Fundación
Miguel Lillo
Tucumán
Argentina

Lilloa 59 (Suplemento): 77-88, Octubre 2022

Kavinia altoandina (Basidiomycota, Gomphales), a new species from the Andean Mountains of northern Chile

Kavinia altoandina (Basidiomycota, Gomphales) una nueva especie de ambientes altoandinos de Chile

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ABSTRACT

Kavinia altoandina is a new species from the Andean Mountains in northern Chile. It is characterized by a hydnoid hymenophore that is white to cream when young but olive green when mature, as well as by the cylindrical to fusiform, verrucose basidiospores, 7.5 11.8 × 3.3 4.5 μm. In addition, phylogenetic relationships inferred from internal transcribed spacer (ITS) sequences support *K. altoandina* as a new species related to *K. chacoserrana* from Argentina.

Keywords — Chilean mycobiota; corticioid fungi; hydnoid fungi; phylogeny; taxonomy.

RESUMEN

Se describe *Kavinia altoandina* como una nueva especie con base en datos morfológicos y evidencia molecular. La especie fue recolectada en ambientes andinos del norte de Chile, y se caracteriza morfológicamente por su himenóforo hidnoide, blanquecino cuando joven a verdoso cuando maduro. Microscópicamente se caracteriza por sus basidiosporas cilíndricas a fusiformes, 7.5 11.8 × 3.3 4.5 μm. Además de los datos morfológicos, las relaciones filogenéticas inferidas de las secuencias del

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➤ Ref. bibliográfica: Sandoval-Leiva, P.; Calle, A.; Robledo, G. 2022. *Kavinia altoandina* (Basidiomycota, Gomphales), a new species from the Andean Mountains of northern Chile. *Lilloa 59* (Suplemento): 77-88. doi: https://doi.org/10.30550/j.lil/2022.59.S/2022.08.17
➤ Recibido: 29 de junio 2022 – Aceptado: 17 de agosto 2022 – Publicado en línea: 18 de octubre 2022.
➤ URL de la revista: http://lilloa.lillo.org.ar

espaciador transcrito interno (ITS) respaldan a *K. altoandina* como una nueva especie relacionada con *K. chacoserrana.*

Keywords — Micobiota chilena; hongos corticioides; hongos hidnoides; filogenia; taxonomía.

INTRODUCTION

Kavinia Pilát is a corticioid genus characterized by resupinate, hydnoid basidiomes with a loose subiculum bearing hymenial aculei. Microscopically by a monomitic hyphal system with clamp connections, fusiform, cylindrical or subcylindrical basidiospores ornamented with cyanophilous warts. (Eriksson & Ryvarden, 1976; Boidin & Gilles, 2000; Bernicchia & Gorjón, 2010; Robledo & Urcelay, 2017). Phylogenetically, *Kavinia* belongs in the Lentariaceae in the Gomphales (Hosaka *et al*., 2006; Giachini *et al*., 2010). Within in the Lentariaceae, *Kavinia* and *Hydnocristella* (R.H. Petersen) are the only genera that develop resupinate basidiomes, but they are phylogenetically and morphologically distinct producing ornamented and smooth basidiospores, respectively (Larsson, 2007).

Five *Kavinia* species are currently recognized: *K. alboviridis* (Morgan) Gilb & Budington, *K. chacoserrana* Robledo & Urcelay from Argentina, *K. globispora* Natarajan & Koland. from India, *K. salmonea* Boidin & Gilles from Reunion, and *K. vivantii* Boidin & Gilles from Guadeloupe. Of these species, only *K. alboviridis* is widely distributed with numerous records from both hemispheres (Boidin & Gilles, 2000; Bernicchia & Gorjón, 2010; Doðan, 2009; Kout & Hajšmanová, 2015), but mainly in temperate regions (Eriksson & Ryvarden, 1976). In contrast, the other species are only known from their type locations (Natarajan & Kolandavelu, 1985; Boidin & Gilles, 2000; Robledo & Urcelay, 2017). New genetic evidence suggests that *K. alboviridis* encompasses multiple phylogenetic species (Kout & Hajšmanová, 2015; Robledo & Urcelay, 2017).

The mycobiota from northern Chile is poorly known, especially from the high-altitude environments in the Andes Mountain range. Only a few studies have reported on the fungi of this region (e.g., Sandoval-Leiva *et al*., 2017; Troncoso *et al*., 2020). During studies on the mycobiota in the Andes Mountain range of northern Chile, we collected specimens that resembled *K. alboviridis*. The specimens were found in shrublands that are exposed to extreme climatic conditions, such as high temperature and solar radiation during the summer and low temperatures in winter. Subsequent morphological and molecular analyses revealed that the specimens represented an undescribed species of *Kavinia*. We contribute to the knowledge of fungi from this unique environment of northern Chile by describing *Kavinia altoandina*, a new species based on morphology and phylogenic evidence of the ITS rDNA.

MATERIALS AND METHODS

Collections

Samples were collected and processed according to Rossman *et al.* (1998). Macroscopic descriptions are based on fresh material according to Lodge *et al*. (2004). Microscopic features are described from material mounted in KOH (5%), Congo Red (1%), Melzer's reagent and Cotton Blue. Basidiospore statistics include x_m, the arithmetic mean of the spore length by spore width (± SD) for n basidiospores spores measured; Q, the ratio of spore length to spore width, expressed as a range for all basidiospores measured; Q_m, the mean of all Q values (± SD). Microscopic measurements were presented as format of (min–) 5th–95th percentile (–max). Voucher specimens have been deposited in the Herbarium of the Museo Nacional de Historia Natural de Santiago, Chile (SGO). Herbarium acronyms follow Thiers (2022).

DNA extraction and sequencing

DNA was extracted from specimens using the Extract N Amp Plant kit (Sigma-Aldrich, St. Louis, Missouri) and the ITS region was amplified and sequenced using primers ITS1F and ITS4 following White *et al*. (1990). For PCR of ITS and 28S, we used Taq Polymerase with Standard Taq Buffer (New England Biolabs, Ipswich, Massachusetts) following the manufacturer's protocols.

Phylogenetic analyses

ITS sequences generated in the present work were combined with those retrieved from GenBank (NCBI) to construct a dataset of 55 taxa. Scientific names and GenBank accession numbers of sequences are listed in Table 1. *Clavaria delphus* Donk was selected as outgroup (Hosaka *et al*., 2006; Giachini *et al*., 2010; Robledo & Urcelay, 2017).

Phylogenetic analyses were performed following Robledo *et al*. (2021). ITS sequences were aligned using MAFFT 7 (Katoh & Standley, 2013) using the G-INS-i alignment method. Alignments were manually inspected and adjusted using MEGA 6 (Tamura *et al*., 2013). ModelFinder (Kalyaanamoorthy *et al*., 2017) as implemented in the IQ-Tree software (Nguyen *et al*., 2015) was used to estimate the best-fit partitioning strategy and the best-fit model of nucleotide evolution for the dataset using three data blocks (ITS1; 5.8S; ITS2). Models were restricted for those implemented in MrBayes 3.2 (Ronquist *et al*., 2012). Bayesian inference (BI) and maximum likelihood (ML) phylogenetic analyses were applied to the dataset using the partition scheme and evolutionary models defined by ModelFinder. BI was performed following Robledo *et al*. (2020, 2021) in the CIPRES science gateway (Miller *et al*., 2010; http://www.phylo.org/). Maximum likelihood searches were conducted with IQ-Tree. The analysis initially involved 100 ML searches, each one starting from one randomized stepwise addition parsimony tree. Branch supports were calculated using the UFBoot (ultrafast bootstrap approximation) (Hoang *et al*., 2018) implemented

Table 1 (part 1 of 2). List of taxa, specimens and sequences used in the phylogenetic analysis. New sequences generated in this study are in boldface. T= Type specimen.

Tabla 1 (parte 1 de 2). Lista de taxones, especímenes y secuencias usadas en los análisis filogenéticos. Las nuevas secuencias generadas en este estudio están en negrita. T = espécimen tipo.

Taxón Voucher reference – Origin	Genbank / Putoff Accesion Nº – ITS
Clavariadelphus occidentalis	
OSC 114281, USA	EU846242
OSC 104664, USA	EU669308
H21536, Tunisia	KU973835
Clavariadelphus pistillaris	
3894, Canada, Quebec	KM248917
K(M):163658, United Kingdom, England	MZ159395
Clavariadelphus truncatus	
SMI278, Canada, British Columbia	HQ650728
UBC:F21557, Canada, British Columbia	MZ836048
UBC:F21603, Canada, British Columbia	MZ836049
Lentaria bambusina	
MHHNU 7302, Liuyang, Hunan, China	KU324496
MHHNU 6794, Sangzhi, Hunan, China	KU870448
Lentaria byssisseda	
TENN61159, USA, TN	FJ596785
RAS454, USA: Tennessee	MT196983
Lentaria gassypina	
UNAM:FCME27625, Mexico: Veracruz,	MK253199
UNAM:FCME27626, Mexico: Veracruz,	MK253200
Lentaria. aff. micheneri	
MA-Fungi 48116, Equatorial Guinea	AJ292289
Lentaria patouillardii	
MHHNU 7829, China: Baihaba, Xinjiang	KU324498
HMJAU:26892, China: Inner Mongolia	KU870449
MA-Fungi 48032, Spain	AJ292290
HMAS 290111	MK966659
Lentaria pinicola	
MushroomObserver.org/355909, USA, California	MW871706
MushroomObserver.org/193851, USA, California	MG979400
Lentaria surculus	
MHHNU 8721 Xishuangbanna, Yunnan, China	KU870450
FHMU 880 Dinghushan, Guangdong, China	KU870451
Lentaria uncispora	
MHHNU7707, China, Gongga mountain, Sichuan	KU324497
Lentaria variabilis	
UNAM:FCME21524, Mexico: Campeche	MK253189
UNAM:FCME19862, Mexico: Campeche	MK253184
Hydnocristella himantia	
CFMR:DLL2011-079, USA: central Wisconsin	KJ140598
2543, Russia	KY769580
CFMR:DLL2011-131, USA: central Wisconsin	KJ140634
Yuan5598, China	KP323407
MA-Fungi 48091, SPAIN	AJ292291
Hydnocristella latihypha	
He 20120911-3 China, Jiuzhaigou Nature Reserve	KM489521
He 20120914-4 China, Jiuzhaigou Nature Reserve	KM489522
Kavinia aff. alboviridis	
UC2022816, USA, AK	KP814530

Table 1 (part 2 of 2).

Tabla 1 (parte 2 de 2).

Taxón Voucher reference – Origin	Genbank / Putoff Accesion Nº – ITS
Kavinia alboviridis	
KM82737, United Kingdom: England	GQ981505
KM141510, United Kingdom: England	GQ981506
K(M)257290, United Kingdom: Wales, Anglesey	MZ159756
Kavinia chacoserrana	
Robledo 2516, Argentina, Córdoba (T)	NR164256
Kavinia altoandina	
PSL2302, Chile (T)	**OP022196**
PSL3014, Chile	**OP022197**
Kavinia sp	
G4620, Estonia	UDB0288438
G4761, Estonia	UDB0445985
G4278, Estonia	UDB0512813
G4646, Estonia	UDB0428073
G2558, Estonia	UDB0437262
G4177, Estonia	UDB0484646
G4705, Estonia	UDB0657677
G4762, Estonia	UDB0455445
G4459, Estonia	UDB0238831
Ramaricium polyporoideum	
TENN:056036, Argentina: Tierra del Fuego	KY352646
TENN:065654, USA: North Carolina	MF992160

in IQ-TREE with 1000 replications. A node was considered strongly supported with BPP ≥ 0.95 or BS ≥ 95% (Hyde *et al*., 2013; Minh *et al*., 2020). Hereafter, support values are presented as BPP/BS in the text.

RESULTS

Phylogenetic analyses

The final dataset included 55 terminals and 688 characters, of which 299 were parsimony informative and 369 were constant. The partitions and evolutionary models selected were K2P+I (5.8S) and SYM+I+G (ITS1 and ITS2). Bayesian and ML analyses resulted in similar topologies; the Bayesian consensus tree is presented in Figure 1. The final topology resolved *Kavinia* specimens from high altitude environments in northern Chile as a well-supported, independent lineage within the genus *Kavinia*. There was strong bootstrap support for a sister relationship between the Chilean *Kavinia* specimens and the Argentinian species *K. chacoserrana* (1/99, Figure 1).

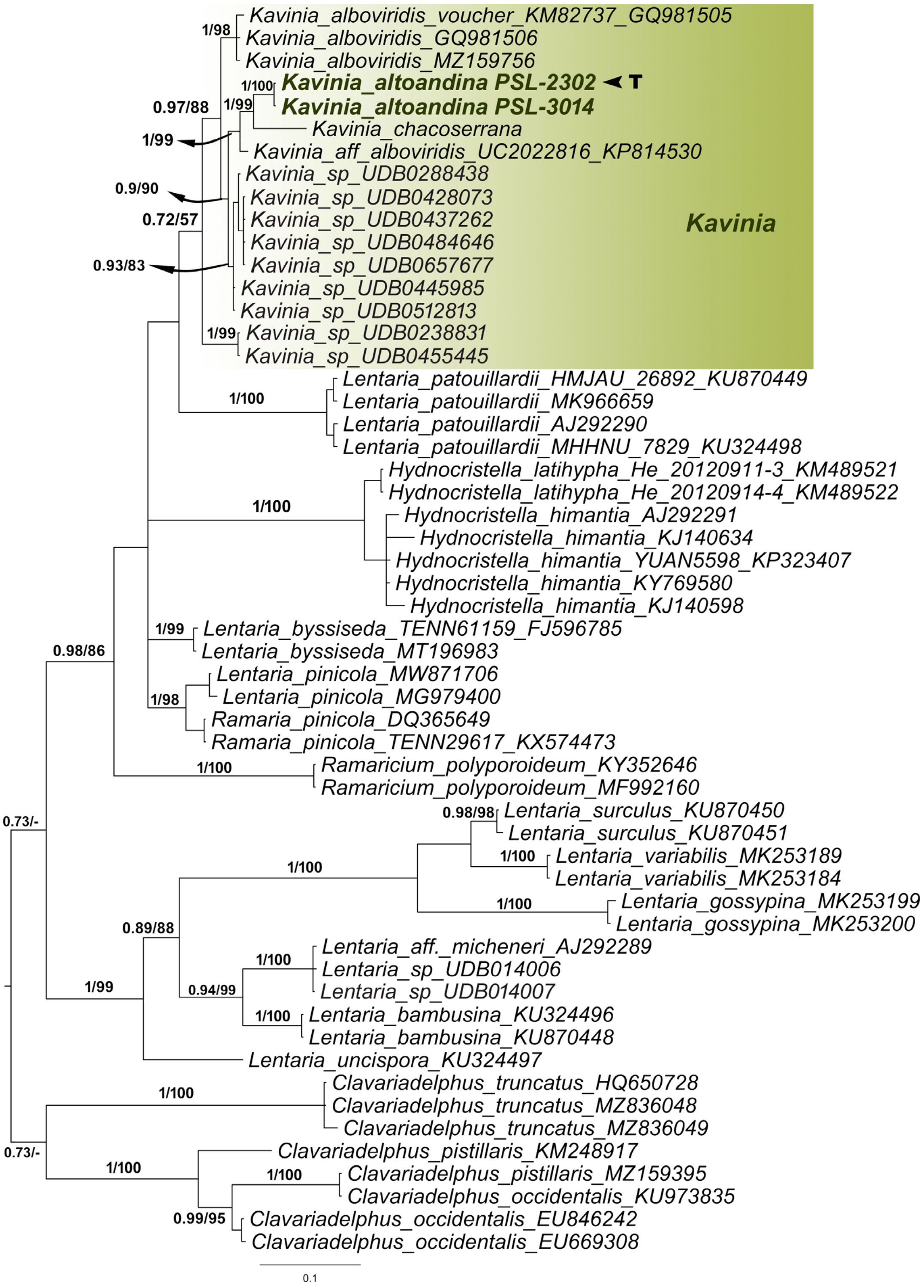

Fig. 1. Strict consensus tree from Bayesian inference (BI) based on ITS sequence data. Branch support values are shown as BPP/BS, Bayesian posterior probability above 0.7 and Bootstrap values above 70%. ➤ **T** = type specimen.

Fig. 1. Árbol de consenso estricto de Inferencia Bayesiana (BI) con base en secuencias ITS. Los valores de soporte de las ramas se muestran como BPP/BS, probabilidad posterior bayesiana superior a 0,7 y valores de Bootstrap superiores al 70 %. ➤ T = espécimen tipo.

Taxonomy

Kavinia altoandina Sandoval-Leiva & Calle ***sp. nov.*** Figs. 2-3
Mycobank: MB844867

Diagnosis.— Hymenophore hydnoid, dark olive-green; Subiculum whitish to cream, arachnoid to cottony; basidospores verrucose, fusiform to cylindrical, 7.5 11.8 × 3.3 4.5 μm; ocurring on dead and partially buried wood of *Adesmia hystrix*, restricted to high Andean environments of the Atacama region in Chile.

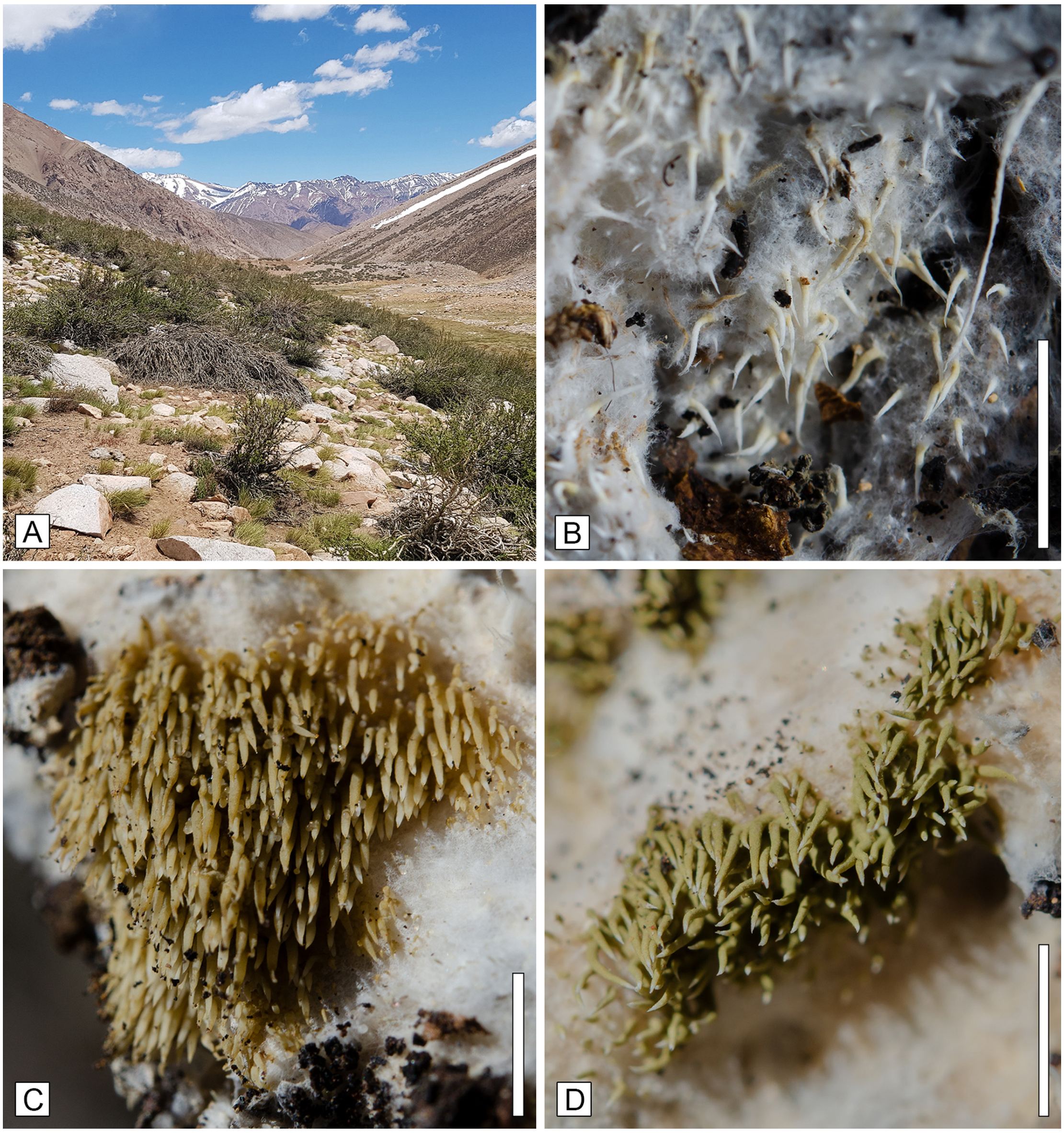

Fig. 2. *Kavinia altoandina*. A) Location of the holotype of *K. altoandina* in a scrubland of *Adesmia hystrix* in the Andes Mountains of Chile. B-D) Macromorpholgy of *Kavinia altoandina* (P. Sandoval-Leiva 2302, holotype). B) Developing aculei arising from arachnoid subiculum. C & D) General view of hymenophore *in situ*. D) Clustered aculei covered by mature basidiospores. Scale bars B-D = 5 mm.

Fig. 2. *Kavinia altoandina*. A) Holotipo de *K. altoandina* en un matorral de *Adesmia hystrix* en la Cordillera de los Andes de Chile. B-D) Macromorfología de *Kavinia altoandina* (P. Sandoval-Leiva 2302, holotipo). B) Dientes en desarrollo surgiendo del subículo aracnoideo. C y D) Vista general del himenóforo *in situ*. D) Agujas agrupadas cubiertas por basidiosporas maduras. Escala B-D = 5 mm.

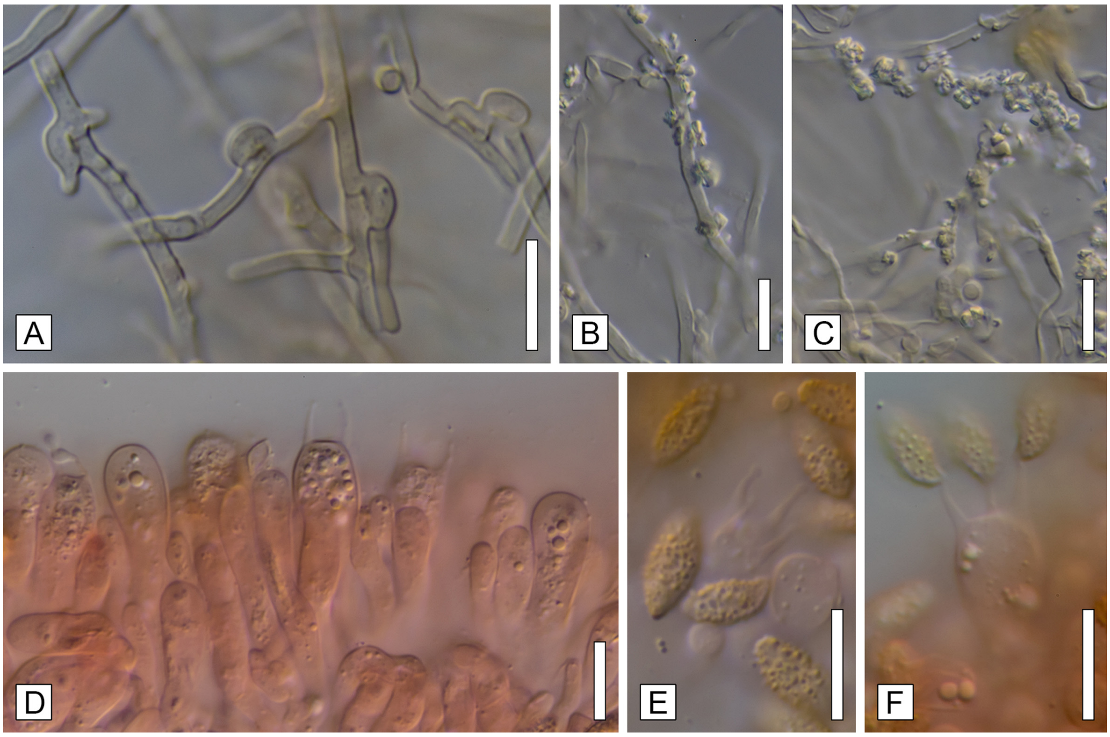

Fig. 3. Microscopic features of *Kavinia altoandina*. A) Loosely interwoven generative hyphae with ampuliform clamps from the subiculum. B-C) Crystalline incrustations in subiculum. D) Close-up of hymenium. E-F) Detail of basidiospores and basidia. Scale bars = 10 µm.

Fig. 3. Características microscópicas de *Kavinia altoandina*. A) Hifas generativas del subículo laxamente entrelazadas con fíbulas ampuliformes. B-C) Incrustaciones cristalinas en el subículo. D) Detalle del himenio. E-F) Basidiosporas y basidios en detalle. Escala = 10 µm.

Typification.— CHILE. Región de Atacama: Province Huasco, Municipality Alto del Carmen, hillsides from quebrada Los Barriales, 29°15’51.8” S, 70°5’2.9” W, 3.633 m asl, on fallen and buried dead wood of *Adesmia hystrix* in a scrubland of *A. hystrix*, 16-XI-2017, *P. Sandoval-Leiva 2302* (holotype, SGO). GenBank OP022196 (ITS).

Etymology.— The epithet “altoandino” is a phytogeographical term that refers to high altitude environment in the Andes Mountains and its vegetation.

Basidiomata annual, resupinate, loosely attached, up to 23 × 7 cm, arising from several points at the substrate and later often confluent. **Hymenophore** hydnoid, aculei narrowly conical up to 3 mm long and up 0.5 mm diam at the base, white to cream when immature (Fig 2C), dark olive green at maturity (Fig 2B, D), smooth, subceraceous, scattered and clustered; apex sterile, subulate, paler. **Subiculum** whitish to cream, loose, arachnoid to cottony, becoming more compact with age, thin, sterile. **Margin** distinct, byssoid or fibrillose, white to cream, sterile, with white, sparsely branched rhizomorphs.

Hyphal system monomitic. Generative hyphae clamped, clamps often ampuliform, hyaline and thin- to slightly thick-walled, commonly up to 5 µm diam, occasionally swollen up to 9 µm. Hyphae regular and parallelly arranged in the trama of aculei, loosely interwoven in the subiculum. Crystalline incrustations abundant in subiculum and rhizomorphs, scarce in aculei.

Cystidia absent. **Basidia** (23.7–)29.5 –39.2(–42.3) × (5.3–)6–8.6(–8.8) μm (x = 33.9 × 7.2 μm), clavate, with a basal clamp, hyaline, commonly with guttules, 4-sterigmata up to 7 μm long. **Basidiospores** fusiform to cylindrical in side view or ellipsoid in dorsi-ventral view, with a distinctly supra-apicular concavity and a rounded to tapering apex, occasionally blunt or truncate, (6.9)7.5 11.8(13.4) × (3.1)3.3 4.5(4.9) [x_m = 8.97 ± 1.20 × 3.82 ± 0.34 μm, Q =(1.83)2.3 2.4 (3.82), Q_m = 2.35 ± 0.30, n = 200], slightly thick-walled, pale yellow to olivaceous yellow, verrucose, with cyanophilous ornamentations, IKI-, occasionally grouped in tetrads.

Distribution.— Known from the Andean Mountains in the Atacama region of Chile.

Specimen studied.— CHILE. Región de Atacama: Province Huasco, Municipality Alto del Carmen, hillsides from quebrada Los Barriales, 29°15’10.4” S, 70°5’42.6” W, 3.534 m asl, on fallen and buried dead wood of *Adesmia hystrix* in a scrubland of *A. hystrix*, 17-XI-2017, *P. Sandoval-Leiva 3014* (SGO). GenBank OP022197 (ITS).

Additional specimen studied.— *Kavinia chacoserrana*: ARGENTINA, Córdoba, Dpto. San Alberto, Los Hornillos, on dead fallen branch of *Lithraea molleoides*, 31°54’0.8”S, 64°58”0.6”W, 1280 m asl, 28-IV-2012, *Robledo 2516* (holotype CORD). GenBank MF377531 (ITS).

DISCUSSION

Kavinia altoandina is most similar to *K. alboviridis* that also has an olivaceous green, hydnoid hymenophore at maturity but with slightly shorter basidiospores. Its closest phylogenetic relative, however, is *K. chacoserrana* that differs by its white to pale hymenophore. In addition, current genetic evidence suggests that *K. alboviridis* is a species complex involving several taxa (Kout & Hajšmanová, 2015; Robledo & Urcelay, 2017). Further molecular and morphological studies are needed to resolve the taxonomic status of this species and its synonyms. The broad distribution of *K. alboviridis* records from both hemispheres is unusual and may represent several different species with restricted distributions.

Although morphologically, *K. altoandina* is similar to *K. alboviridis* the former ecological niche is unique amongst *Kavinia* species because it is restricted to high altitude Andean environments of the Atacama region in Chile. *Kavinia altoandina* has adapted to the extreme temperature variation and high solar radiation present in high elevation areas over 3000 m asl by growing on dead, partially buried wood of *Adesmia hystrix*, thus, obtaining some protection from the inclement climate.

ACKNOWLEDGEMENTS

We thank Francisco Kuhar (IMBIV-CONICET-UNC) who sequenced the fungal specimens, which was possible by a grant from the US National Science Foundation (DEB-1354802 to Matthew Smith). Also, authors kindly acknowledge Dr. Leho Tedersoo (Institute of Ecology and Earth Sciences, University of Tartu, Estonia) for the permission of use *Kavinia* sequences available at Plutoof. Also, we extend our thanks to Dr. Matthew Smith for his valuable comments and suggestions on the manuscript. Finally, the first author of this article, would like to thank Dr. Mario Rajchenberg for all of his selfless support during his early years of mycological studies.

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