page-20-0)). Specimens of these taxa have been the subject of some molecular research (Pino-Bodas et al. [2010](#page-21-0)a, [2013](#page-21-0)b; Osyzcka et al. [2018;](#page-21-0) Stenroos et al. [2019](#page-21-0)), the results of which indicate that C. cervicornis, C. pulvinata and C. verticillata form independent lineages. However, it should be noted that sampling has been mostly focused on the Mediterranean region, where C. cervicornis is particularly common (Burgaz et al. [2020\)](#page-20-0), while less sampling has been carried out in Central and Northern Europe where C. verticillata is more frequent and more difficult to distinguish from C. cervicornis (Ahti & Stenroos [2013\)](#page-20-0). Phylogenetic studies have shown C. verticillata to be polyphyletic (Pino-Bodas et al. [2013](#page-21-0)b; Stenroos et al. [2019](#page-21-0)), and more extensive sampling will be necessary to determine whether European specimens belong to a single species.

The aims of this study were: 1) to evaluate the monophyly of the species within the C. cervicornis group reported for Europe; 2) to estimate the phylogenetic relationships of the species of the C. cervicornis group within the subclade Cladonia; 3) to carry out a morphological study that characterizes each of the lineages found.

Material and Methods

Taxon sampling

This study is based on 160 specimens from 18 countries. Specimens representing all known European species with central proliferations were included in the phylogenetic analyses. New study specimens included: C. cervicornis $(n = 57)$, C. cineracea Ahti $(n = 1)$, C. macrophyllodes $(n = 26)$, C. microphylla $(n = 7)$,

C. pulvinata (n = 15), C. stricta (n = 4), C. trassii (n = 6), C. uliginosa (n = 2) and C. verticillata (n = 32). In addition, a selection of specimens from other regions of the world were included. A small number of specimens of C. rappii A. Evans, a species difficult to distinguish from C. verticillata in North America, were newly sequenced [\(Table 1](#page-2-0)). The specimens studied are deposited in C, H, E, K, MACB and TROM. Types of C. cervicornis (lectotype H-ACH 1672B and isolectotype BM-ACH 722A), C. macrophyllodes (H-ACH 1673), C. pulvinata (lectotype H), and representative specimens of C. sobolifera Nyl. (H-NYL-0608, 0638, 38780, 38784, 38785, 387986) were studied to compare their morphological features with our specimens.

Phenotypic study

The secondary metabolites of each specimen were studied by thin-layer chromatography (TLC). The standard protocol was used as described in White & James ([1985](#page-21-0)) and Orange et al. ([2010\)](#page-21-0), with solvents A (toluene:1,4-dioxane:acetic acid) and C (toluene:acetic acid). The specimens were identified following van Herk & Aptroot ([2003\)](#page-21-0), Ahti ([2007\)](#page-20-0), Ahti & Stenroos ([2013\)](#page-20-0) and Burgaz et al. [\(2020\)](#page-20-0). The morphological study was focused on C. cervicornis, C. pulvinata and C. verticillata which are the more common taxa in Europe and difficult to distinguish from each other. Based on previous studies (van Herk & Aptroot [2003;](#page-21-0) Ahti [2007](#page-20-0); Ahti & Stenroos [2013;](#page-20-0) Burgaz et al. [2020\)](#page-20-0), 13 quantitative traits were selected to conduct the morphological analyses: length of squamules, width at the middle of squamules, maximum width of squamules, squamule incision depth, length of the blackened base of squamules, thickness of squamules, length of first scyphi, total length of podetium, number of proliferations, number of tiers, widening in lower half of podetium, width of scyphi, and thickness of podetial wall. To better represent morphological patterns, the length ratio of the variables 'width of squamules', 'width of scyphi', 'squamules incisions depth' and 'blackened base of squamules' were used. To determine whether the widening of the scyphi is gradual from the base or abrupt above the middle of the podetium, the difference in width of the podetium was analyzed, corrected for length (width at the middle – width at the base / 1/2 (podetium length)). These traits were examined in a selection of 63 specimens, representing all phylogenetic lineages, by measuring three squamules and three podetia per specimen (whenever the amount of material permitted) under a dissecting microscope (Nikon SMZ21000) using a digital caliper. In addition to quantitative characters, the following qualitative features were also studied: colour of the underside of the squamules, colour of the upper side of the squamules, morphology of the squamules, morphology of the squamule lobes, presence of veins on the underside of the squamules, presence of rhizines and continuity of the podetial algal layer.

All statistical analyses were conducted in R v. 4.1.2 (R Core Team [2022](#page-21-0)). The normality and homoscedasticity of the quantitative variables were assessed using the Shapiro-Wilk and Bartlett tests, respectively. It was found that only 'depth of incisions' was normally distributed. Due to the lack of normality, the variables did not meet the assumptions of a principal component analysis (PCA), so the dataset was analyzed using nonmetric multidimensional scaling (NMDS; Kruskal [1964\)](#page-20-0), a more robust method for this type of data (Austin [1985](#page-20-0); Minchin [1987\)](#page-20-0). NMDS was conducted with the Bray-Curtis distances in the vegan package (Oksanen et al. [2013](#page-21-0)). Permutational

Table 1. List of subclade Cladonia specimens included in the study with voucher information, secondary metabolites detected by thin-layer chromatography and GenBank accession numbers. New sequences are in bold.

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ATR = atranorin; FUM = fumarprotocetraric acid; CNSTIC = connorstictic acid; CPH-2 = confumarprotocetraric acid; CPSO = conpsoromic acid; NSTIC = norstictic acid; PHY = physodalic acid; PSO = psoromic acid; USN = usnic aci

multivariate analysis of variance (PERMANOVA) was used to test differences between clades and species, with the Bray-Curtis dissimilarity, 999 permutations and Bonferroni correction for multiple comparisons.

Contingency tables were used to assess the association between qualitative characters and different clades. The morphological characters studied were: upcurled dry squamules, upper surface colour, lanceolate lobes, colour of base squamules, continuous algal layer and basal colour of podetia (alternative states are listed in Supplementary Material Table S1, available online). The analyses were performed using the abind package (Plate & Heiberger [2016\)](#page-21-0). As the number of specimens in clade C was low, Fisher's test was used instead of the chi-square test (Agresti [2018](#page-20-0)).

DNA extraction, PCRs and sequencing

A single podetium per specimen was used for DNA extraction. Exceptionally, for the molecular biology study, specimens with poorly developed podetia or without them were included. Before DNA extraction, the fragment was soaked in acetone for 1 h to remove secondary metabolites. The acetone extracts were used to conduct TLC. Total genomic DNA was extracted using the E.Z.N.A. Forensic Kit (Omega) following the manufacturer's instructions; DNA was dissolved in 100 μl of elution buffer (10 mM Tris-Cl). Based on preliminary studies (Pino-Bodas et al. $2010a$ $2010a$, $2013a$ $2013a$, c; Stenroos et al. 2019), the regions ITS rDNA, IGS rDNA, RPB2 and cox1 were selected to conduct the revision of the C. cervicornis group. The primers and PCR conditions are described in Pino-Bodas et al. [\(2010](#page-21-0)b) and Stenroos et al. [\(2019\)](#page-21-0). PCR reactions were carried out using BIOTAQ polymerase (Bioline), including 0.3 μl of Taq polymerase, 2.5 μl of 10× PCR buffer, 1.4 μl of MgCl₂ (50 μm μ l⁻¹), 1.6 μl of dNTPs (2.5 μm $μl^{-1}$), 1 μl of BSA (1 μm μl⁻¹), 1 μl of each primer (10 μm μl⁻¹), and 1 μl of extracted DNA. PCR products were sequenced at Macrogen Spain [\(http://www.macrogen.com](http://www.macrogen.com)).

Phylogenetic analyses

The dataset used for the phylogenetic analyses included the specimens newly sequenced from the C. cervicornis group, sequences of Cladonia species with central proliferation from other regions of the world included in clade Cladonia, subclade Cladonia, and other species without central proliferations but belonging to this clade (Stenroos et al. [2019\)](#page-21-0). Additionally, specimens of Cladonia species representing other major lineages within the clade Cladonia (Stenroos et al. [2019](#page-21-0)) were included in the phylogenetic analyses ([Table 1\)](#page-2-0). Cladonia boryi Tuck. and C. nipponica Vain., belonging to clade Boryia, were used as an outgroup. The sequences were assembled using Sequencher v. 4.1.4 (Gene Codes Corporation, Inc., Ann Arbor, Michigan, USA). The alignments of each genetic region were performed using the online version of MAFFT (Katoh & Standley [2013\)](#page-20-0), with default parameters. Ambiguous positions of ITS rDNA and IGS rDNA alignments were removed with Gblocks v. 0.91b (Castresana [2000\)](#page-20-0) using less restricted options (allowing final blocks, gap positions and less strict flanking positions).

Maximum likelihood (ML) analyses were performed in RAxML v. 7.04 (Stamatakis et al. [2008](#page-21-0)) for each locus, using 500 pseudoreplicates of rapid bootstrap and the GTRGAMMA model. The congruence among loci was inspected manually, based on the method described by Kauff & Lutzoni ([2002,](#page-20-0) [2003\)](#page-20-0). No incongruences were detected, and the datasets were combined. In addition to the genetic

regions amplified in the specimens of the C. cervicornis group, concatenated analyses also included RPB1 and $efl\alpha$ loci, which were used to estimate the phylogeny of Cladonia (Stenroos et al. [2019](#page-21-0)) and numerous sequences for specimens of the Cladonia subclade were available. This approach increased the number of loci sampled within the clades in the phylogeny. We verified that RPB1 and $efl\alpha$ were not represented exclusively in specimens of some branches of the phylogeny. The concatenated dataset was restricted to specimens represented by at least two loci. The concatenated dataset was analyzed by ML and Bayesian inference. JModelTest (Posada [2008](#page-21-0)) under the Akaike information criterion (AIC) was used to select the best substitution model for each region. The selected models were: $TrNef + G$ for ITS rDNA, IGS rDNA and $RPB2$; $K80 + G$ for cox1; SYM + G for ef1 α and TrNef + I + G for RPB1. The partitioning scheme used to analyze the concatenated datasets considered 15 partitions: ITS rDNA, IGS rDNA and each codon position for the loci cox1, ef1α, RPB1 and RPB2. ML analysis was conducted in RAxML using the GTRGAMMA model for each partition and 1000 pseudoreplicates of rapid bootstrap. The Bayesian analyses were performed using MrBayes v. 3.2.6 (Ronquist et al. [2012\)](#page-21-0). Posterior probabilities were approximated by sampling trees using Markov chain Monte Carlo (MCMC). Two simultaneous runs, each with 20 000 000 generations and employing four chains, were executed. Every 1000th tree was saved into a file. The first 25% of trees was discarded as burn-in. Convergence between chains was assessed using Tracer v. 1.7 (Rambaut et al. [2018\)](#page-21-0). The likelihood versus generation number and the average standard deviation of split frequencies (≤ 0.01) were plotted. Branches with posterior probabilities ≥ 0.95 and bootstrap values $\geq 70\%$ were considered strongly supported. The phylogenetic analyses based on the concatenated dataset were performed on the CIPRES Science Gateway web portal (Miller et al. [2010](#page-20-0)).

Species delimitation analyses

In addition to the clade delimitation obtained in the phylogenetic reconstructions, three species delimitation methods were employed to assess the number of species within the C. cervicornis group: Automatic Partitioning (ASAP) (Puillandre et al. [2021\)](#page-21-0), Poisson Tree Processes (PTP) (Zhang et al. [2013\)](#page-21-0) and General Mixed Yule Coalescent (GMYC) (Pons et al. [2006](#page-21-0)). These algorithms belong to the category of 'discovery' species delimitation methods, since they do not require any prior information on species boundaries. These analyses included only putative species represented by more than two sequences, removing singletons that may create artefacts (Lim et al. [2012](#page-20-0); Pentinsaari et al. [2017](#page-21-0)). ASAP was implemented on the web server (<https://bioinfo.mnhn.fr/abi/public/asap/>) using the Jukes-Cantor (JC69) model to compute the genetic distances. PTP analyses were performed using the best ML tree estimated in RAxML for each locus. The analyses were conducted on the webserver [\(http://species.h-its.org/](http://species.h-its.org/)) with default parameters that included 500 000 generations, with a thinning rate of 100 and 10% burn-in. GMYC was conducted using iTaxoTools (Vences et al. [2021](#page-21-0)), using a single threshold. ML trees of each locus were transformed into ultrametric trees with the 'chromos' function of the ape package (Paradis & Schliep [2019\)](#page-21-0) for R v. 4.3.3 [\(http://www.rproject.org/\)](http://www.rproject.org/) and used for GMYC analyses.

Results

In this study, 469 new DNA sequences were generated (119 of ITS rDNA, 145 of IGS rDNA, 95 of RPB2 and 110 of cox1). The concatenated dataset was composed of 221 specimens and 3798 characters. The ML analysis resulted in a tree with −Lnl = 27581.920. The Bayesian analyses produced a consensus tree with an arithmetic mean of −Lnl = 102147.35. ML and Bayesian consensus trees showed similar topologies. [Figure 1](#page-15-0) shows the Bayesian 50% majority-rule consensus tree, which is consistent with the topology of the subclade Cladonia generated in the phylogeny of Stenroos et al. [\(2019](#page-21-0)). The subclade Cladonia was revealed as monophyletic with high support, while the centrally proliferating species are not monophyletic. All specimens of C. verticillata from Europe form a monophyletic clade, although this is supported only in the Bayesian analysis $(PP = 1)$ Bootstrap = 64). A small number of specimens from North America are included in this clade, which is closely related to C. subulata. The results appear to suggest that C. trassii is polyphyletic; one specimen of C. trassii is basal to the clade formed by C. verticillata and C. subulata, while three other specimens occur distantly, close to a specimen of C. cineracea and C. rappii. Cladonia pulvinata was monophyletic and highly supported in both analyses. Specimens identified as C. cervicornis form two well-supported clades. One clade (clade C), with seven specimens, is closely related to a clade comprising C. ceratophyllina (Nyl.) Vain., C. centrophora Müll. Arg., C. andesita Vain. and C. nitens Ahti. Clade D includes most of the specimens of C. cervicornis in addition to all the specimens studied of C. microphylla. Cladonia macrophyllodes is found to be monophyletic and closely related to C. uliginosa, which is represented by two specimens in the phylogeny. One specimen (Lendemer 22968) morphologically related to C. cervicornis from North America appears to be related to C. mateocyatha Robbins.

The results of species delimitation methods are presented in [Fig. 2](#page-16-0). The number of inferred species ranges from 2 to 115. In general, these methods showed little congruence with each other and with the current species delimitation. However, several of the methods for different loci identified clade C of C. cervicornis as a different species. Specifically, this putative species was inferred by ASAP for ITS rDNA, RPB2 and cox1, by PTP for ITS rDNA and RPB2, and by GMYC for RPB2.

[Table 1](#page-2-0) shows the secondary metabolites detected by TLC in each specimen studied. The results show a high chemical homogeneity within the taxa. As a major substance, all the specimens of C. pulvinata contained psoromic acid, and all the specimens of C. verticillata contained fumarprotocetraric acid. Most C. cervicornis samples contained fumarprotocetraric acid, except for a small number of samples from Cyprus which also contained atranorin. Traces of other substances such as physodalic acid, confumarprotocetraric acid and a fatty acid with an R_f compatible with rangiformic acid were detected in specimens from different geographical origins [\(Table 1\)](#page-2-0).

[Table 2](#page-16-0) presents the PERMANOVA pairwise comparison. PERMANOVA analyses showed a clear morphological differentiation between C. cervicornis and C. verticillata, and between C. cervicornis and C. pulvinata. However, there were no significant differences between C. verticillata and C. pulvinata. Our analyses showed that the specimens of clade C were morphologically very similar to C. pulvinata. These results were confirmed by NMDS analysis ([Fig. 3\)](#page-17-0), where specimens of C. cervicornis and C. verticillata clearly form separate clusters, while those of C. pulvinata and clade C overlap.

The contingency table analyses showed significant associations between the clades and the characters: lower surface colour $(P-value = 0.0001034)$, upper surface colour $(P-value = 0.01213)$, lanceolate/rounded lobes $(P-value = 0.001965)$, basal colour of squamules $(P-value = 1.917e-11)$, and basal colour of podetia $(P-value = 0.01323)$, although there were no significant associations among clades for continuous/discontinuous algal layer $(P$ -value = 0.11).

Discussion

Species delimitation of the Cladonia cervicornis group in Europe

It is well known that many species of Cladonia present a high level of morphological intraspecific variation. This variation may be due to different stages of development, to changes produced by different environmental conditions, such as different light intensity or humidity, or a response to anthropogenic disturbances (Osyzcka & Rola [2013;](#page-21-0) Osyczka et al. [2014,](#page-21-0) [2018](#page-21-0); Pino-Bodas et al. [2015\)](#page-21-0). Therefore, determining which phenotypic traits can be used as diagnostic characters is often challenging. Species delimitation in Cladonia has been hampered by the low genetic variability of the genus, which means that the markers used in phylogenetic and species delimitation studies in fungi often do not have sufficient resolution (Pino-Bodas et al. [2011,](#page-21-0) [2013](#page-21-0)c; Stenroos *et al.* [2019](#page-21-0)). Several studies have shown that phenotypically and ecologically disparate species cannot be genetically distinguished even using multiple loci (Stenroos et al. [2019;](#page-21-0) Steinová et al. [2022\)](#page-21-0). The low genetic variation among Cladonia species may be attributed to recent divergence among species or to the dominance of asexual reproduction (Ahti [2000](#page-20-0); Stenroos et al. [2019](#page-21-0); Steinová et al. [2022](#page-21-0)).

This research investigates the morphological and genetic variation of the C. cervicornis group in Europe, focusing on the three most common species, C. cervicornis, C. pulvinata and C. verticillata. Characters traditionally used to distinguish species of the C. cervicornis group have been: the number of central proliferations, the number of tiers, the presence of a melanotic region at the base of the podetia, gradual or abrupt podetial tapering, morphology of squamules, and the secondary metabolites (Ahti [2000](#page-20-0), [2007;](#page-20-0) van Herk & Aptroot [2003\)](#page-21-0). Although preliminary phylogenetic studies indicated that these three taxa were monophyletic and constituted independent lineages (Pino-Bodas et al. [2010](#page-21-0)a, [2013](#page-21-0)b; Stenroos et al. [2019](#page-21-0)), the large morphological variation documented in C. cervicornis and the difficulty in distinguishing some specimens from C. verticillata (Ahti & Stenroos [2013;](#page-20-0) Søchting [2017](#page-21-0); Burgaz *et al.* [2020\)](#page-20-0) prompted us to perform a new phylogenetic study. In this study, we used an integrative approach, combining the results of phylogenetic analyses, different methods for molecular species delimitation and the phenotypic study of specimens, to address species delimitation in the C. cervicornis group in Europe. Phylogenetic analyses showed five clades ([Fig. 1](#page-15-0)), one corresponding to C. verticillata (clade A), another to C. pulvinata (clade B), two clades including specimens previously identified as C. cervicornis (clades C and D) and one corresponding to C. macrophyllodes (clade E). Nevertheless, these five clades were not identified as distinct species by the different species delimitation methods employed [\(Fig. 2](#page-16-0)). In fact, the results of the different species delimitation methods displayed great inconsistencies between them [\(Fig. 2\)](#page-16-0), most showing an unrealistic amount of oversplitting. Although species delimitation methods have been widely used to establish species boundaries more objectively within different groups of lichen-forming fungi (Parnmen et al. [2012](#page-21-0); Del-Prado et al. [2016](#page-20-0); Pérez-Ortega et al. [2016](#page-21-0); Wei et al.

Figure 1. Phylogeny of subclade Cladonia, based on concatenated ITS rDNA, IGS rDNA, RPB1, RPB2, $efl\alpha$ and cox1, showing the 50% majority-rule consensus tree of the Bayesian analysis. Branches with a bootstrap value of > 70% and a posterior probability of > 0.95 are in bold. Species of the C. cervicornis group are indicated in different colours. The country of origin of the specimen is indicated in brackets using the ISO abbreviations. In colour online.

Figure 2. Results of species delimitation analyses (Automatic Partitioning (ASAP) (Puillandre et al. [2021](#page-21-0)); Poisson Tree Processes (PTP) (Zhang et al. [2013\)](#page-21-0); General Mixed Yule Coalescent (GMYC) (Pons et al. [2006](#page-21-0))) in the Clandonia cervicornis group, based on ITS rDNA, IGS rDNA, cox1 and RPB2. The same colour indicates that the specimens were inferred to belong to the same species. The absence of colour indicates that the specimens were not analyzed. The DNA code corresponds to that shown in [Fig. 1](#page-15-0). Further details of the specimens can be found in [Table 1.](#page-2-0) In colour online.

Table 2. PERMANOVA results of morphological pairwise comparison among subclade Cladonia cervicornis group. Significant P-values are in bold.

Taxon comparisons	P-value
C. cervicornis-C. pulvinata	0.012
C. cervicornis-C. teuvoana	0.006
C. cervicornis-C. verticillata	0.006
C. pulvinata-C. teuvoana	0.528
C. pulvinata-C. verticillata	0.078
C. verticillata-C. teuvoana	0.006

[2016](#page-21-0); Košuthová et al. [2020\)](#page-20-0), it has been common to obtain inconsistent or unrealistic results in terms of the number of species delimited (Pino-Bodas et al. [2018;](#page-21-0) Mercado-Díaz et al. [2020](#page-20-0); Myllys et al. [2023\)](#page-20-0). Inconsistencies may be attributed to breaking assumptions of different methods, employing low numbers of specimens, lack of sampling across the geographical range of species, or recent divergence (Carstens et al. [2013](#page-20-0); Magoga et al. [2021](#page-20-0)). Although our sampling was extensive, with a large number of specimens analyzed, it was focused on Europe and might be geographically biased for some lineages. Reciprocal monophyly has been used as a criterion for species delimitation, since it is indicative of sufficient divergence between lineages (De Queiroz [1998](#page-20-0); Lücking et al. [2021\)](#page-20-0). Based on this criterion and our knowledge of genetic variation in Cladonia, we consider that the lineages found in the phylogenetic analyses represent different species. In addition, most of these lineages are supported by phenotypic differences. Our morphological analyses not only document variation in each lineage, but also show morphological differences among most of them [\(Fig. 3](#page-17-0), Table 2), confirming the results of van Herk & Aptroot [\(2003\)](#page-21-0).

Our analyses show that all European C. verticillata specimens belong to a single lineage, clade A. Therefore, this clade represents C. verticillata s. str. Furthermore, morphological analyses indicate morphological differences with the specimens of C. cervicornis. Clade A not only included European specimens, but also some from North America. Within this clade, two well-supported subclades could be distinguished, one containing three specimens from North America, the other with all European specimens and some from North America. However, these subclades were not delimited as independent species by any of the species delimitation methods. Other specimens of C. verticillata from other regions were not included in this clade, which confirms that a worldwide study is required to clarify the taxonomy of C. verticillata (Ahti [2007](#page-20-0); Pino-Bodas et al. [2021\)](#page-21-0).

Clade B consists exclusively of C. pulvinata specimens. According to our morphological analyses, the distinction between C. pulvinata and C. verticillata is difficult, since they display a large amount of overlap [\(Fig. 3\)](#page-17-0). However, in regions where the species grow side-by-side, they can usually be reliably distinguished (van Herk & Aptroot [2003\)](#page-21-0), and the presence of psoromic acid in C. pulvinata can always be used as a diagnostic character to identify the specimens of this lineage.

Clade C encompasses specimens with a more or less Atlantic distribution. Morphological analyses indicate differences from the rest of the lineages of the C. cervicornis group. This lineage was also supported by some species delimitation analyses (Fig. 2). From a morphological point of view, this lineage is distinguished by the narrower scyphi compared to other taxa within

Figure 3. Non-metric multidimensional scaling (NMDS) plot, illustrating the morphological variation among the species belonging to the Cladonia cervicornis group. Stress = 0.14. In colour online.

the group. These scyphi display abrupt widening and no tier proliferations have been observed. The squamules are smaller than those of the other lineages and may have a blackened zone on the underside, reaching up to 1/3 of the length of the squamules, which are white at the ends. Study of the type material has allowed us to determine that C. cervicornis s. str. corresponds to clade D. The primary thallus of the C. cervicornis type (lectotype and isolectotype) is morphologically similar to that of the specimens of this clade ([Fig. 4](#page-18-0)), characterized by large, deeply incised squamules and an underside with purplish-greyish tinged ends. Possible designations applicable to clade C would be C. cristata Hoffm. or C. sobolifera. However, neither the iconography presented by Dillenius ([1742](#page-20-0)) nor the description by Hoffmann ([1796](#page-20-0)) matches the morphology of the specimens in this clade and we therefore rule out applying C. cristata to this clade. We did not have access to the type of C. sobolifera but we studied the Nylander specimens in the Helsinki herbarium and conclude that they belong to C. cervicornis [\(Fig. 4\)](#page-18-0). Therefore, we consider clade C to be a new species that we describe here under the name Cladonia teuvoana.

Clade D consists of the specimens of C. cervicornis s. str. together with all the analyzed specimens of C. microphylla ([Fig. 1](#page-15-0)), a Macaronesian endemic species characterized by deeply divided squamules (Ahti & Aptroot [2009\)](#page-20-0). Although the analyses performed here did not distinguish this species from C. cervicornis, we do not propose any taxonomic changes since we did not undertake an in-depth morphological study of this taxon. In addition, phylogenomic analyses have resolved relationships between closely related species of lichen-forming fungi that conventional markers (e.g. ITS rDNA, LSU rDNA, RPB2) used in fungal phylogenies failed to separate (Grewe et al. [2018](#page-20-0)). We expect that analyses at the genomic scale will provide a better understanding of the boundaries between C. cervicornis and C. microphylla. Cladonia cervicornis specimens grouped in this clade show a high morphological variation (Fig. 3), but this variation is not related to genetic variation. Despite the low genetic variation found, several of the species delimitation methods divided the clade into several species. Given the lack of congruence among the delimitation methods, we opted for the most conservative option, which is to keep this lineage as a single species, a hypothesis that was supported only by ASAP for ITS rDNA and RPB2.

Cladonia cervicornis has been reported from North America (Hammer & Ahti [1990](#page-20-0); Hammer [1995](#page-20-0); Ahti & Hammer [2002](#page-20-0)) but the identity of these specimens is uncertain. Our results, based on the study of a single specimen, indicate that C. cervicor-nis s. str. is probably not present in North America [\(Fig. 1\)](#page-15-0).

Clade E includes all the analyzed specimens of C. macrophyllodes. No circumscription problems have been reported for this species; although the primary thallus could be confused with that of C. subcervicornis, the two species have somewhat different habitat requirements (Ahti & Stenroos [2013;](#page-20-0) Burgaz et al. [2020](#page-20-0)). However, as for the remaining lineages, most species delimitation analyses inferred more than one species within this lineage, with the exception of ASAP and PTP for cox1. In the absence of other evidence, we maintain C. macrophyllodes as a single species.

Phylogenetic relationships within the Cladonia cervicornis group

The phylogenetic placement of species with central proliferations has been examined in previous studies (Stenroos et al. [2002,](#page-21-0) [2019;](#page-21-0) Beiggi & Piercey-Normore [2007;](#page-20-0) Pino-Bodas et al. [2010](#page-21-0)a, [2013](#page-21-0)b). However, in the present study the sampling is expanded substantially, including specimens from numerous countries and species not sampled to date, or poorly studied, such as C. macrophyllodes, C. trassii or C. stricta. The phylogenetic placement of the species of the C. cervicornis group is consistent with the results obtained by Stenroos et al. [\(2019](#page-21-0)), with all of them belonging to the Cladonia subclade.

The phylogenetic relationships of species in the C. cervicornis group, within the Cladonia subclade, are uncertain. Our results indicate that C. verticillata s. str. is related to C. subulata, a sorediate species without central proliferations, although this relationship was only supported in the Bayesian analysis ([Fig. 1](#page-15-0)). This is a similar result to that found by Beiggi & Piercey-Normore [\(2007](#page-20-0)). However, the phylogeny of Stenroos et al. ([2019\)](#page-21-0) showed a possible relationship between C. verticillata and C. pulvinata, although it was not supported.

In our phylogeny, some clades consisted exclusively of species with central proliferations, but these clades did not always include species with morphological or biogeographical similarities. An example is the clade formed by C. andesita, C. centrophora, C.

Figure 4. A-C, Cladonia teuvoana sp. nov. (MACB 127525-holotype). D, Cladonia sobolifera (H-NYL 0608). E, Cladonia cervicornis (BM-ACH 722A-isolectotype). Scales: A, B & $D = 1$ cm; $C = 0.5$ cm. In colour online.

ceratophyllina, C. nitens and C. teuvoana. While C. teuvoana is restricted to Europe, the rest of the species have very different distribution patterns. Cladonia ceratophyllina and C. centrophora are two morphologically similar African species (Swinscow & Krog [1988;](#page-21-0) Ahti & Aptroot [1992\)](#page-20-0). Cladonia andesita was originally described from Colombia, but other populations later found in Africa, with some morphological differences, could represent a different species (Swinscow & Krog [1988;](#page-21-0) Ahti [2000](#page-20-0)). Cladonia nitens has an amphi-Beringian distribution and is characterized by having slender, shiny podetia and a large melanotic zone (Ahti [2007](#page-20-0)).

Another clade, consisting exclusively of species with central proliferations, is formed by C. aleuropoda Vain., C. calycantha Delise ex Nyl., C. cineracea, C. isabellina Vain., C. mawsonii C.W. Dodge, C. melanopoda Ahti and a specimen of C. rappii. This clade was previously shown in the phylogeny of Stenroos et al. ([2019](#page-21-0)) but without support. With the exceptions of C. mawsonii, which has a disjunct distribution between Australasia and Tierra del Fuego, and C. rappii, with a broader distribution (Stenroos & Ahti [1990;](#page-21-0) Ahti [2000\)](#page-20-0), the remaining taxa in the clade are neotropical, abundant in the páramos of the Andes and morphologically very similar. The delimitation of neotropical species is still not well understood and needs further study (Ahti [2000\)](#page-20-0).

The phylogenetic relationships of C. trassii are studied here for the first time. Although numerous specimens were selected for phylogenetic analysis, sequencing failed for most of the gene regions ([Table 1](#page-2-0)). Only for IGS rDNA were a high number of sequences obtained. Phylogenetic analyses of this region revealed that the specimens identified as C. trassii formed a polyphyletic group. A similar result was found in the multilocus analysis, which included only those specimens with sequences for at least two loci. This result is not surprising, since C. trassii is an extremely variable species, difficult to distinguish from C. stricta and C. uliginosa (Ahti [1998](#page-20-0); Ahti & Stenroos [2013](#page-20-0)). However, phylogenetic analyses did not show that C. trassii specimens are related to C. uliginosa. Our results point out a possible relationship between C. uliginosa and C. macrophyllodes, although it was supported only in the Bayesian analysis. These two species are easily distinguishable. Cladonia macrophyllodes has a welldeveloped and persistent primary thallus, while C. uliginosa has an inconspicuous and evanescent primary thallus. The two species also show considerable discrepancies in the morphology of

the podetia. Cladonia uliginosa has podetia with a discontinuous cortex, with several tiers of proliferations and a strongly melanotic base. None of these characters are shared by C. macrophyllodes, which has podetia with a continuous cortex and abundant squamules on the scyphi, and tiers are rarely present. However, both species synthesize the same secondary metabolites: fumarprotocetraric acid and atranorin (Ahti [1978;](#page-20-0) Hansen & Ahti [2011](#page-20-0); Ahti & Stenroos [2013\)](#page-20-0).

Our analyses did not resolve the phylogenetic relationships of C. stricta. IGS rDNA analysis showed that the specimens of this species formed a polyphyletic group (based on three sequences) and the only RPB2 sequence obtained for it showed a relationship with a specimen of C. trassii. However, these data are not enough to draw conclusions about the taxonomy and phylogenetic relationships of this species. Based on its morphological features, C. stricta has been related to C. phyllophora Hoffm., a species characterized by podetia with a strongly melanotic base, with lateral proliferations that open and rarely produce central proliferations (Osyczka [2006](#page-21-0); Hansen & Ahti [2011;](#page-20-0) Ahti & Stenroos [2013\)](#page-20-0). Our phylogenetic analyses included several specimens of C. phyllophora, which was resolved as a monophyletic group, confirming the findings of Fontaine et al. ([2010\)](#page-20-0). However, C. phyllophora does not belong to the subclade Cladonia, as the phylogeny of Stenroos et al. ([2019](#page-21-0)) showed, but belongs to the subclade Foliosae.

The phylogeny of the subclade Cladonia is in general still poorly resolved ([Fig. 1\)](#page-15-0). Although some well-supported clades have been found within this subclade, the relationships among them are not supported. This result highlights the need for future studies, including sampling in other geographical regions, that will help to better understand both the phylogenetic relationships of species with central proliferations as well as species delimitation. Preliminary data for some species such as C. rappii reveal that they may include more than one species and therefore a thorough morphological and molecular study is necessary to clarify their taxonomy. The use of phylogenomic techniques that increase the number of loci will allow better-founded phylogenetic hypotheses to be established.

Taxonomy

Cladonia teuvoana Pino-Bodas, Burgaz & Aptroot

MycoBank No.: MB 855855

Primary thallus persistent, with small squamules, white on the lower surface. Podetia with narrow scyphi, abruptly widening, with a corticate surface.

Type: The Netherlands, Drenthe, Gasterense zand, on sand, 24 March 2018, A. Aptroot 76154 (MACB 127525—holotype). GenBank Accession nos.: PQ252415, PQ252566, PQ254487.

([Fig. 4A](#page-18-0)–C)

Primary thallus persistent, prostrate or ascendent, squamules $3.7-8.11(9.2)$ mm $\log \times 3.4-5.8$ mm wide, apices sometimes incurved, green to greenish brown on the upper side, white on the lower side, darkening towards the base (up to 1/3 of squamule length). Podetia 4.7–8.7 mm tall, slender, simple, scyphose, rarely with squamules at the base, brownish, without a melanotic base; scyphi regular, with margins entire, very narrow, 1–3 mm wide, abruptly tapering; surface corticate, cortex smooth in the

upper part, verrucose in old parts, faintly pruinose towards the scyphi; podetial wall 183–223 μm wide. Hymenial discs infrequent, dark brown, no well-developed ones observed; ascospores not observed.

Conidiomata at margin of scyphi, globose, pycnidial slime hyaline; conidia $7-10 \times 1$ mm, hyaline, falciform.

Chemistry. PD+ red, K−, UV−; contains the fumarprotocetraric acid complex.

Etymology. This species is named in honour of Prof. Teuvo Ahti, on the occasion of his 90th birthday, for his great contribution to lichenology.

Habitat and distribution. Cladonia teuvoana occurs on heathlands and sandy areas, and is currently known from Denmark, the Czech Republic, the Netherlands, Spain, Sweden and the United Kingdom.

Remarks. The species differs from C. cervicornis s. str. in having a less well-developed primary thallus with a white underside and narrower scyphi that abruptly widen. It can be distinguished from C. pulvinata by the absence of psoromic acid and differs from C. verticillata in having narrow scyphi and a smaller primary thallus. Cladonia teuvoana probably has a wider distribution in Europe. To achieve a more realistic understanding of its distribution, it would be necessary to conduct a comprehensive study of herbarium material.

Additional specimens. Great Britain: England: V.C. 11, South Hampshire, New Forest National Park, Lyndhurst, Bolton Bench, heather with Calluna vulgaris and Erica cinerea, 50° 52ʹ17.2ʺN, 1°33ʹ23ʺW, alt. 36 m, 2019, R. Pino-Bodas & N. Sanderson (MACB).-Denmark: Jutland, Harrild, Hede, 62.07550°N 5.10650°E, 2016, U. Søchting 12520 (C-L 75831).— The Netherlands: Drenthe: Balloo, Ballooerveld, on sand, 2024, Aptroot 76155 (MACB).-Czech Republic: C. Bohemia: Praha, Natural Park Košíře-Motol, path of a heath with grove of Quercus petraea, Betula pendula and Pinus sylvestris with Calluna vulgaris in understorey, 50°03'45.6"N, 14°19'48.7"E, alt. 338 m, 2018, Z. Palice & P. Uhlík 24917.—Spain: Guipúzcoa: Oñate, Aizkorri-Aratz Natural Park, Malkorra, heathland with sandstone. 42°56'36.5"N, 2°21'51.9"W, alt. 1500 m, R. sandstone, 42°56ʹ36.5ʺN, 2°21ʹ51.9ʺW, alt. 1500 m, R. Pino-Bodas 254-2023 (MACB 125083).—Sweden: 2005, B. P. Løfall 10970 (H).

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Author ORCIDs. **D** Raquel Pino-Bodas, [0000-0001-5228-5368;](https://orcid.org/0000-0001-5228-5368) Alberto Herrero, [0009-0005-2007-3172;](https://orcid.org/0009-0005-2007-3172) André Aptroot, [0000-0001-7949-2594](https://orcid.org/0000-0001-7949-2594); Ulrik Søchting, 0000-0001-7122-9425; R. Troy McMullin, [0000-0002-1768-2891;](https://orcid.org/0000-0002-1768-2891) AR Burgaz, [0000-0003-2866-7731.](https://orcid.org/0000-0003-2866-7731)

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References

- Abbayes H des (1949) Some new Cladoniae (lichens) from Panama. Bryologist 52, 92–96.
- Agresti A (2018) An Introduction to Categorical Data Analysis. New York: John Wiley & Sons.
- Ahti T (1978) Nomenclatural and taxonomic remarks on European species of Cladonia. Annales Botanici Fennici 15, 7–14.
- Ahti T (1980) Nomenclatural notes on Cladonia species. Lichenologist 12, 125–133.
- Ahti T (1983) Taxonomic notes on some American species of the lichen genus Cladonia. Annales Botanici Fennici 20, 1–7.
- Ahti T (1998) A revision of Cladonia stricta. Folia Cryptogamica Estonica 32, 5–8.
- Ahti T (2000) Cladoniaceae. Flora Neotropica 78, 1–362.
- Ahti T (2007) Further studies on the Cladonia verticillata group (Lecanorales) in East Asia and western North America. Bibliotheca Lichenologica 96, 5–19.
- Ahti T and Aptroot A (1992) Lichens of Madagascar: Cladoniaceae. Cryptogamie, Bryologie, Lichénologie 13, 117–124.
- Ahti T and Aptroot A (2009) Two new species of Cladonia from the Azores. Bibliotheca Lichenologica 99, 11–17.
- Ahti T and Hammer S (2002) Cladonia. In Nash TH, III, Ryan BD, Diederich P, Gries C and Bungartz F (eds), Lichen Flora of the Greater Sonoran Desert Region, Vol. I. Tempe, Arizona: Lichens Unlimited, Arizona State University, pp. 131–158.
- Ahti T and Marcelli MP (1995) Taxonomy of the Cladonia verticillaris complex in South America. Bibliotheca Lichenologica 58, 5–26.
- Ahti T and Stenroos S (2013) Cladonia. In Ahti T, Stenroos S and Moberg R (eds), Nordic Lichen Flora. Volume 5: Cladoniaceae. Uppsala: Museum of Evolution, Uppsala University, pp. 1–117.
- Aptroot A, Souza MF and Spielmann AA (2021) Two new crustose Cladonia species with strepsilin and other new lichens from the Serra de Maracaju, Mato Grosso do Sul, Brazil. Cryptogamie, Mycologie 42, 137–148.
- Austin MP (1985) Continuum concept, ordination methods, and niche theory. Annual Review of Ecology and Systematics 16, 39–61.
- Beiggi S and Piercey-Normore MD (2007) Evolution of ITS ribosomal RNA secondary structures in fungal and algal symbionts of selected species of Cladonia sect. Cladonia (Cladoniaceae, Ascomycotina). Journal of Molecular Evolution 64, 528–542.
- Brodo IM, Sharnoff SD and Sharnoff S (2001) Lichens of North America. New Haven and London: Yale University Press.
- Burgaz AR, Ahti T, Inashvili T, Batsatsashvili K and Kupradze I (2018) Study of Georgian Cladoniaceae. Botanica Complutensis 42, 19–55.
- Burgaz AR, Ahti T and Pino-Bodas R (2020) Mediterranean Cladoniaceae. Madrid: Spanish Lichen Society (SEL).
- Carstens BC, Pelletier TA, Reid NM and Satler JD (2013) How to fail at species delimitation. Molecular Ecology 22, 4369–4383.
- Castresana J (2000) Selection of conserved blocks from multiple alignments for their use in phylogenetic analysis. Molecular Biology and Evolution 17, 540–552.
- Černajová I, Steinová J, Škvorová Z and Škaloud P (2022) The curious case of Cladonia luteoalba: no support for its distinction. Lichenologist 54, 345–354.
- Charnei AM and Eliasaro S (2013) Verticillate Cladonia species (Lichenized Ascomycota) from high-altitude environments of Serra do Mar in Southern Brazil. Hoehnea 40, 87–97.
- Culberson WL (1986) Chemistry and sibling speciation in the lichen-forming fungi: ecological and biological considerations. Bryologist 89, 123–131.
- De Queiroz K (1998) The general lineage concept of species, species criteria, and the process of speciation. In Howard DJ and Berlocher SH (eds), Endless Forms: Species and Speciation. Oxford: Oxford University Press, pp. 57–75.
- Del-Prado R, Divakar PK, Lumbsch HT and Crespo AM (2016) Hidden genetic diversity in an asexually reproducing lichen forming fungal group. PLoS ONE 11, e0161031.
- Dillenius JJ (1742) Historia Muscorum. Oxford: Sheldonian Theatre.
- Dolnik C, Beck A and Zarabska D (2010) Distinction of Cladonia rei and C. subulata based on molecular, chemical and morphological characteristics. Lichenologist 42, 373–386.
- Fontaine KM, Ahti T and Piercey-Normore MD (2010) Convergent evolution in Cladonia gracilis and allies. Lichenologist 42, 323-338.
- Gheza G, Nascimbene J, Mayrhofer H, Barcella M and Assini S (2018) Two Cladonia species new to Italy from dry habitats in the Po Plain. Herzogia, 31, 293–303.
- Goward T and Ahti T (1997) Notes on the distributional ecology of the Cladoniaceae (lichenized Ascomycetes) in temperate and boreal western North America. Journal of the Hattori Botanical Laboratory 82, 143–155.
- Grewe F, Lagostina E, Wu H, Printzen C and Lumbsch HT (2018) Population genomic analyses of RAD sequences resolves the phylogenetic relationship of the lichen-forming fungal species Usnea antarctica and Usnea aurantiacoatra. MycoKeys 43, 91–113.
- Hammer S (1995) A synopsis of the genus Cladonia in the northwestern United States. Bryologist 98, 1–28.
- Hammer S and Ahti T (1990) New and interesting species of Cladonia from California. Mycotaxon 37, 335–348.
- Hansen ES and Ahti T (2011) A contribution to the lichen genus Cladonia in Greenland and new records from other northern regions. Graphis Scripta 23, 56–64.
- Hoffmann GF (1796) Deutschlands Flora 2. Erlangen: Palm.
- Huovinen K and Ahti T (1982) Biosequential patterns for the formation of depsides, depsidones and dibenzofurans in the genus Cladonia (lichenforming ascomycetes). Annales Botanici Fennici 19, 225–234.
- Katoh K and Standley DM (2013) MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Molecular Biology and Evolution 30, 772–780.
- Kauff F and Lutzoni F (2002) Phylogeny of the Gyalectales and Ostropales (Ascomycota, Fungi): among and within order relationships based on nuclear ribosomal RNA small and large subunits. Molecular Phylogenetics and Evolution 25, 138–156.
- Kauff F and Lutzoni F (2003) Compat.py a program to detect topological conflict between supported clades in phylogenetic trees. [WWW resource] URL <http://www.lutzonilab.net/downloads/index.shtml>
- Košuthová A, Bergsten J, Westberg M and Wedin M (2020) Species delimitation in the cyanolichen genus Rostania. BMC Evolutionary Biology, 20, 1–17.
- Kruskal JB (1964) Nonmetric multidimensional scaling: a numerical method. Psychometrika 29, 115–129.
- Lim GS, Balke M and Meier R (2012) Determining species boundaries in a world full of rarity: singletons, species delimitation methods. Systematic Biology 61, 165–169.
- Litterski B and Ahti T (2004) World distribution of selected European Cladonia species. Symbolae Botanicae Upsalienses 34, 205–236.
- Lücking R, Hodkinson BP and Leavitt SD (2017) The 2016 classification of lichenized fungi in the Ascomycota and Basidiomycota – approaching one thousand genera. Bryologist 119, 361-416.
- Lücking R, Leavitt SD and Hawksworth DL (2021) Species in lichen-forming fungi: balancing between conceptual and practical considerations, and between phenotype and phylogenomics. Fungal Diversity 109, 99–154.
- Magoga G, Fontaneto D and Montagna M (2021) Factors affecting the efficiency of molecular species delimitation in a species-rich insect family. Molecular Ecology Resources 21, 1475–1489.
- Mercado-Díaz JA, Lücking R, Moncada B, Widhelm TJ and Lumbsch HT (2020) Elucidating species richness in lichen fungi: the genus Sticta (Ascomycota: Peltigeraceae) in Puerto Rico. Taxon 69, 851–891.
- Miller MA, Pfeiffer W and Schwartz T (2010) Creating the CIPRES Science Gateway for inference of large phylogenetic trees. In Proceedings of the Gateway Computing Environments Workshop (GCE), 14 November 2010, New Orleans, Louisiana, pp. 1–8.
- Minchin PR (1987) An evaluation of the relative robustness of techniques for ecological ordination. Vegetation 69, 89–107.
- Myllys L, Pino-Bodas R, Velmala S, Wang LS and Goward T (2023) Multi-locus phylogeny of Bryoria reveals recent diversification and unexpected diversity in section Divaricatae. Lichenologist 55, 497–517.
- Oksanen J, Blanchet FG, Kindt R, Legendre P, Minchin PR, O'Hara RB, Simpson GL, Solymos P, Stevens MHH and Wagner H (2013) vegan: Community Ecology Package, version. R package version 2.0. [WWW resource] URL <http://CRAN.R-project.org/package=vegan>.
- Orange A, James PW and White FJ (2010) Microchemical Methods for the Identification of Lichens. London: British Lichen Society.
- Osyczka P (2006) The lichen genus Cladonia (Cladoniaceae, lichenized Ascomycota) from Spitsbergen. Polish Polar Research 27, 207–242.
- Osyczka P and Rola K (2013) Response of the lichen Cladonia rei Schaer. to strong heavy metal contamination of the substrate. Environmental Science and Pollution Research 20, 5076–5084.
- Osyczka P, Rola K, Lenart-Boroń A and Boroń P (2014) High intraspecific genetic and morphological variation in the pioneer lichen Cladonia rei colonising slag dumps. Central European Journal of Biology 9, 579–591.
- Osyczka P, Boroń P, Lenart-Boroń A and Rola K (2018) Modifications in the structure of the lichen Cladonia thallus in the aftermath of habitat contamination and implications for its heavy-metal accumulation capacity. Environmental Science and Pollution Research 25, 1950–1961.
- Paradis E and Schliep K (2019) ape 5.0: an environment for modern phylogenetics and evolutionary analyses in R. Bioinformatics 35, 526–528..
- Parnmen S, Rangsiruji A, Mongkolsuk P, Boonpragob K, Nutakki A and Lumbsch HT (2012) Using phylogenetic and coalescent methods to understand the species diversity in the Cladia aggregata complex (Ascomycota, Lecanorales). PLoS ONE 7, e52245.
- Pentinsaari M, Vos R and Mutanen M (2017) Algorithmic single-locus species delimitation: effects of sampling effort, variation and nonmonophyly in four methods and 1870 species of beetles. Molecular Ecology Resources 17, 393–404.
- Pérez-Ortega S, Garrido-Benavent I, Grube M, Olmo R and de los Ríos A (2016) Hidden diversity of marine borderline lichens and a new order of fungi: Collemopsidiales (Dothideomyceta). Fungal Diversity 80, 285–300.
- Pino-Bodas R, Burgaz AR and Martín MP (2010a) Elucidating the taxonomic rank of Cladonia subulata versus C. rei (Cladoniaceae). Mycotaxon 113, 311–326.
- Pino-Bodas R, Martin MP and Burgaz AR (2010b) Insight into the Cladonia convoluta-C. foliacea (Cladoniaceae, Ascomycota) complex and related species, revealed through morphological, biochemical and phylogenetic analyses. Systematics and Biodiversity 8, 575–586.
- Pino-Bodas R, Burgaz AR, Martín MP and Lumbsch HT (2011) Phenotypical plasticity and homoplasy complicate species delimitation in the Cladonia gracilis group (Cladoniaceae, Ascomycota). Organisms Diversity and Evolution 11, 343–355.
- Pino-Bodas R, Burgaz AR, Martin MP and Lumbsch HT (2012) Species delimitations in the Cladonia cariosa group (Cladoniaceae, Ascomycota). Lichenologist 44, 121–135.
- Pino-Bodas R, Ahti T, Stenroos S, Martín MP and Burgaz AR (2013a) Multilocus approach to species recognition in the Cladonia humilis complex (Cladoniaceae, Ascomycota). American Journal of Botany 100, 664–678.
- Pino-Bodas R, Martín MP, Stenroos S and Burgaz AR (2013b) Cladonia verticillata (Cladoniaceae, Ascomycota), new record to Iberian Peninsula. Botanica Complutensis 37, 21–25.
- Pino-Bodas R, Martin MP, Burgaz AR and Lumbsch HT (2013c) Species delimitation in Cladonia (Ascomycota): a challenge to the DNA barcoding philosophy. Molecular Ecology Resources 13, 1058–1068.
- Pino-Bodas R, Burgaz AR, Martín MP, Ahti T, Stenroos S, Wedin M and Lumbsch HT (2015) The phenotypic features used for distinguishing species within the Cladonia furcata complex are highly homoplasious. Lichenologist 47, 287–303.
- Pino-Bodas R, Burgaz AR, Ahti T and Stenroos S (2018) Taxonomy of Cladonia angustiloba and related species. Lichenologist 50, 267–282.
- Pino-Bodas R, Sanderson N, Cannon P, Aptroot A, Coppins B, Orange A and Simkin J (2021) Lecanorales: Cladoniaceae [revision 1], including the genera Cladonia, Pilophorus and Pycnothelia. Revisions of British and Irish Lichens 26, 1–45.
- Plate T and Heiberger R (2016) abind: Combine Multidimensional Arrays. R package version 1.4-5. [WWW resource] URL [https://cran.r-project.org/](https://cran.r-project.org/package=abind) [package=abind](https://cran.r-project.org/package=abind).
- Pons J, Barraclough TG, Gomez-Zurita J, Cardoso A, Duran DP, Hazell S, Kamoun S, Sumlin WD and Vogler AP (2006) Sequence-based species delimitation for the DNA taxonomy of undescribed insects. Systematic Biology 55, 595–609.
- Posada D (2008) jModelTest: phylogenetic model averaging. Molecular Biology and Evolution 25, 1253–1256.
- Puillandre N, Brouillet S and Achaz G (2021) ASAP: assemble species by automatic partitioning. Molecular Ecology Resources 21, 609–620.
- R Core Team (2022) R: a Language and Environment for Statistical Computing, Version 4.1.2. R Foundation for Statistical Computing, Vienna, Austria. [WWW resource] URL <https://www.R-project.org>.
- Rambaut A, Drummond AJ, Xie D, Baele G and Suchard MA (2018) Posterior summarization in Bayesian phylogenetics using Tracer 1.7. Systematic Biology 67, 901–904.
- Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA and Huelsenbeck JP (2012) MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. Systematic Biology 61, 539–542.
- Søchting U (2017) Lav i klit og hede. Thisted: Biologisk forening for Nordvestjylland.
- Stamatakis A, Hoover P and Rougemont J (2008) A rapid bootstrap algorithm for the RAxML web servers. Systematic Biology 57, 758–771.
- Steinová J, Holien H, Košuthová A and Škaloud P (2022) An exception to the rule? Could photobiont identity be a better predictor of lichen phenotype than mycobiont identity? Journal of Fungi 8, 275.
- Stenroos S and Ahti T (1990) The lichen family Cladoniaceae in Tierra del Fuego: problematic or otherwise noteworthy taxa. Annales Botanici Fennici 27, 317–327.
- Stenroos S, Hyvönen J, Myllys L, Thell A and Ahti T (2002) Phylogeny of the genus Cladonia s. lat. (Cladoniaceae, Ascomycetes) inferred from molecular, morphological, and chemical data. Cladistics 18, 237–278.
- Stenroos S, Pino-Bodas R, Hyvönen J, Lumbsch HT and Ahti T (2019) Phylogeny of the family Cladoniaceae (Lecanoromycetes, Ascomycota) based on sequences of multiple loci. Cladistics 35, 351–384.
- Swinscow TDV and Krog H (1988) Macrolichens of East Africa. London: British Museum (Natural History).
- van Herk CM and Aptroot A (2003) A new status for the Western European taxa of the Cladonia cervicornis group. Bibliotheca Lichenologica 86, 193–203.
- Vences M, Miralles A, Brouillet S, Ducasse J, Fedosov A, Kharchev V, Kostadinov I, Kumari S, Patmanidis S, Scherz MD, et al. (2021) iTaxoTools 0.1: kickstarting a specimen-based software toolkit for taxonomists. Megataxa 6, 77–92.
- Wei X, McCune B, Lumbsch HT, Li H, Leavitt S, Yamamoto Y, Tchabanenko S and Wei J (2016) Limitations of species delimitation based on phylogenetic analyses: a case study in the Hypogymnia hypotrypa group (Parmeliaceae, Ascomycota). PLoS ONE 11, e0163664.
- White FJ and James PW (1985) A new guide to microchemical techniques for the identification of lichen substances. British Lichen Society Bulletin 75(Suppl.), 1–41.
- Zhang J, Kapli P, Pavlidis P and Stamatakis A (2013) A general species delimitation method with applications to phylogenetic placements. Bioinformatics 29, 2869–2876.