

## ***Meridianelia*, a new genus in the *Elixiaceae* (Ascomycota) from Tasmania**

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**Abstract:** *Meridianelia macCarthyana* Kantvilas & Lumbsch, gen. et sp. nov., is described, based on collections from Tasmania. This taxon represents only the second member of the family *Elixiaceae*. It is compared to *Elixia flexella* (Ach.) Lumbsch and to the superficially similar genus *Trapelia*. The family *Elixiaceae* is redefined briefly to account for the inclusion of a second genus.

**Key words:** lichens, flora of Australia, phylogenetic analysis, Lecanoromycetes, *Elixia*, *Trapelia*

### **Introduction**

During the course of the ongoing project to document the lichen flora of the island of Tasmania, a curious epiphytic species was collected in subalpine woodland. This lichen displayed an unusual combination of characters: hemiangiocarpous ascomata, a reduced, cupulate excipulum, delicate, branched and anastomosing paraphyses, eight-spored, lecanoralean asci, and simple, hyaline ascospores. Whereas some of these attributes are also found in the genus *Trapelia* M. Choisy, others suggested alternative relationships within the *Agyriinae* in the sense of Lumbsch (1997). The systematic position of this lichen was ultimately resolved using DNA sequence data that supported our earlier anatomical observations, particularly those pertaining to ascus structure, which had hinted at links with the monotypic family, *Elixiaceae*. We describe this lichen as a new monotypic genus, *Meridianelia*, within this unique family of lichenized fungi.

The *Elixiaceae* was erected by Lumbsch (1997) to accommodate the single species *Elixia flexella* (Ach.) Lumbsch. The relation-

ships of this lichen to other seemingly related groups, such as the families *Agyriaceae* (including *Trapeliaceae*), *Anamylopsoraceae* and *Schaereriaceae*, were elucidated in detail therein (Lumbsch *op. cit.*). These families have subsequently undergone considerable scrutiny using molecular data. The *Agyriaceae* was shown to be unrelated to the *Trapeliaceae*, but grouped with the *Pertusariales* (Lumbsch *et al.* 2007b). The placement of the *Anamylopsoraceae* needs further studies, but preliminary studies suggest it may not be closely related to the *Trapeliaceae* either (Lumbsch *et al.* 2001). The *Schaereriaceae* is also shown to be not closely related to the *Trapeliaceae*, but again, the relationships remain uncertain (Wedin *et al.* 2005). In fact, the *Elixiaceae* appears to be closest to the *Umbilicariaceae* (Lumbsch *et al.* 2004; Wedin *et al.* 2005).

### **Materials and Methods**

#### **Morphology, anatomy and chemistry**

The study is based chiefly on collections housed in the Tasmanian Herbarium (HO) and the Field Museum (F). Anatomical and morphological observations were undertaken using light microscopy, with thin hand-cut sections mounted in water, 10% KOH (K), lactophenol Cotton Blue and Lugol's iodine, either with pretreatment with KOH (indicated as K/I) or without (I). Ascospore measurements are based on at least 100 observations and are presented in the format: smallest measurement–mean–largest measurement; single outlying values are given in parentheses. Nomenclature of

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asci follows Lumbsch (1997). Nomenclature of apothecial pigments follows Meyer & Printzen (2000), although we used concentrated acids for N (HNO<sub>3</sub>) and H (HCl), whereas Meyer & Printzen used 50% N and 10–20% H. Chemical constituents were identified by thin layer chromatography (Culberson 1972; Culberson *et al.* 1981; Culberson & Johnson 1982; Elix & Ernst-Russell 1993).

### Molecular methods

Sequence data of 70 species were assembled using sequences of the mitochondrial small subunit rDNA (Table 1) with a newly obtained sequence extracted from the isotype of *Meridianelia maccarthyana* [Genbank no: FJ763185]. Three *Umbilicaria* species were used as the out-group since the genus has a basal placement in Lecanoromycetes in previous studies (e.g., Lumbsch *et al.* 2007*a,c*). Total DNA was extracted using the DNeasy Plant Mini Kit (Qiagen) following the instructions of the manufacturer. Dilutions (10<sup>-1</sup> up to 10<sup>-2</sup>) of DNA were used for PCR amplifications. Primers for amplification were mr SSU1 (Zoller *et al.* 1999) and MSU 7 (Zhou & Stanosz 2001). The 25 µl PCR reactions contained 2.5 µl buffer, 2.5 µl dNTP mix, 1 µl of each primer (10 µM), 5 µl BSA, 2 µl Taq, 2 µl genomic DNA extract and 9 µl distilled water. Thermal cycling parameters were: initial denaturation for 3 min at 95°C, followed by 30 cycles of 1 min at 95°C, 1 min at 52°C, 1 min at 73°C, and a final elongation for 7 min at 73°C. Amplification products were viewed on 1% agarose gels stained with ethidium bromide and subsequently purified using the QIAquick PCR Purification Kit (Qiagen). Fragments were sequenced using the Big Dye Terminator reaction kit (ABI PRISM, Applied Biosystems). Sequencing and PCR amplifications were performed using the same sets of primers. Cycle sequencing was executed with the following program: 25 cycles of 95°C for 30 sec, 48°C for 15 sec, 60°C for 4 min. Sequenced products were precipitated with 10 µl of sterile dH<sub>2</sub>O, 2 µl of 3 M NaOAc and 50 µl of 95% EtOH, before being loaded on an ABI 3100 (Applied Biosystems) automatic sequencer. Sequence fragments obtained were assembled with SeqMan 4.03 (DNASTAR) and manually adjusted.

### Sequence alignments and phylogenetic analysis

The alignment was carried out using Clustal W (Thompson *et al.* 1994). Ambiguously aligned regions were removed manually. The alignment was analysed by maximum parsimony (MP) and a Bayesian approach (B/MCMC). Maximum parsimony analyses were performed using the program PAUP\* (Swofford 2003). Heuristic searches with 200 random taxon addition replicates were conducted with TBR branch swapping and MulTrees option in effect, equally weighted characters and gaps treated as missing data. Bootstrapping (Felsenstein 1985) was performed based on 2000 replicates with random sequence additions. The B/MCMC analyses were conducted using the MrBayes 3.1.1 program (Huelsenbeck & Ronquist 2001). The analyses

were performed assuming the general time reversible model of nucleotide substitution (Rodriguez *et al.* 1990) including estimation of invariant sites, assuming a discrete gamma distribution with six rate categories. A run with 4 000 000 generations starting with a random tree and employing 12 simultaneous chains was executed. Every 100th tree was saved into a file. The first 200 000 generations (i.e., the first 2000 trees) were deleted as the 'burn in' of the chain. The log-likelihood scores of sample points were plotted against generation time using TRACER 1.0 (<http://evolve.zoo.ox.ac.uk/software.html?id=tracer>) to ensure that stationarity was achieved after the first 200 000 generations by checking whether the log-likelihood values of the sample points reached a stable equilibrium value (Huelsenbeck & Ronquist 2001). Of the remaining 76 000 trees (38 000 from each of the parallel runs) a majority rule consensus tree with average branch lengths was calculated using the sumt option of MrBayes. Posterior probabilities were obtained for each clade. Only clades that received bootstrap support equal or above 70% under MP and posterior probabilities  $\geq 0.95$  were considered as strongly supported. Phylogenetic trees were visualized using the program Treeview (Page 1996).

### Phylogenetic analyses

The new sequences of *Meridianelia maccarthyana* were aligned with sequences obtained from GenBank as listed in Table 1. A matrix of 715 unambiguously aligned nucleotide position characters was produced; 327 characters in the alignment were constant. Maximum parsimony analysis yielded 68 most parsimonious trees (1928 steps long). The strict consensus tree did not contradict the Bayesian tree topology. In the B/MCMC analysis of the combined data set, the likelihood parameters in the sample had the following mean (Variance): LnL = -9628.635 (0.15), base frequencies  $\pi(A) = 0.333$  (0.00046),  $\pi(C) = 0.139$  (0.00025),  $\pi(G) = 0.204$  (0.00026),  $\pi(T) = 0.324$  (0.00017), the gamma shape parameter  $\alpha = 0.776$  (0.0065), and  $p(\text{invar}) = 0.285$  (0.00029).

Since the topologies of the MP and B/MCMC analyses did not show any strongly supported conflicts, only the 50% majority-rule consensus tree of Bayesian tree sampling is shown (Fig. 1). Those nodes that received strong support (i.e. PP  $\geq 0.95$  in B/MCMC analysis and MP bootstrap  $\geq 70\%$ ) in both the MP and Bayesian analyses are in bold as shown in Figure 1. In the

TABLE 1. Sequences obtained from Genbank for the study. Family placement after Eriksson (2006).

Name	Family	nuLSU
<i>Ainoa geochroa</i>	<i>Agyriaceae</i>	DQ871006
<i>A. mooreana</i>	<i>Agyriaceae</i>	AY212828
<i>Arctomia delicatula</i>	<i>Arctomiaceae</i>	AY853355
<i>A. teretiuscula</i>	<i>Arctomiaceae</i>	DQ007346
<i>Arthrorhaphis citrinella</i>	<i>Arthrorhaphidaceae</i>	AY853356
<i>Aspicilia caesiocinerea</i>	<i>Hymeneliaceae</i>	DQ780303
<i>A. cinerea</i>	<i>Hymeneliaceae</i>	DQ780304
<i>Baeomyces placophyllus</i>	<i>Baeomycetaceae</i>	AF356658
<i>B. rufus</i>	<i>Baeomycetaceae</i>	DQ871008
<i>Boreoplaca ultrafrigida</i>	<i>Unclassified Lecanoromycetes</i>	AY853360
<i>Caloplaca flavorubescens</i>	<i>Teloschistaceae</i>	AY300831
<i>Cladonia rangiferina</i>	<i>Cladoniaceae</i>	AY300832
<i>Coccotrema cucurbitula</i>	<i>Coccotremataceae</i>	AF274092
<i>C. pocillarium</i>	<i>Coccotremataceae</i>	AF274093
<i>Elixia flexella</i>	<i>Elixiaceae</i>	AY853368
<i>Everniopsis trulla</i>	<i>Parmeliaceae</i>	EF108290
<i>Gregorella humida</i>	<i>Arctomiaceae</i>	AY853378
<i>Ionaspis lacustris</i>	<i>Hymeneliaceae</i>	AY853371
<i>Hypocenomyce scalaris</i>	<i>Lecideaceae</i>	AY853373
<i>Lecanora hybocarpa</i>	<i>Lecanoraceae</i>	EF105421
<i>L. paramerae</i>	<i>Lecanoraceae</i>	EF105422
<i>Lobaria pulmonaria</i>	<i>Lobariaceae</i>	AF183934
<i>Lobothalia radiosa</i>	<i>Hymeneliaceae</i>	DQ780306
<i>Loxospora lecanoriformis</i>	<i>Loxosporaceae</i>	EF252278
<i>L. ochrophaea</i>	<i>Loxosporaceae</i>	DQ871009
<i>Ochrolechia androgyna</i>	<i>Pertusariaceae</i>	AY300846
<i>O. oregonensis</i>	<i>Pertusariaceae</i>	DQ780308
<i>O. pallescens</i>	<i>Pertusariaceae</i>	DQ780310
<i>O. parella</i>	<i>Pertusariaceae</i>	AF274097
<i>O. turneri</i>	<i>Pertusariaceae</i>	AY568002
<i>Ophioparma ventosa</i>	<i>Ophioparmaceae</i>	AY853380
<i>Orceolina antarctica</i>	<i>Agyriaceae</i>	AF274115
<i>O. kerguelensis</i>	<i>Agyriaceae</i>	AY212830
<i>Peltigera aphthosa</i>	<i>Peltigeraceae</i>	AF286759
<i>Pertusaria albescens</i>	<i>Pertusariaceae</i>	AF329176
<i>P. corallina</i>	<i>Pertusariaceae</i>	AY300850
<i>P. corallophora</i>	<i>Pertusariaceae</i>	DQ780316
<i>P. gibberosa</i>	<i>Pertusariaceae</i>	DQ780322
<i>P. hemisphaerica</i>	<i>Pertusariaceae</i>	AF381556
<i>P. lactea</i>	<i>Pertusariaceae</i>	AF381557
<i>P. leioplaca</i>	<i>Pertusariaceae</i>	AY300852
<i>P. mesotropa</i>	<i>Pertusariaceae</i>	DQ780325
<i>P. ophthalmiza</i>	<i>Pertusariaceae</i>	AY568006
<i>P. pertusa</i>	<i>Pertusariaceae</i>	AF279300
<i>P. subventosa</i>	<i>Pertusariaceae</i>	AY300854
<i>P. velata</i>	<i>Pertusariaceae</i>	AY300855
<i>Placopsis cribellans</i>	<i>Agyriaceae</i>	DQ871010
<i>P. gelida</i>	<i>Agyriaceae</i>	AY212836
<i>P. santessonii</i>	<i>Agyriaceae</i>	AY212845
<i>Placynthiella icmalea</i>	<i>Agyriaceae</i>	AY212846
<i>Protoparmelia badia</i>	<i>Parmeliaceae</i>	DQ871011
<i>Protothelenella corrosa</i>	<i>Protothelenellaceae</i>	AY607734
<i>P. sphinctrinoidella</i>	<i>Protothelenellaceae</i>	AY607735
<i>Rhizocarpon sphaerosporum</i>	<i>Rhizocarpaceae</i>	AY853390

Table 1. *Continued*

Name	Family	nuLSU
<i>Rimularia psephota</i>	<i>Agyriaceae</i>	DQ871012
<i>Schaereria corticola</i>	<i>Agyriaceae</i>	AY300859
<i>Sporastatia polyspora</i>	<i>Catillariaceae</i>	AY640968
<i>S. testudinea</i>	<i>Catillariaceae</i>	AY640969
<i>Thammolia vermicularis</i>	<i>Icmadophilaceae</i>	AY853395
<i>Trapelia chiodectonoides</i>	<i>Agyriaceae</i>	AY212847
<i>T. glebosa</i>	<i>Agyriaceae</i>	AF274103
<i>Trapeliopsis flexuosa</i>	<i>Agyriaceae</i>	AF274118
<i>T. granulosa</i>	<i>Agyriaceae</i>	AF274119
<i>T. percrenata</i>	<i>Agyriaceae</i>	AF279302
<i>Tremolecia atrata</i>	<i>Hymeneliaceae</i>	AY853397
<i>Umbilicaria crustulosa</i>	<i>Umbilicariaceae</i>	AY300869
<i>U. decussata</i>	<i>Umbilicariaceae</i>	AY603113
<i>U. hyperborea</i>	<i>Umbilicariaceae</i>	AY853399
<i>Warvea fruticulosa</i>	<i>Arctomiaceae</i>	DQ007347

majority-rule consensus tree, *Meridianelia maccarthyana* clusters strongly supported with *Elixia flexella* (MP-bootstrap support 99%, B/MCMC posterior probability 1.0) and hence supports placement of the new taxon in the *Elixiaceae* as circumscribed by Lumbsch (1997). Members of the *Trapeliaceae sensu* Lumbsch *et al.* (2007b) form a strongly supported group within Ostropomycetidae. The strongly supported topology of the other parts of the phylogenetic tree is in agreement with previously published phylogenies (Lumbsch *et al.* 2007a, b) and is not discussed further here.

### Taxonomy

#### ***Meridianelia* Kantvilas & Lumbsch gen. nov.**

Mycobank: MB 513000

Genus fungorum lichenisatorum, ad *Elixiaceae* pertinet, thallo crustaceo, algas chlorococcales continenti. Apothecia hemiangiocarpia, excipulo cupulato, prosoplectenchymato, reducto, gelatina hymenialia non-amyloidea, ascis octosporis, *Elixia*-typis, paraphysibus subtilibus, ramosis anastomosantibusque, ascosporis simplicibus, non-halonatis, hyalinis. Pycnidia ignota.

Typus: *Meridianelia maccarthyana* Kantvilas & Lumbsch.

*Thallus* crustose, ecorticate. *Photobiont* chlorococcoid.

*Ascomata* apothecia, hemiangiocarpous. *Excipulum* cupulate, prosoplectenchymatous, very reduced. *Hymenial gel* non-amyloid. *Paraphyses* very delicate, branched and anastomosing, non-capitate. *Asci* 8-spored, of the *Elixia*-type. *Ascospores* simple, non-halonate, thin-walled. *Pycnidia* not seen.

*Etymology.* The generic name is derived from the Latin *meridianus* (meaning 'southern'), in reference to the geographic distribution of the taxon, and also infers the similarity of this lichen to members of the genus *Trapelia* M. Choisy.

The genus contains the single species, *M. maccarthyana* Kantvilas & Lumbsch.

#### ***Meridianelia maccarthyana* Kantvilas & Lumbsch sp. nov.**

Mycobank: MB 513001

*Thallus* crustosus, ecorticatus, sordide griseo-albidus, aliquando soediatus, acidum protolicheterinicum continens. Apothecia adnata vel leviter immersa, 0.3–1 mm lata, disco concavo, plano vel undulato, dense albidopruinosa. *Paraphyses* intricatae, 0.8–1 µm crassae, apicibus non capitatis. *Asci* elongato-clavati, 130–170 µm longi, 17–25 µm lati. *Ascospores* uniseriatae, globosae vel subglobosae vel ovato-ellipsoideae, 14–23(–26) µm longae, 9–20 µm latae.

Typus: Australia, Tasmania, 1 km SE of Lake Fenton, 42°41'S 146°38'E, 950 m altitude, on trunk of *Eucalyptus coccifera* in subalpine woodland,

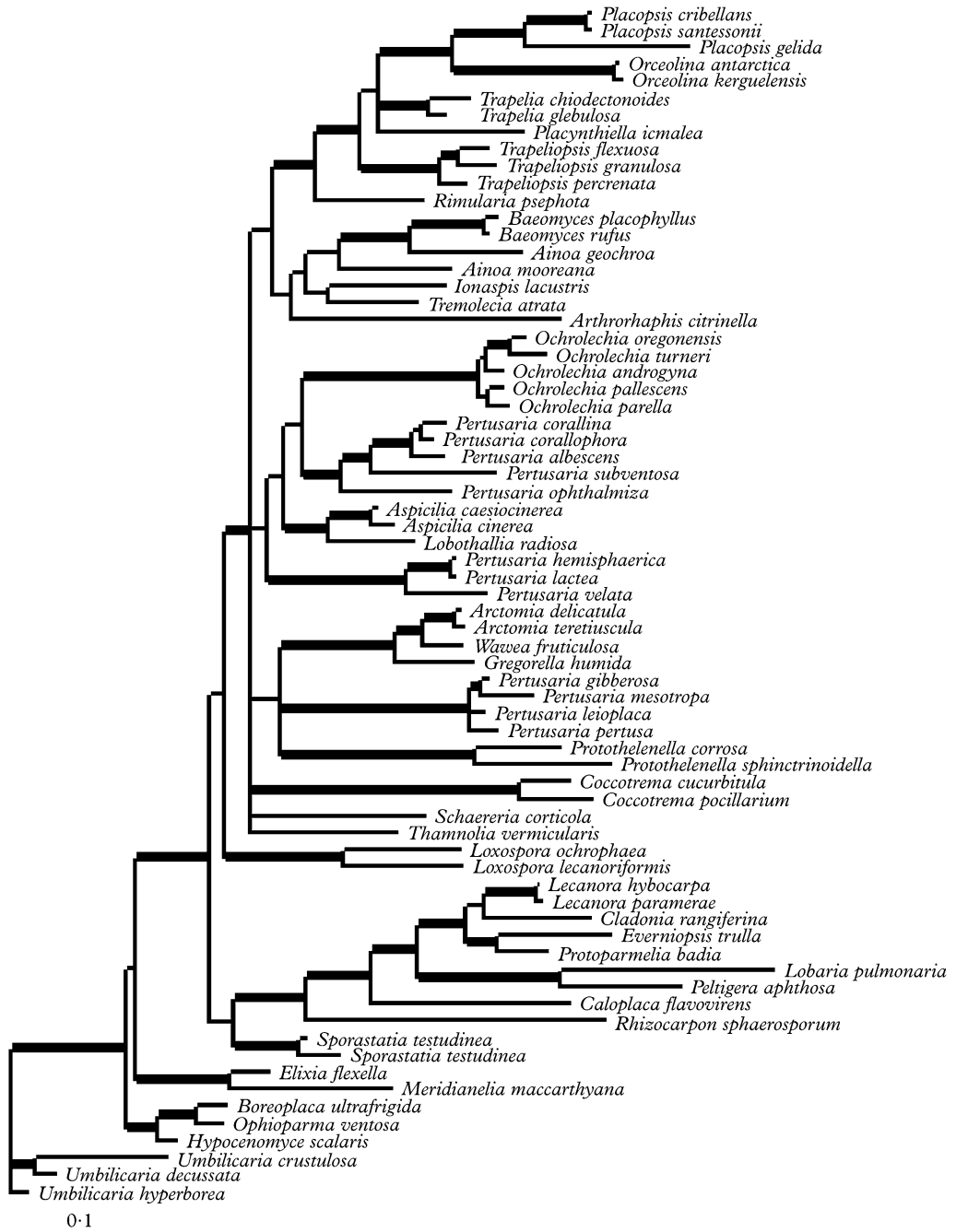


FIG. 1. Phylogeny of Lecanoromycetes as inferred from a mt SSU rDNA sequence analysis to investigate the phylogenetic placement of *Meridianelia macCarthyana*. This is a 50% majority-rule consensus tree based on 38 000 trees from a B/MCMC tree sampling procedure. Branches with posterior probabilities equal to or above 0.95 and MP bootstrap support values above 70% are indicated by wide internodes.

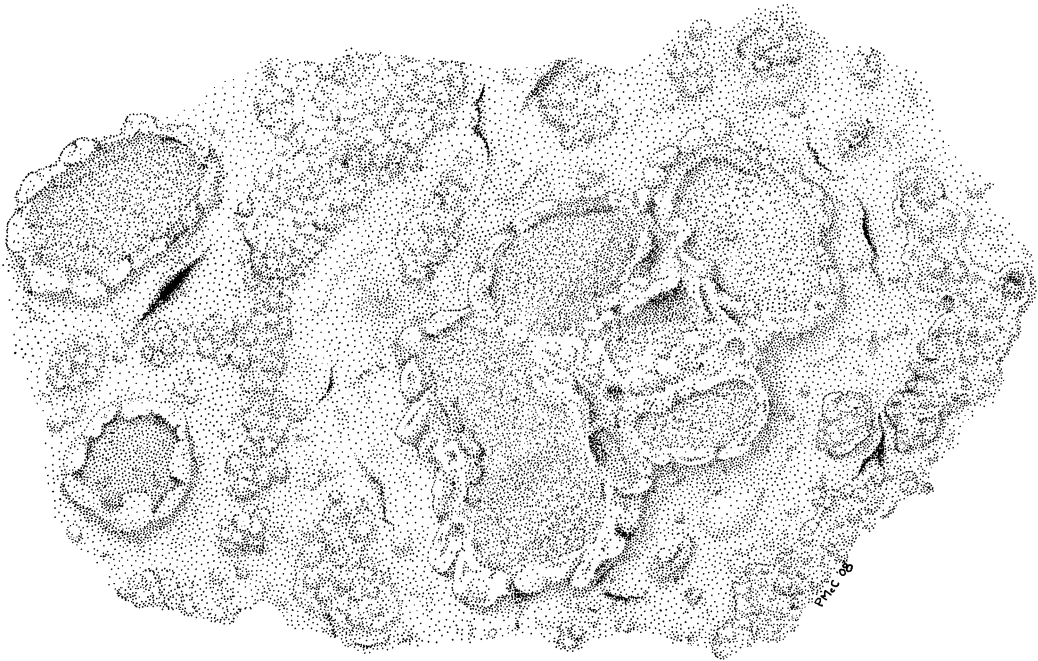


FIG. 2. *Meridianelia macCarthyana*, habitus (holotype). Scale = 1 mm.

17 December 2003, G. Kanwilas 752/03 (HO—holotypus; F—isotypus).

#### Figs (2, 3A–C)

*Thallus* crustose, not delimited, forming spreading colonies to 10–20 cm wide, dull greyish white, somewhat glossy, ecorticate, to 120–200  $\mu\text{m}$  thick, smooth at first, becoming verruculose to tuberculate, with individual verrucae 0.5–1 mm wide, at length becoming abraded, eroded or  $\pm$  coarsely sorediate; soredia generally aggregated in irregularly roundish, erose soralia to c. 1 mm wide, occasionally becoming diffuse and spreading, concolorous with the thallus or occasionally tinged greenish grey, interspersed with angular-rhomboidal crystals to 20  $\mu\text{m}$  wide that fluoresce in polarized light and do not dissolve in KOH. *Photobiont* a unicellular green alga with individual cells globose to broadly ellipsoid, 9–20  $\times$  9–16  $\mu\text{m}$ , generally clustered in fascicles within the thallus.

*Apothecia* erupting from abraded thalline warts, broadly adnate to somewhat im-

mersed in the thallus, roundish to irregularly rhomboidal or angular, 0.3–1 mm wide, generally clustered in groups of 2–3(–5), each usually orientated obliquely to the thallus surface and to each other; disc at first deeply concave, then plane to undulate, dark grey, thickly whitish pruinose; ‘thalline margin’ ragged, incomplete, comprised of abraded, adhering remnants of thallus; proper margin barely evident. *Excipulum* in section cupulate, *Trapelia*-like, very reduced, to c. 10  $\mu\text{m}$  thick, pale greyish green, K $\pm$  olive, composed of poorly differentiated, intertwined, prosoplectenchymatous hyphae to c. 1  $\mu\text{m}$  thick. *Hypothecium* colourless, 40–60  $\mu\text{m}$  thick, poorly differentiated from the hymenium, sparsely interspersed with scattered oil droplets. *Hymenium* colourless, 160–200  $\mu\text{m}$  thick, separating readily in water and KOH, likewise interspersed, I+ and K/I+ blue, with the reaction confined to the asci, with a grey-green, K $\pm$  olive epihymenial layer 30–50  $\mu\text{m}$  thick, composed of the entangled uppermost portions of the paraphyses, interspersed with amorphous crystalline

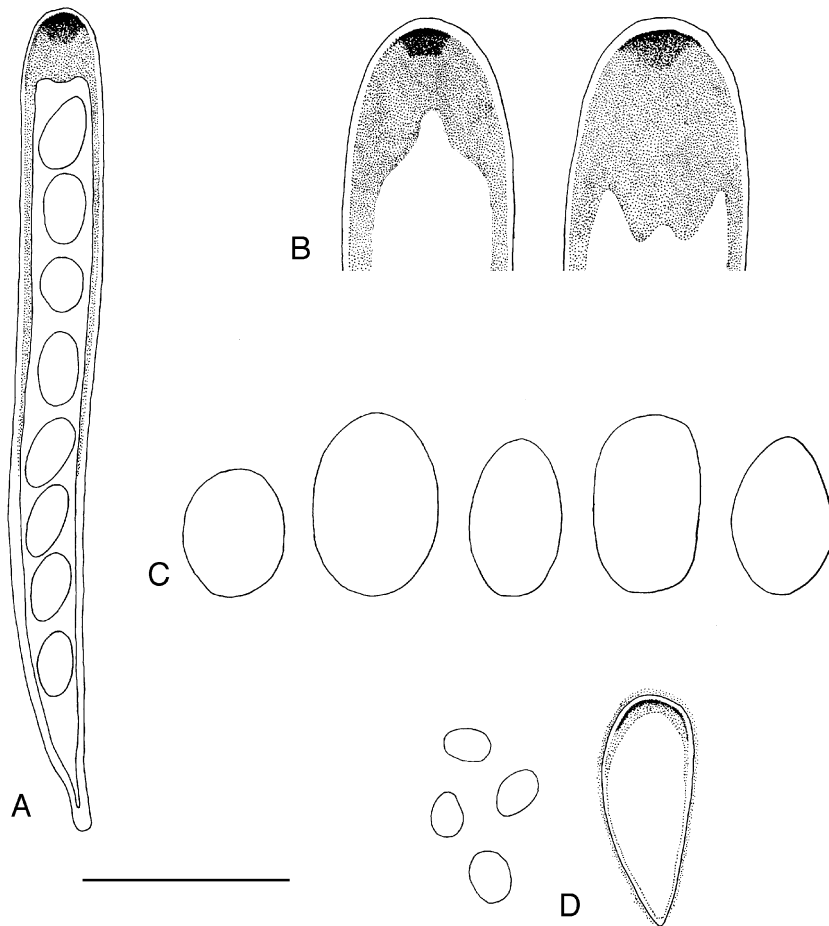


FIG. 3. Scia (with amyloid parts stippled) and ascospores. A–C, *Meridianelia macCarthyana*; D, *Elixia flexella*. Scale: A = 40  $\mu\text{m}$ ; B–D = 20  $\mu\text{m}$ .

material insoluble in KOH. *Asci* 8-spored, 130–170  $\times$  17–25  $\mu\text{m}$ , elongate-clavate with a very long attenuate ‘tail’, approximating the *Elixia*-type: outer wall K/I+ blue; tholus well-developed, K/I+ pale blue, with an intensely K/I+ blue cap or ‘plug’ at the apex; ascoplasm generally truncate or concave at the apex, occasionally with a short, beak-like ocular chamber. *Paraphyses* very delicate, highly branched, anastomosing and entangled, 0.8–1  $\mu\text{m}$  thick; apices tapered. *Ascospores* uniseriate in the ascus, thin-walled, non-halonate, globose to subglobose to ovate-ellipsoid, 14–18.1–23(–26)  $\times$  9–13.4–20  $\mu\text{m}$  [length: width ratio 1.1–1.4–1.8(–2)],

often deformed by mutual pressure when within the ascus, typically with a single, large vacuole.

*Pycnidia* not found.

*Chemistry*. Protolichesterinic acid; thallus K–, KC–, C–, P–, UV–.

*Etymology*. The specific epithet honours our friend and colleague, Dr Patrick McCarthy, who prepared the habit illustration and has made very significant contributions to the knowledge of lichens, especially in Australasia.

*Distribution and ecology.* The new species has been recorded from open subalpine woodland dominated by *Eucalyptus coccifera* Hook. f. growing on a dolerite boulder field. In this vegetation, the understorey is generally sparse and comprises scattered low shrubs, chiefly *Nothofagus gunnii* (Hook.f.) Oerst. and *Olearia pinifolia* (Hook.f.) Benth., or patches of *Bauera rubioides* Andrews intermixed with species of *Epacridaceae* and *Proteaceae*. *Meridianelia macCarthyana* forms conspicuous white patches up to 20 cm wide on the lowermost 1–2 metres of the eucalypt trunks as well as on larger individuals of *Olearia* that have very loose, papery bark. Although a generally lichen-rich environment, particularly with respect to saxicolous and terricolous species, these corticolous habitats are not highly colonized by lichens, and species associated with the new taxon are relatively few. These include *Mycoblastus campbellianus* (Nyl.) Zahlbr., *M. coniophorellus* (Elix & A.W. Archer) Kantvilas & Elix, *Ochrolechia* sp., *Pertusaria jamesii* Kantvilas, *P. perractata* Stirt., *Pseudoramonia richeae* Kantvilas & Vězda, *Ramboldia stuartii* (Hampe) Kantvilas & Elix, *Trapeliopsis granulosa* (Hoffm.) Lumbsch and *Usnea oncodes* Stirt. On the eucalypts, below this 'Meridianelia-zone', there is a basal stocking of bryophytes and species of *Cladia* and *Cladonia*, whereas above, the eucalypt bark is generally too unstable for epiphytes. At a second locality, the new taxon was found in subalpine eucalypt woodland at the margins of a *Nothofagus cunninghamii* (Hook.) Oerst.-dominated cool temperate rainforest.

*Meridianelia* occurs most frequently in sunny conditions, being restricted to trees where the understorey is most sparse; it is absent where the undershrubs form a closed cover. It is curious that the new lichen has been encountered so infrequently. The vegetation community in which it has been found is not uncommon in Tasmania, nor is the lichen itself uncommon at the localities where it has been recorded. Further field observations are clearly required to better understand its ecological requirements.

*Remarks.* This new species is a most enigmatic lichen. Its spreading, white thallus is reminiscent of such unrelated taxa as *Pertusaria* or *Ochrolechia*, both of which occur in the same or similar habitats. The often-clustered, pruinose ascomata, arising from ruptured thalline warts, are not unlike those seen in certain species of *Phlyctis*, which is likewise unrelated. Only with careful study of the asci do the relationships to *Elixia* become evident. The asci of *Meridianelia* have a prominent, weakly amyloid tholus with an intensely amyloid cap that sometimes extends down into the tholus as a 'plug' (Fig. 3A & B). The asci of *Elixia* are very short and compact and rather more difficult to observe, but display essentially the same salient features (Fig. 3D).

The differences between *Elixia* and *Meridianelia* are stark, leaving no doubt that a new genus for the latter is justified. Superficially the two taxa are completely dissimilar, with *Elixia* having a highly reduced to inapparent thallus and often rather angular to almost lirelliform apothecia to only c. 0.4 mm wide. The excipulum of *Elixia* is well-developed and opaque dark brown, not unlike that seen in *Rimularia*. The hymenial gel is hemiamyloid in *Elixia*, whereas in *Meridianelia*, the amyloid reaction is confined to the asci. The paraphyses in *Elixia* are also robust and apically brown-pigmented. Furthermore, the ascospores of *Elixia* are rather small (8.5–13 × 4.5–6.5 μm), whereas those of *Meridianelia* are comparatively large (Fig. 3C & D).

The genus shows the strongest superficial links with *Trapelia*, which also has hemiangiocarpous apothecia, surrounded by a 'margin' of adhering thallus fragments, delicate, branched and anastomosing paraphyses, a highly reduced excipulum of prosoplectenchymatous hyphae, and uniseriate, often-vacuolate ascospores. The grey-green apothecial pigment in the new taxon approximates caesiocinerea-green of Meyer & Printzen (2000); this has also been recorded in *Trapeliopsis*, *Xylographa* and a range of other, unrelated taxa. Furthermore, the shape of the asci is very *Trapelia*-like, being very elongate-clavate, and with the apex of the ascoplasm being generally concave or



truncate. Only after staining with Lugol's solution do the fundamental structural differences between the asci of the two genera become evident.

The addition of a further genus to the *Elixiaceae* necessitates a recircumscription of the family. Accordingly, the *Elixiaceae* is defined as: lichenized Ascomycetes with the thallus crustose, containing a coccoid, green photobiont; ascomata apothecia, hemiangiocarpous, with excipulum cupulate, prosoplectenchymatous, often reduced; asci 8-spored, of the *Elixia*-type; ascospores simple, hyaline, non-halonate, thin walled; pycnidia unknown; chemistry: aliphatic acids or nil.

*Specimens examined. Australia: Tasmania:* 1 km SE of Lake Fenton, 42°41' S 146°38' E, 950 m alt., 2003, *G. Kantvilas* 752/03 (HO); Lake Fenton Hut, 42°41' S 146°38' E, 1010 m alt., 2008, *G. Kantvilas* 345/08 (HO); Hartz Mountains Road, 43°12' S 146°46' E, 730 m, 2008, *G. Kantvilas* 376/08 (HO) (all specimens sterile only); track to Lake Nicholls, 42°40' S 146°39' E, 1000 m, 2008, *G. Kantvilas* 353/08 (BM, HO).

*Selected comparative material examined. Elixia flexella* (Ach.) Lumbsch. **Great Britain: Scotland: V.C. 105,** West Ross: Kinlochewe, Beinn Eighe NNR, 150–200 m, 2001, *B. J. Coppins* 19753 & *A. M. Coppins* (HO).—**Austria:** Salisburgia, Hohe Tauern, 960 m, 1986, *R. Türk* (A. Vězda: *Lich. Sel. Exsicc.* 2101) (HO).

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