Lopadostoma taeniosporum revisited and a new species of *Coniochaeta*

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Friebes G., Jaklitsch W.M., García S. & Voglmayr H. (2016) *Lopadostoma taeniosporum* revisited and a new species of *Coniochaeta*. Sydowia 68: 87–97.

Phylogenetic analyses of ITS-LSU rDNA sequence data revealed that *Anthostoma taeniosporum*, currently classified as *Lopadostoma taeniosporum*, does not belong to Xylariales but to the genus *Coniochaeta* (Coniochaetales), in which it is formally combined. *Anthostoma taeniosporum* is epitypified with a recent specimen for which sequence data are available. *Coniochaeta taeniospora* differs macro-morphologically from most other species of *Coniochaeta* in the immersed habit of ascomata. Furthermore, this species is well defined by its light brown, obtuse hairs, green peridium in KOH, and relatively large, ellipsoid to ovoid ascospores. A Spanish specimen initially identified as *Coniochaeta taeniospora* turned out to be phylogenetically distinct from the other two accessions sequenced, and is described as the new species *Coniochaeta navarrae*. This species differs morphologically from *C. taeniospora* in ascomatal habit, lack of clearly developed hairs on the peridium, colour of the peridium in KOH, and size of the ascospores, which are slightly larger and sometimes show a hyaline sheath in *C. navarrae*.

Keywords: Ascomycota, Coniochaetaceae, phylogenetic analysis, pyrenomycetes, Sordariomycetes.

In a monographic revision of the genus *Lopadostoma*, Jaklitsch et al. (2014) briefly redescribed *L. taeniosporum* based on its type extant in PAD. Subsequently fresh specimens were collected, which match or nearly match this taxon morphologically. Micromorphology and phylogenetic analyses based on LSU and ITS-LSU rDNA matrices revealed that *L. taeniosporum* belongs to the genus *Coniochaeta* (Coniochaetaceae). *Coniochaeta* is characterised by black, usually superficial, perithecial, sometimes cleistothecial, solitary or aggregated, typically setose ascomata, a paraphysate centrum, unitunicate, cylindrical to clavate, thin-walled asci with a small inamyloid apical ring, and by 1-celled, usually dark brown, often laterally compressed ascospores with a germ slit (García et al. 2006). Its asexual morphs are hyphomycetous, phialidic, with the phialide often reduced to a collarette lateral on a hyphal cell (*Lecythophora*). The genus occurs on wood and bark, dung or in soil and is primarily saprobic; however, some species are also known as pathogens of woody plants (Damm et al. 2010) or can cause serious opportunistic infections in animals or humans

(Drees et al. 2007, Hoog et al. 2000, Perdomo et al. 2011, Taniguchi et al. 2009, Troy et al. 2013). Remarkably, *Coniochaeta* species have also been shown to produce potent antibiotics (Segeth et al. 2003) or have a high potential of biological detoxification of lignocellulosic biomass (López et al. 2004).

Coniochaeta, typified by *C. ligniaria*, is a large genus. Many species have been described, but there are mostly morphological studies and keys to species (Asgari et al. 2007, Checa et al. 1988, Romero et al. 1999). First molecular studies on the Coniochaetaceae (Coniochaetales) were published by Weber et al. (2002), who emphasised the connection of *Coniochaeta* with the asexual morph genus *Lecythophora*, by Huhndorf et al. (2004), who showed the family as an integral part of the Sordariomycetes, and by García et al. (2006), who detected that the Coniochaetaceae were polyphyletic. They determined that *Coniochaetidium*, *Ephemeroascus* and *Poroconiochaeta* are synonyms of *Coniochaeta* and transferred two species to the new genera *Coniocessia* (see also Asgari & Zare 2011) and *Coniolariella*

(see also Checa et al. 2008, Zare et al. 2010) in the Xylariales. Other genera of the Coniochaetaceae are *Barrina* and possibly *Synaptospora*. The latter was recently proposed to belong to the Helminthosphaeriaceae, based on DNA data of a non-type species (Miller et al. 2014). The fungicolous genus *Immersisphaeria* (Jaklitsch 2007), which is only known from an old herbarium specimen and matches *Coniochaeta* except for a hyaline peridium, may also belong to the family. Raja et al. (2012) added a new species occurring in freshwater to *Coniochaeta*. The most recent contribution was published by Vázquez-Campos et al. (2014). Unfortunately for most species only LSU and, to a lesser extent, ITS sequences are available, which is most probably insufficient for satisfactory resolution at the species level.

Materials and methods

Isolates and specimens

All newly prepared isolates used in this study originated from ascospores of fresh specimens. Numbers of strains including NCBI GenBank accession numbers of gene sequences used to compute the phylogenetic trees are listed in Tab. 1. Isolates have been deposited at the CBS-KNAW Fungal Biodiversity Centre, Utrecht, The Netherlands (CBS). Details of the specimens used for morphological investigations are listed in the Taxonomy section under the respective descriptions. Specimens have been deposited in the Herbarium of the Institute of Botany, University of Graz (GZU).

Culture preparation, growth rate determination and phenotype analysis

Cultures were prepared and maintained as described previously (Jaklitsch 2009). Microscopic observations were made in tap water except where noted. Morphological analyses of microscopic characters were carried out as described earlier (Jaklitsch 2009). Methods of microscopy included stereomicroscopy using Nikon SMZ 1500 and Euromex Novex RZ 65.560, light microscopy using Euromex XHR MIC 625 and Nomarski differential interference contrast (DIC) using the compound microscope Nikon Eclipse E600. Images and data were gathered using Nikon Coolpix 4500, Nikon DS-U2, and Nikon D90 digital cameras and measured directly with the microscope or with NIS-Elements D v. 3.0. Measurements are reported as maximum and minimum in parentheses and the mean plus and minus the standard deviation of a number of measurements given in parentheses.

DNA extraction and sequencing methods

The extraction of genomic DNA was performed as reported previously (Voglmayr & Jaklitsch 2011, Jaklitsch et al. 2012) using the DNeasy Plant Mini Kit (QIAgen GmbH, Hilden, Germany). The following loci were amplified and sequenced: the complete internally transcribed spacer region (ITS1-5.8S-ITS2) and a c. 900 bp fragment of the large subunit nuclear ribosomal DNA (nLSU rDNA), amplified and sequenced as a single fragment with primers V9G (Hoog & Gerrits van den Ende 1998) and LR5 (Vilgalys & Hester 1990); a c. 1.2 kb fragment of the RNA polymerase II subunit 2 (*rpb2*) with primers fRPB2-5f and fRPB2-7cr (Liu et al. 1999); and a c. 1.3 kb fragment of the translation elongation factor 1-alpha (*tef1*) with primers EF1-728F (Carbone & Kohn 1999) and TEF1LLErev (Jaklitsch et al. 2005). PCR products were purified using an enzymatic PCR cleanup (Werle et al. 1994) as described in Voglmayr & Jaklitsch (2008). DNA was cycle-sequenced using the ABI PRISM Big Dye Terminator Cycle Sequencing Ready Reaction Kit v. 3.1 (Applied Biosystems, Warrington, UK) with the same primers as in PCR; in addition, primers ITS4 (White et al. 1990) and LR3 (Vilgalys & Hester 1990) were used for the ITS-LSU region. Sequencing was performed on an automated DNA sequencer (3730xl Genetic Analyzer, Applied Biosystems).

Analysis of sequence data

NCBI nucleotide BLAST searches of the ITS and LSU revealed *Coniochaeta* as closest matches (98% and 99% sequence identities for ITS and LSU, respectively). For the majority of *Coniochaeta* species, only partial LSU rDNA are available; for comparatively few also ITS rDNA. Therefore, phylogenetic analyses were only possible with these two markers. Based on critical inspection of the sequence data available in GenBank, we decided to produce an LSU and a combined ITS-LSU matrix, if available from the same strains, for further phylogenetic analyses. No ITS matrix was produced, because for only few *Coniochaeta* species reliably labelled sequences are available in GenBank, as most are either inaccurately identified or unidentified (see e.g. also the ITS tree fig. 2 of Raja et al. 2012). ITS and LSU sequences of a representative selection of *Coniochaeta* species were downloaded from GenBank, preferably from ex-type cultures; for rooting the trees, two *Chaetosphaeria* species (*C. innumera* AF178551, *C. pygmaea* AF178545) were included. For the LSU matrix, the GenBank accession numbers are given in the tree, for the ITS-LSU matrix in

Tab. 1. Strains and NCBI GenBank accessions used in the phylogenetic analyses of the combined ITS-LSU rDNA matrix. Sequences in bold were generated during the present study.

Taxon	Strain	Type	ITS	LSU
Coniochaeta africana	CBS 120868	ex-type	GQ154539	GQ154601
C. canina	UAMH 11702	ex-type	NR_120211	NG_042720
C. cateniformis	CBS 131709	ex-type	NR_111517	HE610329
C. decumbens	CBS 153.42	ex-type	HE610337	AF353597
C. fasciculata	CBS 205.38	ex-type	HE610336	AF353598
C. fodinicola	CBS 136963	ex-type	JQ904603	KF857172
C. gigantospora	ILLS 60816	ex-type	JN684909	JN684909
C. hoffmannii	CBS 245.38	ex-type	HE610332	AF353599
C. lignicola	CBS 267.33	ex-type	NR_111520	AF353601
C. luteorubra	CBS 131710	ex-type	HE610330	HE610328
C. luteoviridis	CBS 206.38	ex-type	HE610333	AF353603
C. mutabilis	CBS 157.44	ex-type	NR_111519	NG_042382
C. polymorpha	CBS 132722	ex-type	HE863327	HE863327
C. prunicola	CBS 120875	ex-type	GQ154540	GQ154602
C. prunicola	CBS 121445		GQ154541	GQ154603
C. velutina	CBS 120874		GQ154542	GQ154604
C. velutina	CBS 121444		GQ154544	GQ154605
C. taeniospora	LTA	ex-type	**KU762324**	**KU762324**
C. taeniospora	LTA1		**KU762325**	**KU762325**
C. navarrae	LTA3	ex-type	**KU762326**	**KU762326**

Tab. 1. All alignments were produced with the server version of MAFFT (www.ebi.ac.uk/Tools/mafft), checked and refined using BioEdit version 7.0.4.1 (Hall 1999). For phylogenetic analyses, an LSU and a combined ITS-LSU matrix were produced containing 474 and 1105 nucleotide characters, respectively.

Maximum likelihood (ML) analyses were performed with RAxML (Stamatakis 2006) as implemented in raxmlGUI 1.3 (Silvestro & Michalak 2012), using the ML + rapid bootstrap setting and the GTRGAMMAI substitution model with 1000 bootstrap replicates.

Maximum parsimony (MP) analyses were performed with PAUP v. 4.0a142 (Swofford 2002), using 1000 replicates of heuristic search with random addition of sequences and subsequent TBR branch swapping (MULTREES option in effect, steepest descent option not in effect). All molecular characters were unordered and given equal weight; analyses were performed with gaps treated as missing data; the COLLAPSE command was set to MAX-BRLEN. Bootstrap analyses with 1000 replicates were performed in the same way, but using 5 rounds of random sequence addition and subsequent branch swapping during each bootstrap replicate; in addition, each replicate was limited to 1 million rearrangements in the analyses of the LSU matrix.

Results

Of the 474 characters of the LSU matrix, 74 were parsimony informative. Figure 1 shows the phylogram of the best ML tree (lnL = -1873.2991) obtained by RAxML. MP analysis revealed one tree of length 229, which is similar to the ML tree except for minor topological differences at the basal nodes of the tree (not shown). Most of the tree topologies are unsupported in both ML and MP analyses. In both ML and MP analyses, *Coniochaeta taeniospora* and *C. navarrae* are embedded within *Coniochaeta* and form a clade with medium support, but the two species are not resolved. A sister group relationship of the *C. taeniospora - C. navarrae* clade to the clade containing *C. savoryi*, *C. punctulata* and *C. ornata* is also revealed in both ML and MP analyses but does not receive significant internal support.
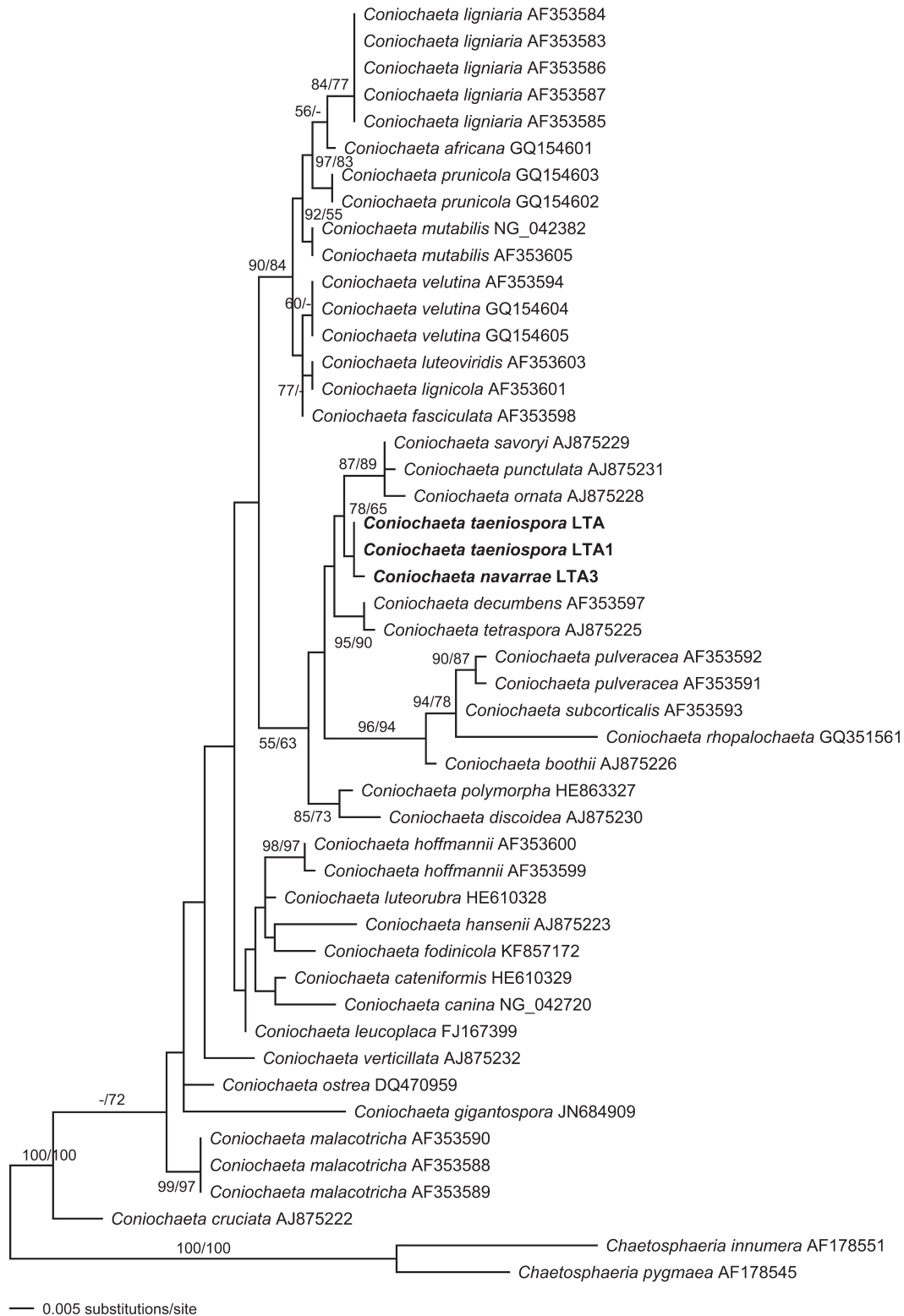
Fig. 1. Phylogram of the best maximum likelihood tree (lnL = –1873.2991) revealed by RAxML from an analysis of the LSU rDNA matrix of *Coniochaeta*, showing the phylogenetic position of *C. taeniospora* and *C. navarrae*. ML and MP bootstrap support above 50% are given above or below the branches. GenBank accession numbers are given following the taxon names. The tree was rooted with 2 species of *Chaetosphaeria*.
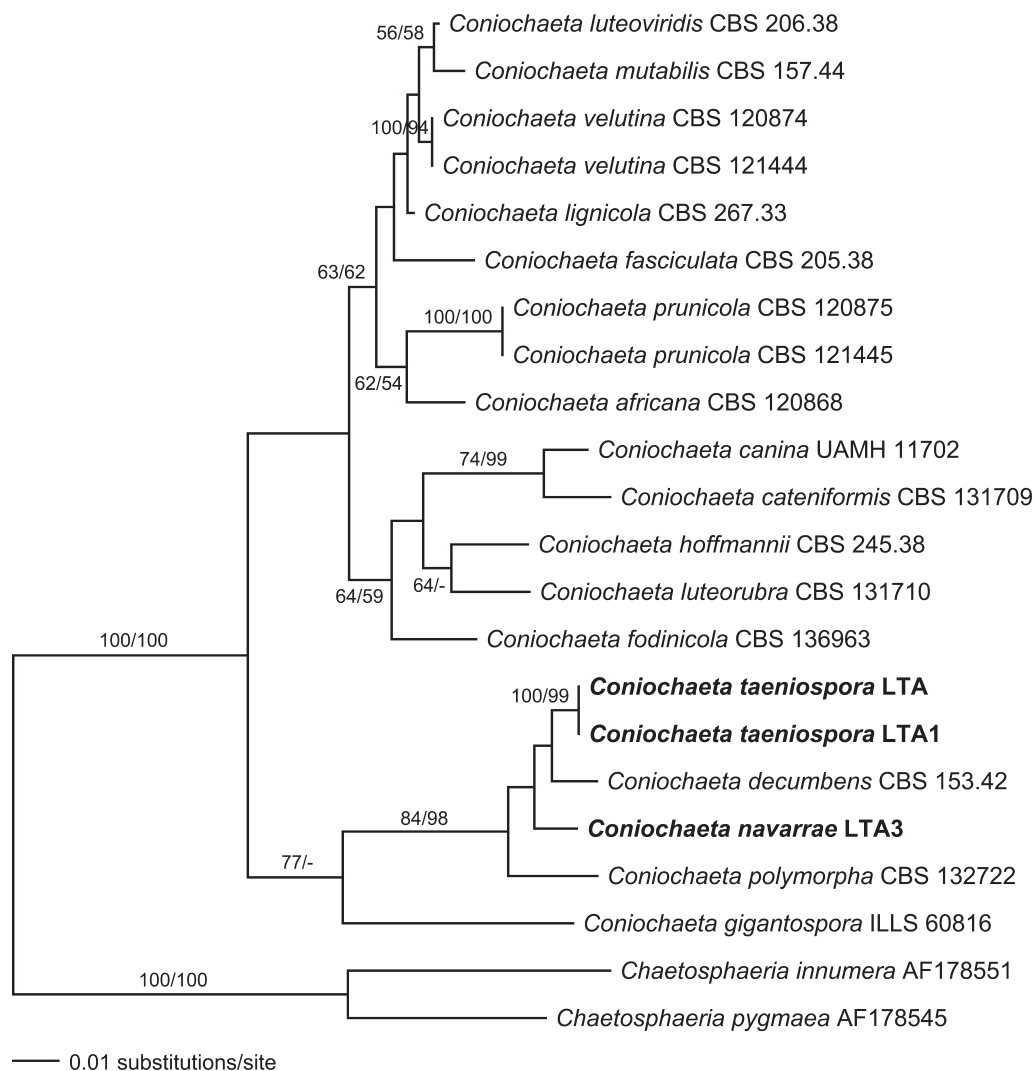
Fig. 2. Phylogram of the best maximum likelihood tree (lnL = -4506.09195) revealed by RAxML from an analysis of the ITS-LSU rDNA matrix of *Coniochaeta*, showing the phylogenetic position of *C. taeniospora* and *C. navarrae*. ML and MP bootstrap support above 50% are given above or below the branches. Strain numbers are given following the taxon names. The tree was rooted with 2 species of *Chaetosphaeria*.

Of the 1105 characters of the ITS-LSU matrix, 215 were parsimony informative. Figure 2 shows the phylogram of the best ML tree (lnL = -4506.09195) obtained by RAxML. MP analysis revealed three trees of length 609, which differed from the ML tree in many nodes of the tree lacking bootstrap support (not shown). *Coniochaeta taeniospora* and *C. navarrae* are phylogenetically clearly distinct and placed in a highly supported clade together with *C. decumbens* and *C. polymorpha*; however, the phylogenetic relationships within this clade remain unresolved due to lack of significant internal support. Sister group relationship of *Coniochaeta gigantospora* to this clade is moderately supported only in the ML analysis.

Taxonomy

Coniochaeta taeniospora (Sacc.) Friebes, Jaklitsch & Voglmayr, **comb. nov.** – Fig. 3.
MycoBank no.: MB 815856

B a s i o n y m . – *Anthostoma taeniosporum* Sacc., Atti Soc. Veneto-Trentino Sci. Nat. Padova 2: 143. 1873.

S y n o n y m . – *Lopadostoma taeniosporum* (Sacc.) Traverso, Fl. Ital. Crypt., Pars 1: Fungi. Pyrenomycetae, Xylariaceae, Valsaceae, Ceratostomataceae 1, 1: 171. 1906.

H o l o t y p e . – ITALY, Montello, on corticated branches of *Quercus robur* (given as *Quercus pedunculata*), without date, P. Saccardo (PAD).

E p i t y p e of *Anthostoma taeniosporum*, here designated. – AUSTRIA, Niederösterreich, Krems, Egelsee, on corticated,

Fig. 3. *Coniochaeta taeniospora*. **a, b**. ascomata in face view; **c, e**. vertical section of a perithecium; **d**. perithecia in transverse section; **f**. ostiole in section; **g**. asci; **h, i**. peridium in section (i in 3% KOH); **j**. ascospores and paraphyses; **k, o**. ascospores; **l, p**. ascospores showing germ slits (l in Congo Red); **m, n**. hairs; **q, r**: ascus apex in Congo Red. (a, b, g–i, l, q, r. GZU000313628 (LTA); c–f, j, k, m, n. GZU000313629 (LTA1); o, p. holotype). Scale bars: a, b, d = 500 µm; c = 300 µm; e = 200 µm; f, g, j = 20 µm; h, i = 50 µm; k–o, q, r = 10 µm; p = 5 µm.

0.8–1.1 cm thick twigs of *Quercus petraea* on the ground, 27. October 2013, *leg.* W. Jaklitsch & H. Voglmayr (GZU000313628, culture LTA = CBS 141014; ex-epitype sequences: ITS-LSU: KU762324, *rpb2*: KU762327, *tef1*: KU762330). MBT 204266.

D e s c r i p t i o n . – A s c o m a t a forming inconspicuous groups of 0.5–2 mm diam. in cracks of bark or erumpent through the bark, more rarely growing solitarily, often with a brown, amorphous substance between them rendering a stromatic appearance. Ascomata immersed or semi-immersed in the bark, often with only the ostiole visible, perithecial, 200–410 µm high and 200–450 µm wide (n=15), subglobose to ellipsoid, sometimes pyriform or lageniform, black, with smooth to somewhat rough surface, often with some hyaline hyphae at the base. P e r i d i u m brittle when dry, softer when rehydrated, 20–40 µm thick at the base (n=15), 30–45(–55) µm near the ostiole (n=23), two-layered. Inner layer consisting of hyaline to subhyaline, strongly compressed cells, 5–12(17) × 2–5(8) µm (n=25), turning green in 3% KOH; outer layer consisting of densely packed, moderately thick-walled, brown cells measuring 4–10(12) × 2–7 µm (n=30), tending to be darker and more isodiametric towards the outside; near the ostiole some protruding, thick-walled, elongated, apically rounded cells and sparse, pale, often apically darker, 0–2-septate hairs, 19–28 × 2.0–3.2 µm (n=12), present. O s t i o l a r n e c k s papillate to cylindrical, with circular outline, densely filled with 1–1.5 µm wide periphyses (n=15). P a r a p h y s e s filiform, septate, hyaline, 2.5–3.5(4) µm wide (n=25). A s c i 169–184(196) × 9–14 µm (n=20), cylindrical, (4–)8-spored (aborted ascospores sometimes visible in 4-spored asci), with slender stipe, apical apparatus inconspicuous, more clearly visible in Congo Red, inamyloid (Melzer- and IKI-negative). A s c o s p o r e s (12.5)15.5–19.2(24.5) × (8.0)9.5–12.3 (14.5) µm, l/w (1.3)1.4–1.8(2.5) (n=106), ellipsoid to ovoid, slightly laterally compressed, dark brown, darker in 3% KOH, with a conspicuous, straight germ slit across the entire length, smooth, multiguttulate, without sheath or appendages.

H a b i t a t . – On corticated branches of *Quercus* spp.

D i s t r i b u t i o n . – Central and Southern Europe (Austria, Italy).

O t h e r s p e c i m e n e x a m i n e d : AUSTRIA, Steiermark, Bad Waltersdorf, Leitersdorfberg, on corticated, 0.4 cm thick twigs of *Quercus petraea* on the ground, 20. April 2014, *leg.* A. Draxler & W. Maurer (GZU000313629, culture LTA1 = CBS 141015; sequences: ITS-LSU: KU762325, *rpb2*: KU762328, *tef1*: KU762331).

N o t e s . – Apart from two gaps in the ITS, the two collections have identical ITS-LSU sequences. However, the *rpb2* and *tef1* sequences differ in 20 and 26 nucleotide substitutions, respectively, which may indicate that actually two cryptic species are involved. Sequence data from additional strains are necessary to clarify this.

Coniochaeta navarrae Friebes, Jaklitsch, S. García & Voglmayr, **sp. nov.** – Fig. 4.
MycoBank no.: MB 815857

H o l o t y p e . – SPAIN, Navarra, Sarasibar, elev. 590 m, on bark of *Ulmus* sp., 3. April 2015, *leg.* S. García (GZU000313630, culture LTA3 = CBS 141016; ex-holotype sequences: ITS-LSU: KU762326, *rpb2*: KU762329, *tef1*: KU762332).

D e s c r i p t i o n . – A s c o m a t a solitary to gregarious, with bases immersed in bark, not forming pustulate groups, non-stromatic, globose to pyriform, 200–450 µm high and 120–320 µm wide (n=15), with black, somewhat roughened surface. P e r i d i u m brittle when dry, softer when rehydrated, 33–45(60) µm thick (n=30), two-layered. Inner layer composed of hyaline to subhyaline, strongly compressed cells measuring 7–12 × 1–4 µm (n=20), faintly turning greenish in 3% KOH; outer *textura angularis* consisting of compressed to isodiametric, thick-walled, dark brown cells measuring 3–13 × 2–4 µm (n=25), encrusted with a dark brown substance, more elongate towards the ostiole and sometimes slightly protruding; surface clothed with inconspicuous, scattered to densely grouped, short, thick-walled, dark brown, seta-like cells. O s t i o l e s inconspicuous to papillate, with circular outline, filled with 1–1.5 µm wide periphyses (n=12). P a r a p h y s e s filiform, 2.5–4 µm wide (n=20), filled with droplets. A s c i 165–189 × (14–)16–20 µm (n=20), cylindrical, (4–)8-spored, ascospores uniseriate, with short but distinct, sometimes twisted stipe, apical apparatus inamyloid (Melzer-negative), faintly visible in Melzer and Congo Red. A s c o s p o r e s (17)18–20(20.5) × (10)11–13.5(16) µm, l/w (1.2)1.4–1.7(1.9) (n=32), ellipsoid to broadly ellipsoid, sometimes ovoid, dark brown when mature, with a conspicuous, straight germ slight across the entire spore length, smooth, sometimes with a hyaline sheath, usually filled with one or two bigger and several smaller droplets, turning almost black in 3% KOH.

E t y m o l o g y . – For its occurrence in Navarra.

H a b i t a t . – On bark of *Ulmus*.

D i s t r i b u t i o n . – Spain, only known from the holotype.

Discussion

The main objective of this work was to clarify the phylogenetic position of *Lopadostoma taenio-*
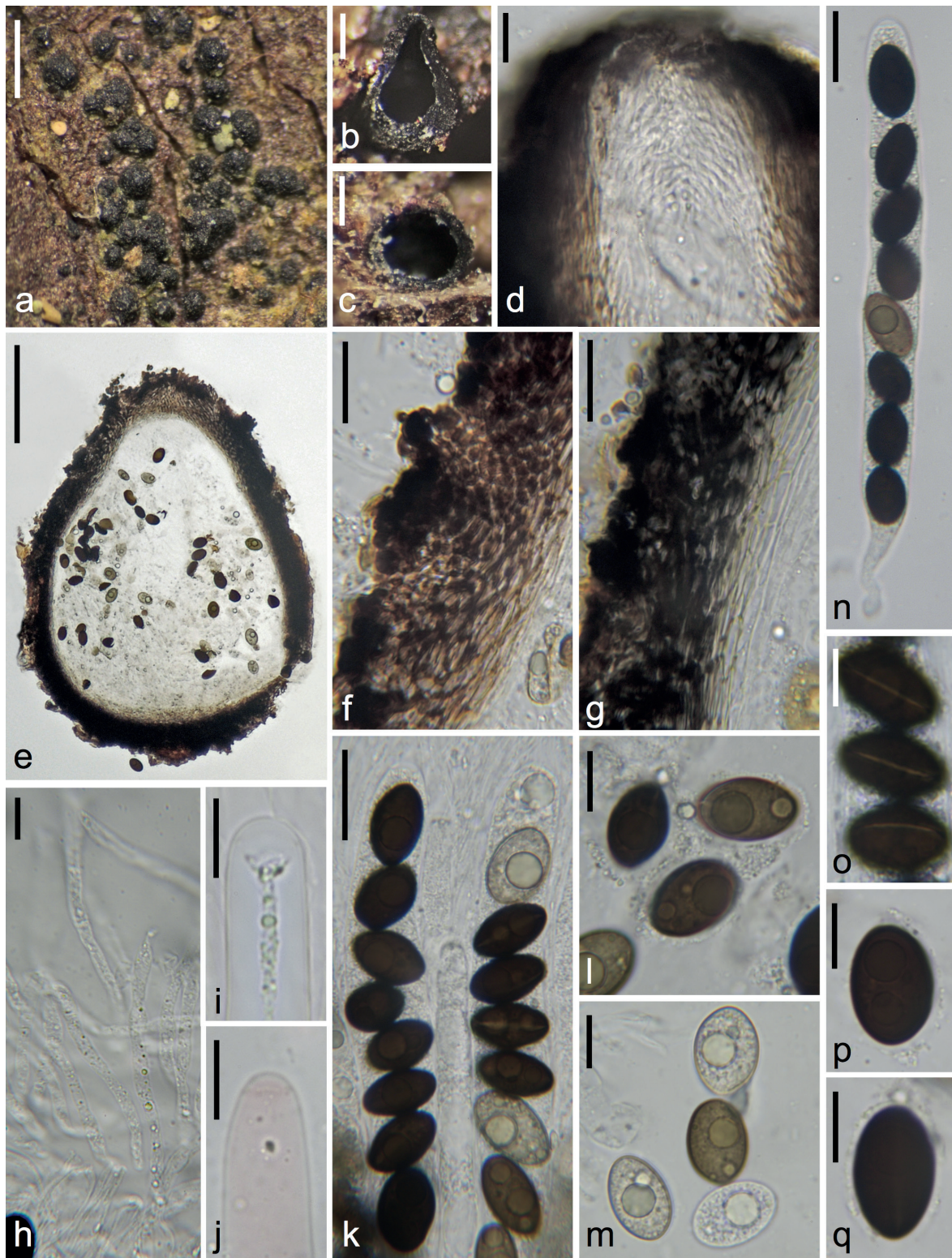
Fig. 4. *Coniochaeta navarrae* (Holotype GZU000313630). **a**. ascomata in face view; **b, e**. vertical section of a perithecium; **c**. transverse section of a perithecium; **d**. ostiole in section; **f, g**. peridium in section (g in 3% KOH); **h**. paraphyses; **i, j**. ascus apex in Congo Red; **k**. asci with ascospores; **l, p, q**. ascospores with sheath; **m**. immature ascospores; **n**. ascus; **o**. ascospores showing germ slits. Scale bars: a = 500 µm; b = 125 µm; c = 150 µm; e = 100 µm; f, g, k, n = 20 µm; d, h–j, l, m, o–q = 10 µm.

sporum. Phylogenetic analyses of ITS and LSU rDNA data clearly place this taxon in *Coniochaeta*, which requires a generic transfer. The Spanish specimen was revealed as closely related to *L. taeniosporum*, but the ITS sequence clearly separated it from the latter, which was also corroborated by morphological differences (see below). However, the LSU data are insufficient to elucidate the detailed phylogenetic relationships within *Coniochaeta*. The combined ITS-LSU matrix revealed better resolution; however, ITS sequences are available for only a few *Coniochaeta* species. In addition, many of the ITS sequences deposited at GenBank are unidentified or require critical taxonomic revision. It is therefore urgently needed to sequence the ITS for additional well documented strains for which the LSU is already available, and additional markers with higher resolution like the *rpb2*, *tef1* or *tub2* should be sequenced for reliable delimitation of closely related *Coniochaeta* species.

Coniochaeta taeniospora is an untypical representative of the genus due to its immersed ascomata, which tend to be clustered in groups with stromatic appearance. Also the relatively large, non-appendiculate, ellipsoid to ovoid ascospores, as well as peridial cells, which show a green reaction to KOH, and sparse, obtuse, light brown hairs on the peridium characterise this species well. Most lignicolous *Coniochaeta* species have more or less superficial ascomata on the natural substrate; however, immersed ascomata have been reported for *C. renispora* (Crane & Shearer 1995), which differs from *C. taeniospora* in having much smaller, kidney-shaped ascospores. *Coniochaeta myricariae* is described as having glabrous, gregarious ascomata, which develop under the bark and finally become erumpent, in a similar fashion as *C. taeniospora*, but the former species has much smaller and laterally compressed ascospores (Arx & Müller 1954).

Coniochaeta taeniospora has a stromatic appearance due to a dark amorphous substance between the ascomata, which is unusual for the typically non-stromatic genus *Coniochaeta*. Similarly, ascomata of *C. phalacrocarpa* are described as being glabrous and surrounded by an "amorphous hyphal weft" rendering a stromatic appearance (Carroll & Munk 1964). This species differs from *C. taeniospora* in superficial ascomata and lenticular, much smaller ascospores. Some other species of *Coniochaeta* have occasionally been described as having more or less well developed stromatic parts towards the basal part of the ascomata, e.g. *C. malacotricha* and *C. niesslii* (Arx & Müller 1954), which also differ in ascospores and other traits.

Most *Coniochaeta* species have setose ascomata but in some species setae may occasionally be absent or very sparse while other species are reported without setae or hairs. The ascomata of *C. taeniospora* appear smooth under the stereomicroscope but light microscopy reveals some sparse, light brown, obtuse hairs, which differ quite clearly from the stiff, dark brown, pointed setae typically found in this genus. Some hairs are apically darker and thus resemble the setae of *C. rhopalochaeta* (Romero et al. 1999) even though the latter differ in being apically inflated.

The peridial cells of *C. taeniospora* show a green reaction to KOH similar to *C. alkalivirens* (Checa et al. 1988). The latter differs in smaller ascospores, which are subfusiform in side view, as well as in superficial ascomata. Furthermore, *C. taeniospora* is distinguished from most other species mentioned in the literature (Asgari et al. 2007, Checa et al. 1988, Mahoney & LaFavre 1981, Romero et al. 1999) by its relatively large, ellipsoid to ovoid ascospores with rounded, non-appendiculate ends. Only few *Coniochaeta* species possess ascospores with similar shape and size, e.g. *C. niesslii* (Arx & Müller 1954) with narrower ascospores (16–20 × 8–9 µm) and dark brown setae, and *C. sanguinolenta* (Checa et al. 1988) with red peridium and long, pointed hairs. *Coniochaeta caryotae* (Rao 1970) and *C. gigantospora* (Raja et al. 2012) also have large, ellipsoid ascospores (measuring 20–24 × 7–10 µm and 23–30 × 11–13 µm, respectively), which are considerably longer than those of *C. taeniospora*.

The newly described *C. navarrae* shares some morphological features with *C. taeniospora*. The ascomata of both species appear glabrous under the stereomicroscope and the ascospores are of similar size and shape, although they are slightly larger in *C. navarrae*. *Coniochaeta navarrae* has solitary to gregarious ascomata, which do not form well defined groups and are not covered by sparse, light brown, obtuse hairs like *C. taeniospora*. Instead, the peridium of *C. navarrae* is occasionally covered with short, dark brown, sometimes densely grouped, setae-like cells. The reaction of the peridium to KOH is another differentiating characteristic of these species: while the peridium of *C. taeniospora* shows a noticeable green reaction, the peridial cells of *C. navarrae* react only weakly. The ascospores of *C. navarrae*, in addition to being slightly larger than those of *C. taeniospora*, are sometimes surrounded by a hyaline sheath, which was not observed in *C. taeniospora*. Hyaline gelatinous sheaths are usually found in some coprophilous *Coniochaeta* species (Chang & Wang 2011)

and are more rarely reported from species growing on wood or other plant material, e.g. *C. caryotae* (Rao 1970), *C. niesslii* (Arx & Müller 1954), and *C. tilakii* (Kale 1968). For further comparison of *C.navarrae* to other species of *Coniochaeta* regarding ascospore morphology the above discussion of *C. taeniospora* applies.

Acknowledgements

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(Manuscript accepted 1 March 2016; Corresponding Editor: I. Krisai-Greilhuber)