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Standard Paper

Using morphological, chemical, and molecular data to study the diversity of *Xanthoparmelia* species from South Africa (*Ascomycota, Parmeliaceae*)

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Abstract

There is still a high diversity of lichen-forming fungi that remains undescribed, especially cryptic lineages at the species level. Integrating morphological, chemical, and DNA sequence data has proved useful in corroborating species descriptions and delimitations. Here we reviewed morphological features, secondary metabolites and the DNA sequences of ITS, mtSSU and nuLSU markers to study the diversity of *Xanthoparmelia* in southern Africa. A total of 37 species were recorded. Three of these appear undescribed, and we therefore describe them here as new: *Xanthoparmelia nimisii*, with a sorediate thallus and broad lobes, is well supported as a clade separate from *X. annexa*; *X. pseudochalybaeizans* with a white medulla is phylogenetically distinct from the otherwise similar *X. chalybaeizans*; and *X. sipmaniana*, well supported as a separate clade from the similar *X. hypoprocetrarica*. In addition, the separation of *Xanthoparmelia capensis* and *X. tinctina* requires further studies.

Keywords: cryptic species; lichens; new species; phylogeny; Southern Hemisphere; species delimitation

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Introduction

Xanthoparmelia is the most speciose genus of lichen-forming fungi (*c.* 800 species) (Thell *et al.* 2012; Jaklitsch *et al.* 2016). The genus has a worldwide distribution and is found in temperate to tropical, semi-arid and arid regions (Hale 1990). South Africa and Australia are the distribution centers (Elix *et al.* 1986; Hale 1990). While *Xanthoparmelia* species are equally species-rich in both regions, macro-evolutionary patterns of lineage diversification are quite distinct. South Africa and nearby regions have been suggested as the areas of evolutionary origin for *Xanthoparmelia*, which is estimated to be close to the Oligocene-Miocene boundary (Divakar *et al.* 2015; Leavitt *et al.* 2018). Multiple early-diverging lineages diversified in South Africa, with several migration events into Australia (Leavitt *et al.* 2018; Autumn *et al.* 2020). The species diversity in Australia might result from several subsequent radiation events (Leavitt *et al.* 2018). In contrast, the Northern Hemisphere was colonized recently by the genus, with an estimated age of the Holarctic clade of 7.2 Mya (Leavitt *et al.* 2013, 2018). We focused our study on southern Africa, where currently more than 300 species are known, including the synonymized genera *Karoowia*, *Namakwa*, *Neofuscelia*, *Paraparmelia* and *Xanthomaculina* (Esslinger 1981, 1986, 2000; Hale 1985, 1988, 1989, 1990; Elix

1997, 1999*a*, *b*, 2001, 2002, 2003; Elix *et al.* 1999; Blanco *et al.* 2004; Thell *et al.* 2004; Amo de Paz *et al.* 2010; Sipman 2017). We used the available data from recent collections by one of our researchers (VW) through somewhat opportunistic sampling. Therefore, the sampling has limitations and does not include all South African *Xanthoparmelia* species. However, a thorough sampling of specimens in the studied area has been carried out (Wirth & Sipman 2018; Wirth *et al.* 2018). This study aims to contribute to a better understanding of species delimitation and phylogenetic relationships of *Xanthoparmelia* in South Africa.

Material and Methods

Study area

Our study is based on 61 *Xanthoparmelia* specimens collected during an inventory of natural vegetation remnants in the Cederberg and Renosterveld Reserve regions of the Western Cape, South Africa, by VW (Wirth & Sipman 2018; Wirth *et al.* 2018), for which new sequences were generated. The specimens are deposited in B and STU, and we used collections in F for comparison.

Anatomical studies

Thallus morphology was studied using a Zeiss Stemi 2000-C stereomicroscope, and conidia and spore shape and size were observed using a Zeiss Axioscope. Secondary metabolites were identified using spot tests with 10% KOH, C (sodium hypochlorite),
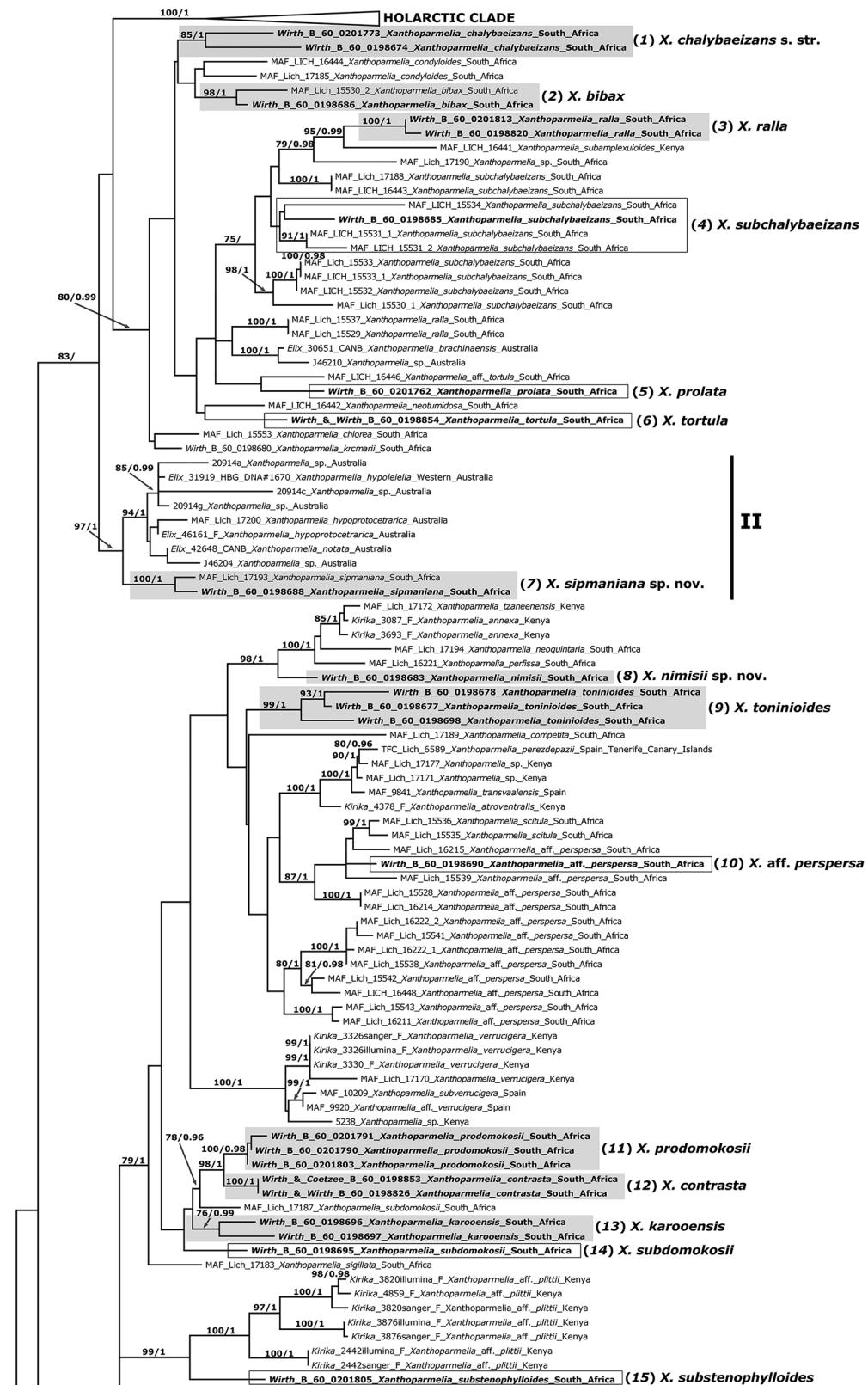
Figure 1. Phylogenetic relationships of *Xanthoparmelia* based on concatenated alignments of ITS, mtSSU and nuLSU markers. Topology based on maximum likelihood (ML) analyses. Bootstrap values > 75 and posterior probabilities > 0.95 are indicated on each branch. The 61 samples from South Africa generated in this study are indicated in bold. Highlighted in bold and enlarged font at the tree tips are 37 lineages, including XV major groups (well-supported lineages indicated with grey boxes, poorly-supported lineages with white boxes). Information provided includes the collector, specimen voucher, species name and country. Further information regarding these samples and those of the collapsed nodes (Holarctic Clade, Australian Clades A-D and *pulla* Clade) can be found in Supplementary Materials S1 (available online).
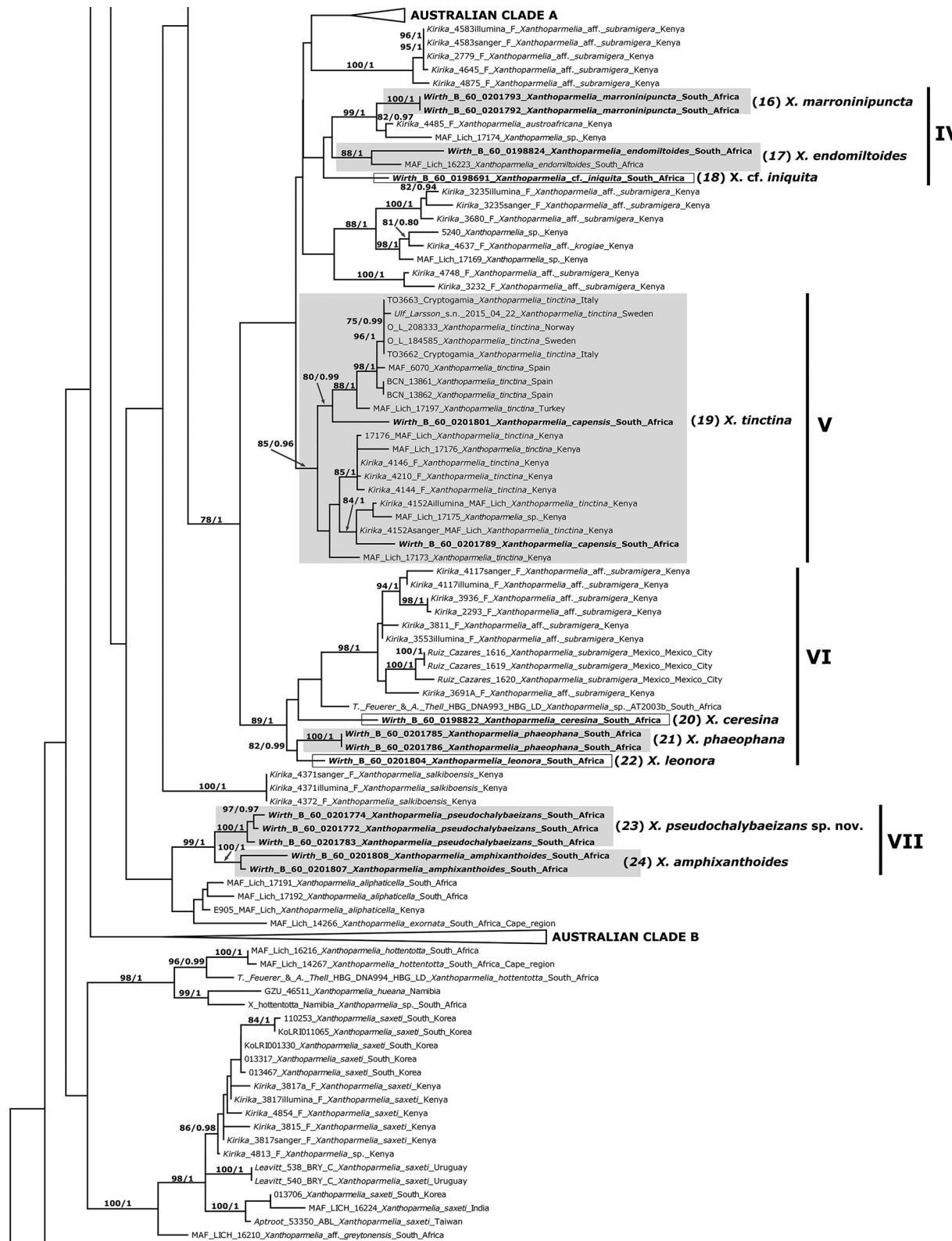
Figure 1. Continued.
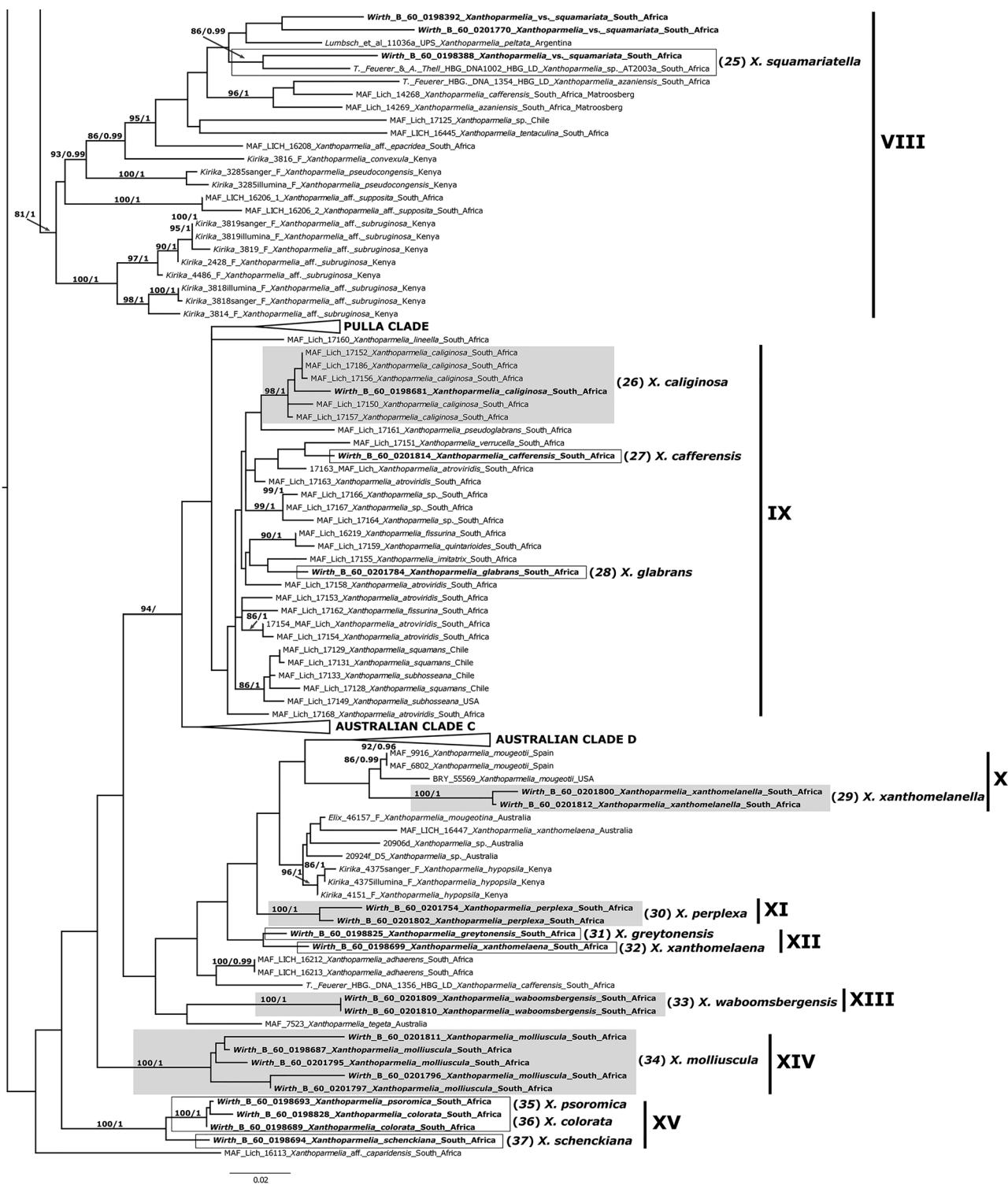
Figure 1. Continued.

KC and PD (paraphenylenediamine) and high-performance thin-layer chromatography (HPTLC) (Culberson & Johnson 1982; Arup et al. 1993; Orange et al. 2010).

Molecular methods

Sixty-one specimens from South Africa were selected for molecular analysis. Total genomic DNA was extracted from thallus fragments using the ZR Fungal/Bacterial DNA Miniprep Kit (Zymo Research Corp., Irvine, CA, USA), following the manufacturer's instructions. DNA sequences were generated for three markers using the polymerase chain reaction (PCR): the nuclear ribosomal internal transcribed spacer region (ITS), a region of the mitochondrial small subunit rDNA (mtSSU), and a region of the nuclear large subunit rDNA (nuLSU). PCR reactions contained 6.25 μl of MyTaq™ Red DNA Polymerase (Bioline,

Taunton, MA, USA), 5.25 µl of H$_2$O, 0.25 µl of forward and reverse primers (10 µM), and 0.5 µl of template DNA (10×), for a total reaction volume of 12.5 µl. The ITS region was amplified using the primers ITS1F (Gardes & Bruns 1993) and ITS4 (White *et al.* 1990), mtSSU using primers mrSSU1 and mrSSU3R (Zoller *et al.* 1999), and nuLSU rDNA using primers AL2R (Mangold *et al.* 2008) and LR6 (Vilgalys & Hester 1990). PCR products were sequenced with the same primers used for amplification on an ABI Prism 3730 DNA Analyzer (Applied Biosystems, Waltham, MA, USA) at the Pritzker Laboratory for Molecular Systematics and Evolution at The Field Museum, Chicago, Illinois, USA.

Sequence alignment and phylogenetic analysis

ITS, mtSSU and nuLSU sequences were aligned independently using the 'auto' option with the FFT-NS-i algorithm in MAFFT v. 7 (Katoh *et al.* 2019), with the remaining parameters set to default values. SequenceMatrix software (Vaidya *et al.* 2011) was used to concatenate all three alignments. Phylogenetic analyses were performed using maximum likelihood (ML) and Bayesian analyses (BA). ML trees were calculated with RAxML-HPC2 on XSEDE v. 8.2.10 (Stamatakis 2014) on the Cipres Science Gateway (http://www.phylo.org) (Miller *et al.* 2010) using the GTR + G + I substitution model with 1000 bootstrap pseudoreplicates, and the data partitioned by loci. For the BA, substitution models for each locus were estimated using jModelTest v. 2.1.9 (Guindon & Gascuel 2003; Darriba *et al.* 2012), which recommended the TIM2ef + I + G model for the ITS and nuLSU loci, and the F81 + I model for the mtSSU locus. Since the TIM2ef substitution models are not implemented in MrBayes, they were replaced by the GTR model (Ronquist & Huelsenbeck 2003). The proportion of invariable sites (I) and gamma distributed rates (G) defined in jModelTest were conserved in both cases. Two parallel Markov chain Monte Carlo (MCMC) runs were performed in MrBayes v. 3.2.6 (Huelsenbeck & Ronquist 2001; Ronquist & Huelsenbeck 2003), each using 10 000 000 generations which were sampled every 100 steps. A 50% majority-rule consensus tree was generated from the combined sampled trees (150 002) of both runs after discarding the first 25% of trees as burn-in. The convergence diagnostic of the potential scale reduction factor (PSRF) was close to 1.0 for all parameters, and the average deviation of split frequencies was below 0.01 (Gelman & Rubin 1992). Tree files were visualized with FigTree v. 1.4.2 (Rambaut 2014). The ITS, mtSSU and nuLSU sequences are deposited in GenBank (see Supplementary Material Table S1, available online).

Results and Discussion

Phylogenetic analysis

The phylogenetic analyses of the concatenated dataset under maximum likelihood (ML) and the Bayesian analysis (BA) were congruent, and therefore only the ML tree is shown here with the BA support values added. Our new material clusters in 37 lineages, including three distinct lineages that are described as new species below (Fig. 1). In addition, our data suggest that the distinction of *Xanthoparmelia capensis* Hale and *X. tinctina* (Maheu & Gillet) Hale requires further study since the species do not form separate monophyletic groups (Figs 1 & 2). The two species are not separated but there is some geographical pattern that suggests more than one species might be present in the complex.

Lineages found in the South African material

The relationships of the 37 lineages (indicated with italicised numbers in parentheses) identified in the newly sequenced material cluster into 15 major groups (I–XV), which are briefly discussed below. Within Fig. 1, only these 37 lineages are indicated: the well-supported lineages are indicated by grey boxes, while white boxes represent clades that lack support. More studies will be necessary to understand the relationships and delimitation of several species mentioned in this study.

Clade I: (*1*) We interpret the samples in this clade as representing *Xanthoparmelia chalybaeizans* (J. Steiner & Zahlbr.) Hale s. str. since our new specimens are phenotypically identical to the type of *X. chalybaeizans*. *Xanthoparmelia chalybaeizans* and (*2*) *X. bibax* (Brusse) Hale contain salazinic and chalybaeizanic (trace) acids, but *X. chalybaeizans* lacks pruina on the lobes. Our sample of *X. bibax* (B 60 0198686) clusters with MAF-Lich 15530-2 identified as *X. chalybaeizans* in Amo de Paz *et al.* (2010) and Leavitt *et al.* (2018), and is interpreted here as belonging to *X. bibax*. (*3*) Some of our samples of *X. ralla* (Brusse) G. Amo *et al.* (B 60 0201813, B 60 0208820) are closely related to *X. subamplexuloides* Hale. The latter species differs from *X. ralla* by its larger foliose thallus (4–7 cm) and lobes (0.4–1.3 mm), the presence of isidia and lack of pycnidia and apothecia. However, the added specimens (B 60 0201813, B 60 0208820) did not cluster with the other *X. ralla* from South Africa (MAF-Lich 15537/15529) (Leavitt *et al.* 2018). The polyphyly of *X. ralla* requires additional sampling to clarify the species delimitation within this complex of subcrustose species. (*4*) *Xanthoparmelia subchalybaeizans* (Hale) G. Amo *et al.* is found to consist of at least two separate clades: *X. subchalybaeizans* MAF-LICH 16443 and *X. subchalybaeizans* MAF-LICH 15532 (Amo de Paz *et al.* 2010; Leavitt *et al.* 2018). Our additional specimen (B 60 0198685) is closely related to MAF-LICH 15531-1, 15531-2 and 15534, but does not form a monophyletic group with the other *X. subchalybaeizans* specimens. (*5*) *Xanthoparmelia prolata* (Hale) Elix is closely related to *X.* aff. *tortula* (MAF-LICH 16446), which has shorter and more adnate lobes and produces norlobaridone. (*6*) *Xanthoparmelia tortula* (Kurok.) Elix has previously been found to be closely related to *X. neotumidosa* Hale and *X. brachinaensis* (Elix) O. Blanco *et al.* (Amo de Paz *et al.* 2010; Leavitt *et al.* 2018). Our additional specimen of *X. tortula* (B 60 0198854) does not cluster with the other *X.* aff. *tortula* from South Africa (MAF-LICH 16446).
Clade II: (*7*) *Xanthoparmelia sipmaniana* Barcenas-Peña, Lumbsch & Grewe sp. nov. and (*8*) *X. nimisii* Barcenas-Peña, Lumbsch & Grewe sp. nov. (Clade III) will be discussed under 'Taxonomy'.
Clade III: (*9*) *Xanthoparmelia toninioides* Hale is supported as a monophyletic clade. (*10*) *Xanthoparmelia* aff. *perspersa* (Stizenb.) G. Amo *et al.* (B 60 0198690) agrees phenotypically with *X. perspersa* but does not form a monophyletic clade. Instead, it clusters together with *X.* aff. *perspersa* '3' (MAF-Lich 15539) of Leavitt *et al.* (2018). However, this relationship lacks support. (*11*) *Xanthoparmelia prodomokosii* Hale *et al.* is closely related to (*12*) *X. contrasta* Hale. Both species have a similar chemistry but *X. contrasta* differs from *X. prodomokosii* by having a black
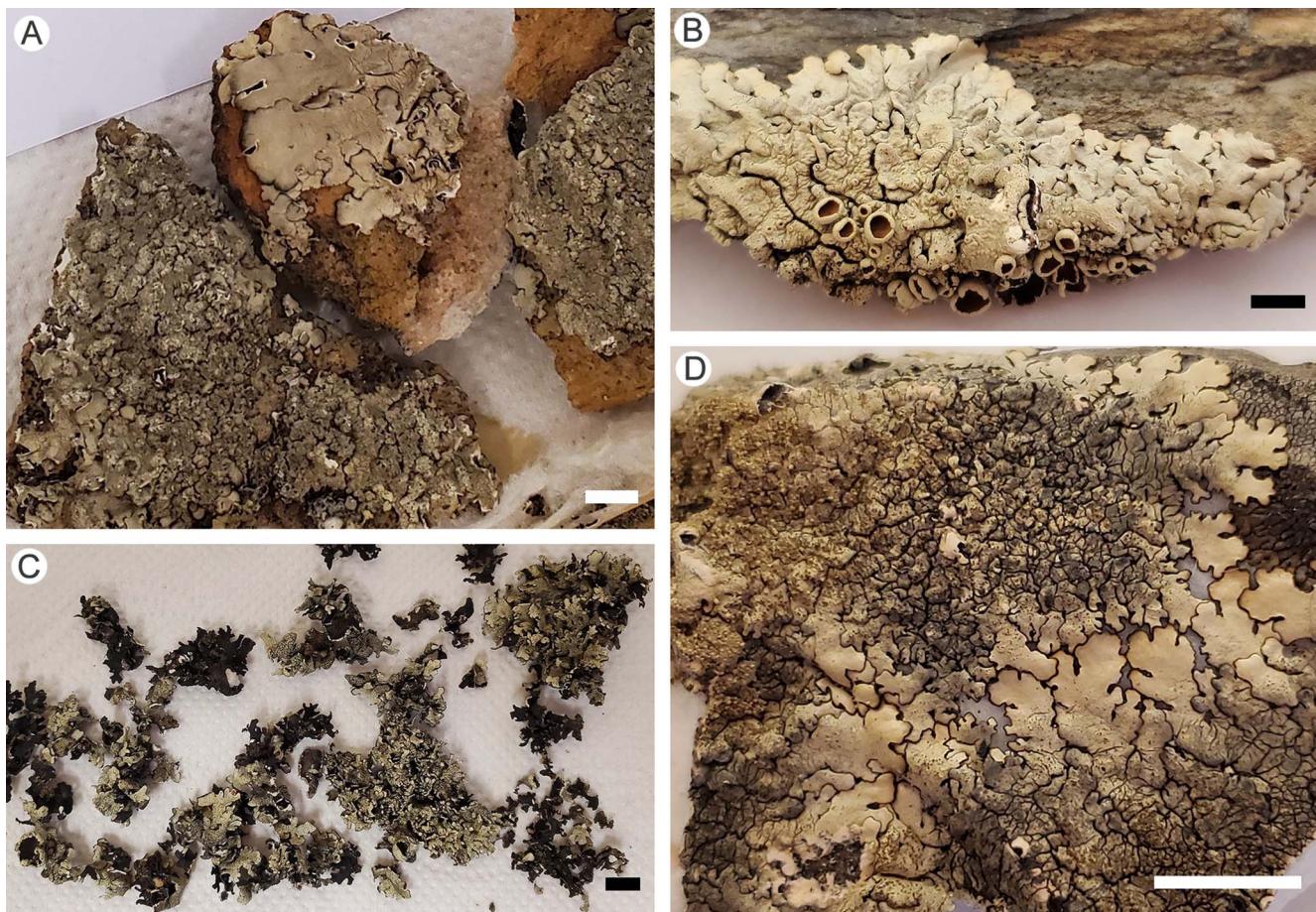
Figure 2. New species and probable synonyms of *Xanthoparmelia* in South Africa. A, habitus of *X. nimisii* sp. nov. (B, holotype). B, habitus of *X. pseudochalybaeizans* sp. nov. (B, holotype). C, habitus of *X. sipmaniana* sp. nov. (B, holotype). D, habitus of *X. capensis* (B 60 0201801). Scales: A–D = 5 mm. In colour online.

lower surface and a lack of pycnidia and apothecia. (*13*) *Xanthoparmelia karooensis* Hale is a well-supported clade. (*14*) *Xanthoparmelia subdomokosii* (Hale) Hale does not cluster with the other *X. subdomokosii* specimen MAF-Lich 17187, which was also collected in South Africa. However, both samples are in the same clade as *X. karooensis*. Both species differ only slightly in *X. subdomokosii* having a wider thallus (3–12 cm) and lobes (2–4 mm) than *X. karooensis* (4–7 cm and 0.8–1.5 mm). Thus, the three samples could belong to the same species and more studies are necessary. (*15*) *Xanthoparmelia substenophylloides* Hale is closely related to *X.* aff. *plittii* from Kenya, a similar species that differs in having a larger thallus (4–10 cm) and contiguous to imbricate lobes (1–2 mm).

Clade IV: (*16*) *Xanthoparmelia marroninipuncta* (Brusse) Hale is closely related to *X. austroafricana* (Stirt.) Hale, which produces protocetraric and usnic acids and is also restricted to southern Africa. However, *X. austroafricana* has a white maculate upper surface and broader thallus (4–12 cm) than *X. marroninipuncta* (3–8 cm). Our study supports the monophyly of (*17*) *X. endomiltoides* (Nyl.) Hale. (*18*) *Xanthoparmelia* cf. *iniquita* does not match completely with the *X. iniquita* of Elix *et al.* (1986), differing in having an adnate thallus and sublinear and broader lobes (up 4 mm). Whether *X.* cf. *iniquita* represents an undescribed taxon requires additional studies.

Clade V: (*19*) The distinction of *Xanthoparmelia capensis* and *X. tinctina* requires further study. The two species are similar in their morphology and chemistry, and also have overlapping geographical distributions (Hale 1986, 1990). Our analysis shows that the two newly sequenced samples identified as *X. capensis* (see Fig. 2D) fall into a clade with *X. tinctina*. We refrain from synonymizing the two species here since there is geographical structure in the phylogenetic tree and additional sampling might show that more than one species is involved in this clade.

Clade VI: (*20*) *Xanthoparmelia ceresina* (Vain.) Hale is closely related to *X. subramigera* (Gyeln.) Hale. Both species contain fumarprotocetraric and succinprotocetraric acids. However, *X. ceresina* has a very adnate and narrow thallus (3–8 cm) and lobes (0.8–2 mm), and lacks maculae. (*21*) *Xanthoparmelia phaeophana* (Stirt.) Hale is closely related to (*22*) *X. leonora* (A. Massal.) Hale. Both species have a white maculate upper surface and contain fumarprotocetraric and succinprotocetraric acids, but *X. phaeophana* can also contain protocetraric (±), physodalic (±), virensic (±) and caperatic (±) acids. In addition, *X. leonora* differs from *X. phaeophana* by its terricolous thallus, weakly convoluted lobes and less distinctive maculae (Hale 1990). In other studies (Leavitt *et al.* 2018), *X. phaeophana* was closely related to *X.* aff. *krogiae* Hale & Elix.

Clade VII: (*23*) *Xanthoparmelia pseudochalybaeizans* Barcenas-Peña, Lumbsch & Grewe sp. nov. is closely related to (*24*) *X. amphixanthoides* (J. Steiner & Zahlbr.) Hale. The former species differs in having an adnate, saxicolous thallus, wider lobules (1–3 mm), not being terete, and the presence of chalybaeizanic acid (see also 'Taxonomy' below).

Clade VIII: (*25*) *Xanthoparmelia squamariatella* (Elix) O. Blanco *et al.* includes distinct chemical components: B 60 0198388 contains norstictic, connorstictic and salazinic acids, whereas B 60 0201770 and B 60 0198392 contain fumarprotocetraric, protocetraric and succinprotrotocetraric acids. Additional studies are needed to understand their relationship.

Clade IX: (*26*) *Xanthoparmelia caliginosa* (Essl.) O. Blanco *et al.* is sister to *X. pseudoglabrans* (Essl.) O. Blanco *et al.*, which is also endemic to southern Africa. The two species differ because *X. pseudoglabrans* has lobes that are often somewhat maculate, a black lower surface, and contains alectoronic and α-collatolic acids, whereas *X. caliginosa* lacks maculae, has a dark brown to black lower surface, and contains olivetoric acid. (*27*) *Xanthoparmelia cafferensis* (Essl.) O. Blanco *et al.* clusters (without support) with the similar *X. verrucella* (Essl.) O. Blanco *et al.*, which occurs in southern Africa and Australasia (Culberson *et al.* 1977). (*28*) *Xanthoparmelia glabrans* (Nyl.) O. Blanco *et al.* from southern Africa clusters separately from *X. glabrans* from Europe, South America and Australia (collapsed clades: Australian Clade C and *pulla* Clade). In contrast, *X. glabrans* clustered in an unsupported clade with *X. imitatrix* (Taylor) O. Blanco *et al.* from southern Africa. Both species are morphologically similar but *X. imitatrix* has a different chemistry (physodic acid and often trace amounts of 4-*O*-methylphysodic acid) (Esslinger 1977, 2000; Elix 1994).

Clade X: (*29*) *Xanthoparmelia xanthomelanella* Elix forms a monophyletic clade.

Clade XI: (*30*) *Xanthoparmelia perplexa* (Stizenb.) Hale forms a monophyletic clade.

Clade XII: (*31*) *Xanthoparmelia greytonensis* Hale and (*32*) *X. xanthomelaena* (Müll. Arg.) Hale cluster together but this relationship lacks support. Note that *X.* aff. *greytonensis* from South Africa (MAF-LICH 16210) is only distantly related to our *X. greytonensis* material. *Xanthoparmelia xanthomelaena* also shows differences among specimens from different continents. The southern African material does not cluster with material from Australia (MAF-LICH 16447).

Clade XIII: (*33*) *Xanthoparmelia waboomsbergensis* Elix is related to *X. tegeta* Elix & J. Johnst. However, *X. tegeta* is readily distinguished by its loosely adnate, pulvinate, dark yellowish green and larger thallus (6–9 cm), and contiguous to imbricate lobes (0.7–1.5 mm) (Elix *et al.* 1986; Hale 1990).

Clade XIV: (*34*) *Xanthoparmelia molliuscula* (Ach.) Hale forms a monophyletic clade. **Clade XV:** The southern African material identified here as (*35*) *X. psoromica* Hale is morphologically similar but differs in chemical constituents, with (*36*) *X. colorata* (Gyeln) Hale containing salazinic and norstictic acids, and *X. psoromica* containing psoromic acid. Both species are members of a group of species with the *schenckiana* pigment that also includes *X. colorata* and *X. schenckiana* (Müll. Arg.) Hale. In our analysis, *X. colorata* and *X. psoromica* cluster in the same clade, whereas (*37*) *X. schenckiana* is only distantly related.

Taxonomy

Xanthoparmelia nimisii Barcenas-Peña, Lumbsch & Grewe sp. nov.

MycoBank No.: MB 847480

Differs from *Xanthoparmelia annexa* by the presence of soredia and the broader lobes (5–6 mm). In addition, the new species forms a well-supported clade based on a dataset of ITS, mtSSU and nuLSU sequences.

Type: South Africa, Western Cape, Cape Winelands, Breede River DC, Klein Cedarberg, on sunny siliceous rock, 985 m alt., 32°55.4′S, 19°30.55′E, 24 September 2014, *V. Wirth* B 60 0198683 (B—holotype). GenBank Accession nos: OQ356389 (ITS) and OQ366463 (mtSSU).

(Figs 1 (Clade III (*8*)) & 2A)

Thallus foliose, tightly to loosely adnate, 4–5 cm diam., lobate; *lobes* subirregular, elongate, plane, separate, contiguous, 5–6 mm wide, not lobulate; *apices* subrotund, smooth, eciliate; *upper surface* yellow-green, smooth, shiny, epruinose and emaculate, not isidiate; *soralia* laminal and orbicular to irregular masses, soredia granular; *medulla* white, with continuous algal layer; *lower surface* black, plane, moderately rhizinate; *rhizines* black, simple, 0.3–0.4 mm long.

Apothecia not observed; *pycnidia* not observed.

Chemistry. Upper cortex K+ yellow, UV−; medulla K−, C+ deep red, KC+ red, P−. Atranorin and lecanoric acid.

Etymology. The new species is named in honour of Pier Luigi Nimis for his successful career devoted to the study of lichens.

Distribution and habitat. South Africa, on siliceous rocks.

Remarks. The new species resembles *X. annexa* because both species share the same chemistry. However, *X. annexa* is an isidiate species, it does not have soredia and has narrower lobes (0.7–3.5 mm) than the new species (5–6 mm), which is sorediate (Hale & Kurokawa 1964).

Additional specimen examined. **South Africa:** *Western Cape*: Klein Cedarberg, on shaded vertical cliff faces, siliceous rock, 985 m alt., 32°55′08″S, 19°30′26″E, 2014, *V. Wirth* 36287 (STU).

Xanthoparmelia pseudochalybaeizans Barcenas-Peña, Lumbsch & Grewe sp. nov.

MycoBank No.: MB 847482

Same chemistry and similar morphology to *Xanthoparmelia chalybaeizans*, but differs by not forming an imbricate thallus, and having a white medulla. Its distinction is supported by a phylogenetic study based on a concatenated dataset of ITS, mtSSU and nuLSU rDNA.

Type: South Africa, Western Cape, Overberg, 32 km NE of Bredasdorp, Renosterveld Nature Reserve, on rock, 190 m alt., 34°21.18′S, 20°19.05′E, 13 October 2015, *V. Wirth* RENO-2, B 60 0201783 (B—holotype). GenBank Accession nos: OQ356405 (ITS), OQ366468 (mtSSU) and OQ366517 (nuLSU).

(Figs 1 (Clade VII (*23*)) & 2B)

Thallus foliose, adnate, (1.8)3–7 cm diam.; *lobes* subirregular, elongate, plane, contiguous, 1–3 mm wide, not lobulate, apices rotund, smooth, eciliate; *upper surface* yellow-green, smooth, shiny, epruinose and emaculate, isidia and soredia lacking; *medulla* white, with continuous algal layer; *lower surface* brown, plane, moderately rhizinate; *rhizines* brown to dark brown, simple, 0.5–0.7 mm long.

Apothecia substipitate, with a brown to dark brown disc, not pruinose, (0.5)2–6 mm diam.; *spores* 10–12 × 5–7 µm.

Pycnidia common; *conidia* bifusiform, 5–6 × 0.5 µm.

Chemistry. Upper cortex K−, UV−; medulla K+ yellow to dark red, C−, KC−, P+ orange. Usnic, norstictic (trace), chalybaeizanic, salazinic, consalazinic acids, and an unknown substance (R_f 15/norstictic 30).

Etymology. The new species is named for its close similarity to *X. chalybaeizans.*

Distribution and habitat. South Africa, on siliceous rocks.

Remarks. This new species has the same chemistry (salazinic, consalazinic, norstictic (±trace), usnic and chalybaeizanic acids) and a similar morphology to *X. chalybaeizans* (Hale 1990). However, *X. chalybaeizans* has a thallus that is 4–8 cm diam., with contiguous to imbricate lobes, that are 1–3 mm wide, and a white to slightly yellow medulla. In contrast, *X. pseudochalybaeizans* has no imbricate lobes and a white medulla. Furthermore, the distinction of *X. chalybaeizans* and *X. pseudochalybaeizans* is supported by the phylogenetic study based on ITS, mtSSU and nuLSU rDNA sequence data.

Additional specimens examined. **South Africa:** *Western Cape*: Overberg, 32 km NE of Bredasdorp, Renosterveld Nature Reserve, on rock, 185 m alt., 34°21.25′S, 20°19.03′E, 2015, *V. Wirth* B 60 0201774 (B); *ibid.,* 190 m alt., 34°21.21′S, 20°19.017′E, *V. Wirth* B 60 0201772 (B).

Xanthoparmelia sipmaniana Barcenas-Peña, Lumbsch & Grewe sp. nov.

MycoBank No.: MB 847483

Morphologically and chemically similar to *X. hypoprotocetrarica* (Kurok. & Elix) Hale but differs by its phylogenetic relationships based on ITS, mtSSU and nuLSU rDNA sequence data. In addition, both differ in their geographical distribution (Australia vs South Africa).

Type: South Africa, Western Cape, Cape Winelands, Breede River DC, Klein Cedarberg, on sunny siliceous rock, 985 m alt., 32°55.4′S, 19°30.55′E, 24 September 2014, *V. Wirth* B 60 0198688 (B—holotype). GenBank Accession nos: OQ356383 (ITS) and OQ366502 (nuLSU).

(Figs 1 (Clade II (7)) & 2C)

Thallus foliose, adnate to loosely attached, 7–9 cm diam.; *lobes* subirregular, elongate, plane, imbricate, subascending, 1–3 mm wide, lobulated margins, apices rotund, smooth, eciliate; *upper surface* yellow-green, smooth, shiny, epruinose, effigurate maculate, isidia and soredia lacking; *medulla* white, with continuous algal layer; *lower surface* black, plane, sparsely rhizinate; *rhizines* black, simple to furcate, 0.5–0.7 mm long.

Apothecia substipitate, with a dark brown disc, not pruinose, 2–5 mm diam.; *spores* 8–11 × 4–6 μm.

Pycnidia common; *conidia* bifusiform, 5–6 × 0.5 μm.

Chemistry. Upper cortex K−, UV−; medulla K−, C−, KC−, P−. Usnic and hypoprotocetraric acids.

Etymology. The new species is named in honour of Harrie Sipman for his important contribution to lichenology.

Remarks. *Xanthoparmelia sipmaniana* and *X. hypoprotocetrarica* both share an identical morphology and chemistry and can be interpreted as cryptic species, as indicated by molecular data. The two species exhibit different distributional ranges, with *X. hypoprotocetrarica* occurring in Australia, and *X. sipmaniana* currently known only from South Africa (Kurokawa & Elix 1971; Hale 1974, 1990).

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