

***Krogia australasiatica* (Ramalinaceae, lichenized fungi), a new species from Australia and New Caledonia, with new records of *Krogia* from New Caledonia**

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Abstract

The new species *Krogia australasiatica* Timdal is described from tree trunks in humid forests/rainforests in Australia (Queensland) and New Caledonia, partly based on a phylogenetic reconstruction using the ITS marker. The new species shares the secondary chemistry with the neotropical *K. antillarum* Timdal, i.e. 4-O-methylcryptochlorophaeic acid, and the vegetative dispersal units, i.e. isidia, with the New Caledonian *K. isidiata* Kistenich & Timdal and *K. macrophylla* Kistenich & Timdal. The trivial name hyperboninic acid is introduced for a secondary compound occurring in *K. coralloides* Timdal and *K. macrophylla*. The genus *Krogia* Timdal is new to Australia and new localities are given for *K. isidiata* and *K. macrophylla* in New Caledonia.

Introduction

The lichen genus *Krogia* Timdal was described for the single species *K. coralloides* Timdal from Mauritius (Timdal 2002). Subsequently, five more species of *Krogia* have been described: *K. antillarum* Timdal from the West Indies (Timdal 2009), *K. microphylla* Timdal from in the Dominican Republic (Timdal in Lumbsch *et al.* 2011), and the three species *K. borneensis* Kistenich & Timdal from Borneo, *K. isidiata* Kistenich & Timdal from New Caledonia, and *K. macrophylla* Kistenich & Timdal from New Caledonia by Kistenich *et al.* (2018a).

The genus is corticolous and occurs in tropical and subtropical humid forests and rainforests. It shares the squamulose growth form with the much more common genus *Phyllopsora* Müll. Arg. Both genera belong in the Ramalinaceae, but even though easily confused, are not closely related as *Krogia* belongs in the *Toninia*-group and *Phyllopsora* in the *Biatora*-group of that family (Kistenich *et al.* 2018b). Anatomically, *Krogia* differs from *Phyllopsora* in having a weak or absent amyloid reaction in the tholus of the asci, and filiform, curved, spirally arranged ascospores (Timdal 2002). In *Phyllopsora*, the tholus shows a deeply amyloid conical structure (*Bacidia*-type) and the ascospores vary from ellipsoid to fusiform (Kistenich *et al.* 2018b). Nearly every examined specimen of *Krogia* has at least some scattered red or purple patches on the thallus or apothecia caused by non-crystalline, acetone-insoluble pigment(s); this is perhaps the best diagnostic feature to distinguish *Krogia* from *Phyllopsora* in the field. The only published molecular studies of *Krogia* are those of Kistenich *et al.* (2018a, b).

Recent field work in New Caledonia by the lichen group at the Natural History Museum at the University of Oslo, Norway (NHMO) resulted in several collections of *Krogia*. Three species were identified in the material, *K. isidiata*, *K. macrophylla*, and a third species which turned out to be new to science and is described here as *K. australasiatica* Timdal.

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Material and Methods

The lichen group at NHMO made 24 collections of *Krogia* in New Caledonia in October–December 2022. A complete set is stored in O, with selected duplicates in NOU and the holotype of the new species in PC. A specimen of *Krogia* that we had earlier found as an admixture in a collection of *Eschatogonia marivelensis* (Vain.) Kalb from Australia in UPS was included in the study. The specimen had been examined by morphology and thin-layer chromatography by Kistenich *et al.* (2018a) but not included in that paper due to very scanty material and unclarified taxonomy. The geographical coordinates for the material from New Caledonia are given with 10 m precision and in the WGS84 map datum.

The collections were studied under dissecting and compound microscopes, in the latter in water and lactophenol cotton blue (LCB). The iodine reaction in the hymenium and asci was studied after pretreatment with 10% KOH in a modified Lugol's solution where water was replaced by 50% lactic acid. Polarized light was used to locate crystals of secondary compounds.

All specimens of *Krogia* collected in New Caledonia in 2022, except for one scanty one, were subjected to thin-layer chromatography (TLC), performed in accordance with the methods of Culberson (1972) and Culberson and Johnson (1982) on aluminium plates and mainly in solvent system B'.

DNA extraction, PCR amplification, and sequencing were performed at two different labs. Eleven sequences were produced at the Canadian Centre for DNA Barcoding (<https://ccdb.ca>), using the primer pair ITS1F/ITS4 (Gardes and Bruns 1993, White *et al.* 1990). Those sequences were provided through the DNA barcode project OLICH at NHMO (Marthinsen *et al.* 2019). In addition, three sequences were produced in-house at NHMO, using the DNA extraction kit Chelex 100 (Bio-Rad, Hercules, California) following the procedure described by Ferencova *et al.* (2017) and sequenced using the same primer pair, ITS1F/ITS4. The 14 sequences we had obtained were added to the 11 ITS sequences produced by Kistenich *et al.* (2018a, b); the data set hence consisted of all available ITS sequences of *Krogia* (25 sequences). We added eight sequences from related genera, including two species of *Bacidia* as outgroup, following Kistenich *et al.* (2018a) although with a slightly reduced taxon sampling. Two *Krogia* species are missing in this data set: *K. borneensis* (only mtSSU available) and *K. microphylla* (no sequence available).

The data set was iteratively aligned by SATé-II ver. 2.2.7 (Liu *et al.* 2012), using MAFFT ver. 6.717 (Katoh *et al.* 2005, Katoh and Toh 2008) as aligner, MUSCLE ver. 3.7 (Edgar 2004) as merger, FastTree ver. 2.1.4 (Price *et al.* 2010) as tree evaluator (i.e. under an approximate maximum likelihood criterion), and with the default settings in the GUI except that the number of iterations after last improvement in the maximum likelihood score was set to 10. The alignment was inspected in BioEdit ver. 7.2.5 (Hall 1999) and trimmed to exclude flanking regions, but not further adjusted. It is available for download from ResearchGate. The phylogeny was reconstructed under the Bayesian inference (BI) by MrBayes 3.2.7a (Huelsenbeck and Ronquist 2001, Ronquist and Huelsenbeck 2003) and under the maximum likelihood

criterion (ML) by RAxML 8.2.12 (Stamatakis 2014). MrBayes ran for 1 million generations (terminated at ASDSF = 0.0083), every 1000th generation was sampled, the burnin was set to 25%, and the phylogenetic tree is the 50% majority rule consensus tree. RAxML was run under raxmlGUI ver. 2.0.10 (Edler *et al.* 2021), using the bundled software ModelTest ver. 0.1.7 (Darriba *et al.* 2020) which estimated the best substitution model to be GTRGAMMAIX. We ran 1000 rapid bootstrap replicates. The BI consensus tree and the ML best tree were edited in TreeGraph 2 (Stöver and Müller 2010). In the BI tree, the branches were collapsed at posterior probability (PP) < 0.95, and in the ML tree at bootstrap support (BS) < 70%. The bootstrap values of the ML tree were manually transferred to the BI consensus tree.

The Saté-II alignment was used for calculating a pairwise distance matrix in MEGA 11 (Tamura *et al.* 2021). The calculation was based on p-distances, pairwise deletion, and uniform rates. After the taxonomic species were decided, the matrix was manually inspected for maximum intraspecific distances and minimum interspecific distances. The barcode gap is the latter minus the former, i.e. a species' genetic distance to the nearest neighbour minus the maximum distance within the species (see, e.g. Schoch *et al.* 2012).

Results

Five secondary compounds were identified on the chromatograms (Figs 1, 2; Table 1): 4-O-methylcryptochlorophaeic acid, boninic acid, homosekikaic acid, sekikaic acid, and one unknown compound occurring above boninic acid in all three standard solvent systems and here referred to as hyperboninic acid. Additional unknown compounds were present as minor or traces, but apparently not giving further taxonomic information and were hence disregarded. The compounds were the basis for recognizing four chemotypes: (1) 4-O-methylcryptochlorophaeic acid (only), (2) homosekikaic acid (major) and sekikaic acid (submajor), (3) hyperboninic acid (major) and boninic acid (minor), and (4) hyperboninic acid (only).

Fourteen new ITS sequences were produced (GenBank: PV029845–47, PV137641–51). The alignment was 651 bp long and the ingroup contained 307 variable and 237 parsimony informative sites. The BI consensus tree is shown in Fig. 2. The genus *Krogia* was not recovered as a supported clade, but rather as five separate clades in a polytomy with species of *Aciculopsora* Aptroot & Trest, *Bacidina* Vězda, *Eschatogonia* Trevis. and *Toninia* A.Massal. Those five *Krogia* clades, however, were all strongly supported, with PP=1 and with BS ranging from 97% to 100%.

The chemotypes largely followed the clades (Fig. 2), i.e. chemotype 1 occurred in two clades, chemotype 2 in one clade, chemotype 3 in two clades, and chemotype 4 in one clade. Four of the clades contained only one chemotype, and one clade contained two chemotypes (chemotypes 3 and 4).

The maximum genetic distance within each of the five *Krogia* clades, the minimum distance from each clade to its nearest neighbour, and each clade's barcode gap to the nearest neighbour are detailed in Table 2. The barcode gaps ranged from 9.9 to 14.3 percentage points.

Table 1. Sequences used for the phylogenetic reconstructions, with specimen ID, current species identification, voucher information, geographical origin, type status, and chemotype. New sequences are indicated in bold. 4MCC: 4-O-methylcryptochlorophaeic acid, BON: boninic acid, DID: didymic acid, HBON: hyperboninic acid, HSEK: homosekikaic acid, NONE: no lichen substances, SEK: sekikaic acid.

GenBank ID	Species	Voucher	Country	Type	Chemotype
MG925948	<i>Aciculopsora longispora</i>	Lücking 17543 (BR)	Costa Rica	isotype of <i>A. salmonea</i>	NONE
AF282086	<i>Bacidia rosella</i>	Ekman 3117 (BG)	Sweden	–	–
JQ796852	<i>Bacidia rubella</i>	van den Boom, DNA 578 (LG)	Switzerland	–	–
JQ796854	<i>Bacidina delicata</i>	Serussiaux, DNA 369 (LG)	France	–	–
JQ796855	<i>Bacidina neosquamulosa</i>	van den Boom, DNA 490 (LG)	Netherlands	–	–
OQ717322	<i>Bacidina phacodes</i>	Vondrak 25994 (PRA)	Austria	–	–
MG925969	<i>Eschatogonia prolifera</i>	Timdal 10207 (O L-144577)	Peru	–	DID
MH174281	<i>Krogia antillarum</i>	Rui & Timdal 10844 (O L-152141)	Trinidad & Tobago	paratype	4MCC
MH174282	<i>Krogia antillarum</i>	Wolf & Sipman 2052 (B)	Mexico	–	4MCC
MH174283	<i>Krogia antillarum</i>	Dahl et al. AM39 (O L-202829)	Brazil	–	4MCC
PV029845	<i>Krogia australasiatica</i>	Timdal 20061 (PC)	New Caledonia	holotype	4MCC
PV137648	<i>Krogia australasiatica</i>	Möller NC146 (O L-400782)	New Caledonia	paratype	4MCC
MG925977	<i>Krogia coralloides</i>	Krog & Timdal MAU51/83 (O L-21909)	Mauritius	holotype	BON, HBON
MH174284	<i>Krogia coralloides</i>	Diederich 18455 (hb Diederich)	Mauritius	–	BON, HBON
MH174285	<i>Krogia isidiata</i>	Elvebakk 05:633 (O L-186393)	New Caledonia	holotype	HSEK, SEK
MH174286	<i>Krogia isidiata</i>	Rikkinen 34385 (H)	New Caledonia	paratype	HSEK, SEK
PV029846	<i>Krogia isidiata</i>	Simon 1093 (O L-400510)	New Caledonia	–	HSEK, SEK
PV137643	<i>Krogia isidiata</i>	Timdal 20010 (O L-400822)	New Caledonia	–	HSEK, SEK
PV137646	<i>Krogia isidiata</i>	Timdal 20008 (O L-400820)	New Caledonia	–	HSEK, SEK (trace)
PV137647	<i>Krogia isidiata</i>	Haugan RH20509 (O L-401083)	New Caledonia	–	HSEK, SEK
MH174287	<i>Krogia macrophylla</i>	Rikkinen 36047 (H)	New Caledonia	paratype	HBON
MH174288	<i>Krogia macrophylla</i>	Rikkinen 36077 (H)	New Caledonia	holotype	HBON
MH174289	<i>Krogia macrophylla</i>	Rikkinen 35037 (H)	New Caledonia	paratype	HBON
MH174290	<i>Krogia macrophylla</i>	Rikkinen 38565 (H)	New Caledonia	paratype	HBON
PV029847	<i>Krogia macrophylla</i>	Timdal 20241 (O L-401051)	New Caledonia	–	HBON, BON
PV137641	<i>Krogia macrophylla</i>	Timdal 20248 (O L-401059)	New Caledonia	–	HBON, BON
PV137642	<i>Krogia macrophylla</i>	Timdal 20089 (O L-400901)	New Caledonia	–	HBON
PV137644	<i>Krogia macrophylla</i>	Simon 1018 (O L-400435)	New Caledonia	–	HBON
PV137645	<i>Krogia macrophylla</i>	Simon 1023 (O L-400440)	New Caledonia	–	–
PV137649	<i>Krogia macrophylla</i>	Simon 801 (O L-400218)	New Caledonia	–	HBON
PV137650	<i>Krogia macrophylla</i>	Timdal 20009 (O L-400821)	New Caledonia	–	HBON
PV137651	<i>Krogia macrophylla</i>	Evankow NC011 (O L-400011)	New Caledonia	–	HBON, BON
AF282104	<i>Toninia cinereovirens</i>	Haugan & Timdal 7953 (O L-33355)	Norway	–	–

Table 2. Genetic distances within and between *Krogia* species, based on all available ITS sequences.

Species	No. of specimens	Maximum distance	Minimum distance to				Barcode gap	
		Intraspecific	<i>K. austroasiatica</i>	<i>K. coralloides</i>	<i>K. isidiata</i>	<i>K. macrophylla</i>	Percentage points	Nearest neighbour
<i>K. antillarum</i>	3	3.6 %	14.7 %	15.4 %	21.4 %	17.2 %	11.1	<i>K. australasiatica</i>
<i>K. australasiatica</i>	2	0.8 %	–	18.1 %	22.1 %	18.4 %	13.9	<i>K. antillarum</i>
<i>K. coralloides</i>	2	0.0 %	–	–	20.1 %	14.3 %	14.3	<i>K. macrophylla</i>
<i>K. isidiata</i>	6	7.6 %	–	–	–	20.9 %	12.5	<i>K. coralloides</i>
<i>K. macrophylla</i>	12	4.4 %	–	–	–	–	9.9	<i>K. coralloides</i>

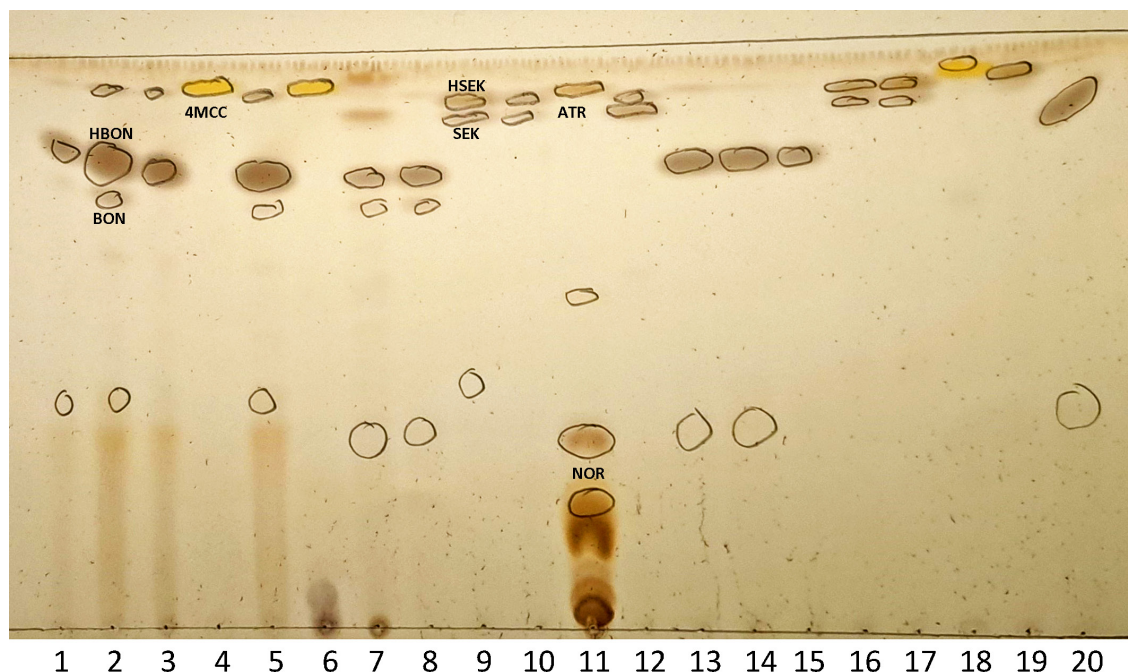


Figure 1. TLC chromatogram in solvent system B' of *Krogia* specimens from New Caledonia. *Krogia australasiatica* [lanes 4 (O L-400141), 6 (O L-400782), 18 (O L-400627)], *K. isidiata* [lanes 9 (O L-401081), 10 (O L-401083), 16 (O L-400439), 17 (O L-401316), 19 (O L-400820)], *K. macrophylla* [lanes 1 (O L-400009), 2 (O L-400011), 3 (O L-400015), 5 (O L-400651), 7 (O L-401051), 8 (O L-401059), 13 (O L-400218), 14 (O L-400361), 15 (O L-400435), 20 (O L-400821)], and references [lanes 11 (atranorin, norstictic acid), 12 (homosekikaic acid, sekikaic acid)]. Abbreviations: 4MCC: 4-O-methylcryptochlorophaeic acid, ATR: atranorin, BON: boninic acid, HBON: hyperboninic acid, HSEK: homosekikaic acid, NOR: norstictic acid, SEK: sekikaic acid.

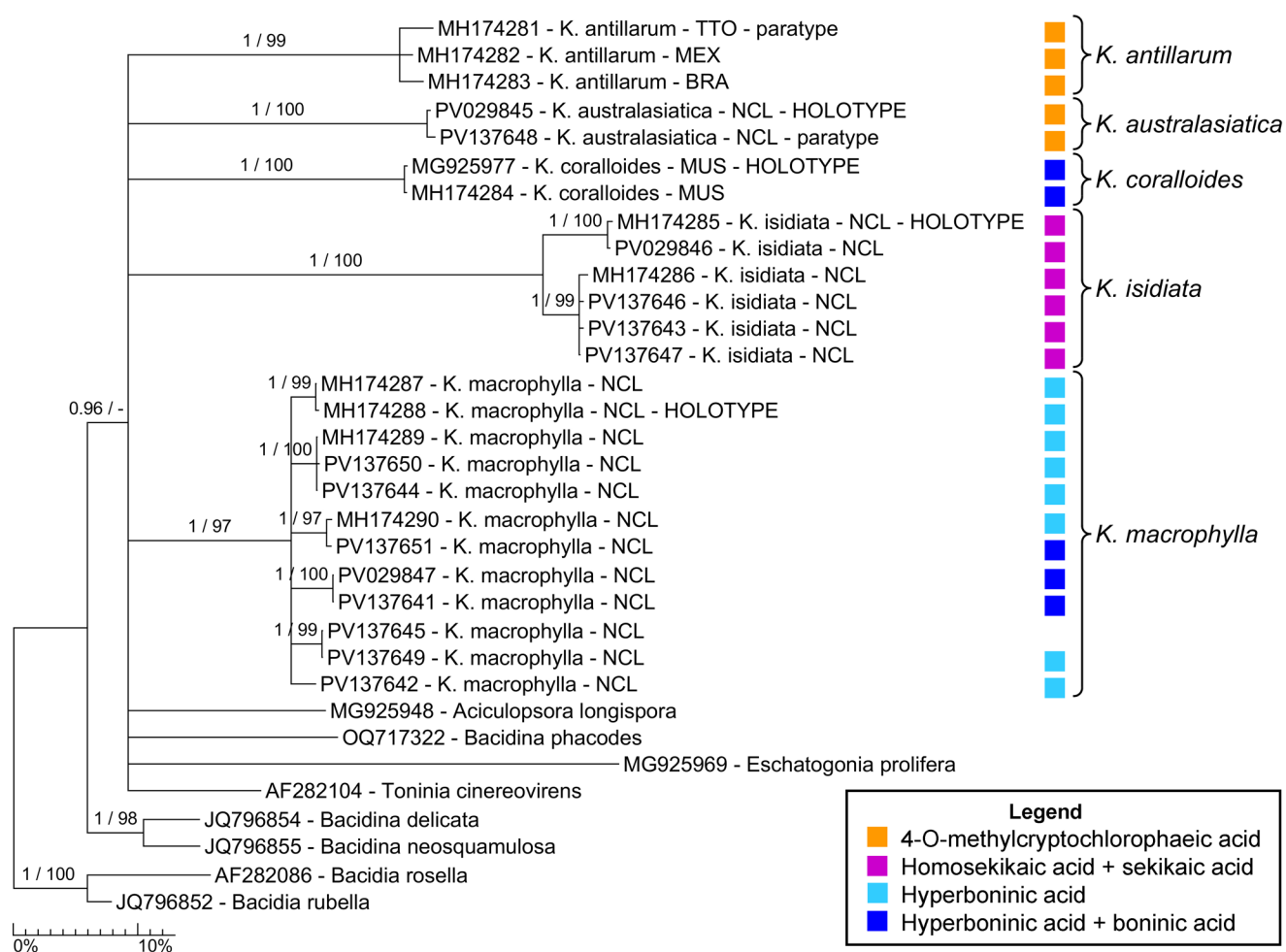


Figure 2. Bayesian 50% majority rule consensus tree, collapsed where posterior probability (PP) < 0.95, of all known ITS sequences of *Krogia*, with representatives from related genera added and *Bacidia* used as outgroup. Bootstrap support (BS) values from a congruent maximum likelihood tree are added; the support values are given as PP/BS on the branches. The scale bar indicates numbers of substitutions per site (as percent). Geographical origins: BRA: Brazil, MEX: Mexico, MUS: Mauritius, NCL: New Caledonia, TTO: Trinidad and Tobago. Chemotypes are colour-coded, and braces indicate current species hypotheses.

Discussion

The high support for the five *Krogia* clades and their long branches (Fig. 2), their large barcode gaps (Table 2), and the strong correlation between clades and chemotypes (Fig. 2) indicate that the five clades should be regarded as separate species hypotheses. Four of them are here identified by morphology and chemistry as *K. antillarum*, *K. coralloides*, *K. isidiata*, and *K. macrophylla*, following the key and taxonomy of Kistenich *et al.* (2018a).

The fifth clade is represented by squamulose, isidiate specimens containing 4-O-methylcryptochlorophaeic acid. This chemistry is shared with *K. antillarum*, but that species differs in morphology by lacking isidia and is apparently propagating by the breaking-off of flattened, ascending squamules (Timdal 2009). The two isidiate species of *Krogia*, *K. isidiata* and *K. macrophylla*, differ in chemistry (Fig. 2); the former also in forming a black hypothallus and the latter in forming larger, up to 3 mm wide, squamules (Kistenich *et al.* 2018a). The two *Krogia* species missing in the molecular data set, *K. borneensis* and *K. microphylla*, differ from the specimens in the fifth clade in both morphological and chemical characters. *Krogia borneensis* forms lacinules (flattened diaspores budding off from the end of the squamules) and contains homosekikaic and sekikaic acids (Kistenich *et al.* 2018a). *Krogia microphylla* forms minute squamules (< 0.3 mm wide), which are soon coalescing into a microphyllinous crust, and does not contain secondary compounds (Timdal in Lumbsch *et al.* 2011). It hence appears that the fifth *Krogia* clade represents an undescribed species, and it is here described as *K. australasiatica*.

The lack of support for *Krogia* as a monophyletic genus (Fig. 2) is explained by the use of only the ITS marker in this study. ITS is apparently too variable to give sufficient backbone support at the genus level although it seems good in distinguishing clades at the species level. Kistenich *et al.* (2018a), using additionally the more conservative mtSSU marker, recovered *Krogia* as monophyletic (PP=0.99, BS=73%). The morphological and chemical similarity between the seven *Krogia* species (e.g. the red spots on the thallus and apothecia, the weakly amyloid to non-amyloid tip of the asci, and the filiform, curved, spirally arranged ascospores; all here interpreted as synapomorphies within the family Ramalinaceae) also indicate that *Krogia* is monophyletic.

The unknown compound found in *K. coralloides* and *K. macrophylla* which resembles boninic acid in colour and fluorescence on the developed chromatograms and moves just above boninic acid in all three standard solvent systems (R_f -classes A:5, B:5, C:6; Timdal 2002, Kistenich *et al.* 2018a), does not seem to match any of the biosynthetically related compounds of boninic acid listed by Elix (2014), i.e. 4,4'-di-O-methylcryptochlorophaeic acid, 2,4'-di-O-methylnorsekikaic acid, homosekikaic acid, 4'-O-methylpaludosic acid, 2-O-methylsekikaic acid, paludosic acid, and sekikaic acid. Although the molecular structure is unknown, introducing a trivial name seems justified and it is here referred to as hyperboninic acid.

Taxonomy

Krogia australasiatica Timdal, *sp. nov.*

MycoBank No.: MB 857416

Type: NEW CALEDONIA: South Province: Mont Dore: Port-Boisé, 1–1.5 km NW of Pointe Puka, 22.3480°S, 166.9652°E, 1–10 m alt., on tree trunk at forest edge, 30 Nov 2022, E. Timdal 20061 (holotype: PC; isotype: O L-400873), TLC: 4-O-methylcryptochlorophaeic acid, DNA: PV029845 (ITS).

Diagnosis: Differs from the two other isidiate species of *Krogia*, *K. isidiata* and *K. macrophylla*, in containing 4-O-methylcryptochlorophaeic acid, and from the chemically identical *K. antillarum* in forming isidia.

Description: Thallus effuse, squamulose; squamules up to 1.6 mm wide, at first rounded, later elongated and becoming incised and deeply divided into up to 0.2 mm wide lobes, adnate when young, later ascending, often imbricate, flattened or with an up-turned to involute tip, green, with patches of red (K+ purple) spots, epruinose, glabrous; margin concolorous with upper side, not fibrillose; lower side white; isidia attached marginally to the squamules or sometimes free on the substrate, simple or sparingly branched, up to 1 mm long and 0.1 mm wide. Upper cortex composed of thick-walled, irregularly orientated hyphae with angular lumina, 15–25 µm thick, lacking an epinecral layer, not containing crystals (polarised light!); algal layer 30–40 µm thick, filled with crystals dissolving in K; medulla composed of loosely interwoven hyphae, upper part containing crystals dissolving in K; lower cortex lacking; prothallus lacking. Apothecia up to 0.7 mm diam. when simple, often forming aggregates up to 1.5 mm diam., pale to medium brown, with red patches (K+ purple), plane to weakly convex, with a slightly paler, often flexuose margin; excipulum colourless, composed of radiating, closely conglutinated, thick-walled hyphae with narrowly cylindrical lumina, filled with crystals in inner part; hypothecium colourless or patchily with red pigment especially in upper part, composed of closely conglutinated, thick-walled hyphae with narrowly cylindrical lumina, not containing crystals; epithecium colourless or patchily red, not containing crystals. Ascus clavate, surrounded by a thin amyloid sheet; tholus well-developed, with a wide, amyloid, conical structure. Ascospores simple, filiform, curved, spirally arranged in ascus, 23–27 × c. 1 µm (estimate of curved spores). Conidiomata not seen. **Fig. 3.**

Chemistry: 4-O-methylcryptochlorophaeic acid (by TLC) and unidentified red pigment(s) occurring scattered in thallus and apothecium; thallus PD–, K– (red spots K+ purple), C–, KC–, UV–.

Notes: The ascus of *Krogia australasiatica* showed a deeper amyloid conical structure in the tholus of the ascus than what is previously reported (Timdal 2002, 2009; Kistenich *et al.* 2018a), approaching the *Bacidia* type which is common in the Ramalinaceae (Fig. 3B). This is the first record of the genus *Krogia* from Australia.

Etymology: The name indicates its geographical distribution, Australia and New Caledonia.



Figure 3. *Krogia australasiatica*, paratype (O L-400627). A, lab photo of the specimen in dry condition; scale bar = 1 mm. B, ascus, stained in Lugol's solution after pretreatment in K; scale bar = 10 μ m. C, D, field photos of the same specimen in moist condition. Photographs by E. Timdal (A, B) and A. Simon (C, D).

Distribution and habitat: The species is known from two localities in New Caledonia (North Province and South Province) and from Australia (Queensland). The species grows on tree trunks in humid primary forests or rainforest. Accompanying species include *Chiodecton congestulum*, *Cryptothecia atropunctata*, and *Eschatogonia marivelensis* (Queensland; from searches performed in the UPS collection database published by Myrdal 2022) and *Bacidia cylindrophora*, *Krogia isidiata*, *K. macrophylla*, *Normandina pulchella*, and *Phyllopsora breviscula* (New Caledonia; own collections).

Additional specimens examined: **Australia: Queensland:** Noosa Head National Park, c. 1 km from the sea near road to the Lookout, 26°23'S, 153°07'E, 110 m alt., rainforest with emergent *Araucaria cunninghamii*, G. Thor 4913, p.p., 7 Nov 1985 (UPS L-174920 p.p., immixture in *Eschatogonia marivelensis*). **New Caledonia: North Province: Koné:** along Rivière de Confiance, valley S of Mt Koniambo, 21.0308°S, 164.8199°E, 200 m alt., on tree, in low-elevation rainforest, A.M. Evankow NC141, 12 Dec 2022 (O L-400141); *ibid.*, 21.0310°S, 164.8195°E, 180 m alt., R. Haugan RH220773 (O L-401328); *ibid.*, 21.0308°S, 164.8200°E, 200 m alt., E.J. Möller NC146 (O L-400782); *ibid.*, 21.0303°S, 164.8214°E, 230 m alt., A. Simon 1210 (NOU, O L-400627).

Krogia isidiata Kistenich & Timdal

Notes: The species was previously known from three localities in New Caledonia (Kistenich et al. 2018a). Four new localities are reported here. All specimens contain homosekikaic acid and sekikaic acid, and all have a well-developed black hypothallus which is unique within the genus (Kistenich et al. 2018a).

New records: **New Caledonia: North Province: Koné:** along Rivière de Confiance, valley S of Mt Koniambo, 21.0309°S, 164.8193°E, 180 m alt., tree trunk in rainforest, R. Haugan RH220762, 12 Dec 2022 (NOU, O L-401316); **South Province: Boulouparis:** Réserve de Faune et de Flore du Mont Do, just N of the peak, 21.7533°S, 165.9999°E, 1020 m alt., epiphytic, in high-elevation rainforest, A. Simon 1093, 2 Dec 2022 (NOU, O L-400510); **Païta:** along trail to Mont Humboldt from mine Gallieni, 21.9088°S, 166.3705°E, 955 m alt., tree trunk in shady ravine, E. Timdal 20035, 28 Nov 2022 (O L-400848); **Yaté:** E of Mt Pic du Pin, 22.2487°S, 166.8285°E, 280 m alt., epiphytic, in sclerophyllous forest, A. Simon 1022, 26 Nov 2022 (O L-400439); *ibid.*, 22.2487°S, 166.8285°E, 280 m alt., tree trunk in dense forest, E. Timdal 20008 (O L-400820); *ibid.*, 22.2486°S, 166.8286°E, 280 m alt., tree trunk in dense forest, E. Timdal 20010 (NOU, O L-400822); *ibid.*, 22.2480°S, 166.8286°E, 280 m alt., tree trunk in forest, R. Haugan RH220507 (O L-401081); *ibid.*, 22.2478°S, 166.8293°E, 280 m alt., tree trunk in forest, R. Haugan RH220509 (O L-401083).

Krogia macrophylla Kistenich & Timdal

Notes: The species was previously known from three localities in New Caledonia (Kistenich et al. 2018a). Six new localities

are reported here. In addition to hyperboninic acid, which was reported as the only major compound by Kistenich et al. (2018a, as unknown compound resembling boninic acid), boninic acid is here reported from three specimens (Fig. 2; Table 1).

New records: **New Caledonia: North Province: Koné:** along Rivière de Confiance, valley S of Mt Koniambo, 21.0310°S, 164.8192°E, 190 m alt., tree trunk in rainforest, E. Timdal 20241, 12 Dec 2022 (NOU, O L-401051); *ibid.*, 21.0308°S, 164.8197°E, 200 m alt., tree trunk in rainforest, E. Timdal 20248 (NOU, O L-401059); **Poya:** mountain N of route RT1 between Poya and Nepoui, 21.3001°S, 165.0909°E, 590 m alt., epiphytic, in shrubby maquis transitioning into sclerophyllous forest, A. Simon 944, 18 Nov 2022 (O L-400361); **South Province: Boulouparis:** Réserve de Faune et de Flore du Mont Do, along the road near the peak, 21.7576°S, 166.0008°E, 955 m alt., tree trunk in rainforest, E. Timdal 20089, 2 Dec 2022 (O L-400901); **Mont Dore:** along trail NC1 SE of Camping des Bois du Sud, 22.1719°S, 166.7597°E, 200 m alt., epiphytic, in low-elevation rain forest, A. Simon 801, 23 Oct 2022 (NOU, O L-400218); **Thio:** Réserve Spéciale Botanique du Mont Humboldt, Refuge du Humboldt, 21.8824°S, 166.4132°E, 1350 m alt., on tree, in high-elevation rain forest, A.M. Evankow NC009, 28 Nov 2022 (O L-400009); *ibid.*, 21.8823°S, 166.4133°E, 1350 m alt., A.M. Evankow NC011 (O L-400011); *ibid.*, 21.8825°S, 166.4126°E, 1350 m alt., A.M. Evankow NC015 (O L-400015); **Yaté:** Réserve Spéciale Botanique des Chutes de la Madeleine, near route 10, 22.2301°S, 166.8525°E, 255 m alt., epiphytic, in shrubby *Gymnostoma* maquis, including *Dacrydium araucarioides*, *Sannantha leratii*, etc, A. Simon 1018, 26 Nov 2022 (O L-400435); E of Mt Pic du Pin, 22.2487°S, 166.8285°E, 280 m alt., epiphytic, in sclerophyllous forest, A. Simon 1023, 26 Nov 2022 (O L-400440); *ibid.*, 22.2486°S, 166.8287°E, 280 m alt., tree trunk in dense forest, E. Timdal 20009 (NOU, O L-400821).

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References

- Culberson CF (1972) Improved conditions and new data for the identification of lichen products by a standardized thin-layer chromatographic method. *Journal of Chromatography* 72: 113–125. [DOI](#)
- Culberson CF, Johnson A (1982) Substitution of methyl tertbutyl ether for diethyl ether in the standardized thin-layer chromatographic method for lichen products. *Journal of Chromatography* 238: 483–487. [DOI](#)
- Darriba D, Posada D, Kozlov AM, Stamatakis A, Morel B, Flouri T (2020) ModelTest-NG: A New and Scalable Tool for the Selection of DNA and Protein Evolutionary Models. *Molecular Biology and Evolution* 37: 291–294. [DOI](#)
- Edgar RC (2004) MUSCLE: a multiple sequence alignment method with reduced time and space complexity. *BMC Bioinformatics* 5: 113. [DOI](#)
- Edler D, Klein J, Antonelli A, Silvestro D (2021) raxmlGUI 2.0: A graphical interface and toolkit for phylogenetic analyses using RAxML. *Methods in Ecology and Evolution* 12: 373–377. [DOI](#)
- Elix J (2014) A catalogue of standardized chromatographic data and biosynthetic relationships for lichen substances. Third edition. ([PDF](#)) (Accessed 7 Oct 2024)
- Ferencova Z, Rico VJ, Hawksworth DL (2017) Extraction of DNA from lichen-forming and lichenicolous fungi: a low-cost fast protocol using Chelex. *Lichenologist* 49: 521–525. [DOI](#)
- Gardes M, Bruns TD (1993) ITS primers with enhanced specificity for basidiomycetes – application to the identification of mycorrhizae and rusts. *Molecular Ecology* 2: 113–118. [DOI](#)
- Hall TA (1999) BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic Acids Symposium Series* 41: 95–98.
- Huelsenbeck JP, Ronquist F (2001) MRBAYES: Bayesian inference of phylogeny. *Bioinformatics* 17: 754–755. [DOI](#)
- Katoh K, Toh H (2008) Recent developments in the MAFFT multiple sequence alignment program. *Briefings in Bioinformatics* 9: 286–298. [DOI](#)
- Katoh K, Kuma K-I, Toh H, Miyata T (2005) MAFFT version 5: improvement in accuracy of multiple sequence alignment. *Nucleic Acids Research* 33: 511–518. [DOI](#)
- Kistenich S, Rikkinen JK, Thüs H, Vairappan CS, Wolseley PA, Timdal E (2018a) Three new species of *Krogia* (Ramalinaceae, lichenised Ascomycota) from the Paleotropics. *MycKeys* 40: 69–88. [DOI](#)
- Kistenich S, Timdal E, Bendiksby M, Ekman S (2018b) Molecular systematics and character evolution in the lichen family Ramalinaceae (Lecanorales, Ascomycota). *Taxon* 67: 871–904. [DOI](#)
- Liu K, Warnow TJ, Holder MT, Nelesen SM, Yu J, Stamatakis AP, Linder CR (2012) SATéII: very fast and accurate simultaneous estimation of multiple sequence alignments and phylogenetic trees. *Systematic Biology* 61: 90–106. [DOI](#)
- Lumbsch HT, Chaves-Chaves JL, Umaña-Tenorio L, Lücking R (2011) One hundred new species of lichenized fungi: A signature of undiscovered global diversity. *Phytotaxa* 18: 1–127. [PDF](#)
- Marthinsen G, Rui S, Timdal E (2019) OLICH: A reference library of DNA barcodes for Nordic lichens. *Biodiversity Data Journal* 7: e36252. [DOI](#)
- Myrdal M (2022). Botany (UPS). Museum of Evolution, Uppsala University. Occurrence dataset [DOI](#) (accessed via GBIF.org on 8 Oct 2024)
- Price MN, Dehal PS, Arkin AP (2010). FastTree 2 – approximately maximum-likelihood trees for large alignments. *PLoS One* 5: e9490. [DOI](#)
- Ronquist F, Huelsenbeck JP (2003) MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* 19: 1572–1574. [DOI](#)
- Schoch CL, Seifert KA, Huhndorf S, Robert V, Spouge JL, Levesque CA, Chen W, Fungal Barcoding Consortium (2012) Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for Fungi. *PNAS* 109: 6241–6246. [DOI](#)
- Stamatakis A (2014) RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics* 30: 1312–1313. [DOI](#)
- Stöver BC, Müller KF (2010) TreeGraph 2: Combining and visualizing evidence from different phylogenetic analyses. *BMC Bioinformatics* 11: 7. [DOI](#)
- Tamura K, Stecher G, Kumar S (2021). MEGA 11: Molecular Evolutionary Genetics Analysis Version 11. *Molecular Biology and Evolution* 38: 3022–3027. [DOI](#)
- Timdal E (2002) *Krogia coralloides*, a new lichen genus and species from Mauritius. *The Lichenologist* 34: 293–296. [DOI](#)
- Timdal E (2009) *Krogia antillarum* (Ramalinaceae), a new lichen species from the West Indies. *The Bryologist* 112: 387–389. [DOI](#)
- White TJ, Bruns T, Lee S, Taylor J (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. Pp. 315–322 in Innis MA, Gelfand DH, Sninsky JJ, White TJ (eds) *PCR protocols: A guide to methods and applications*. (Academic Press: New York)