



Article

Doi 10.5943/mycosphe/8/6/3

Copyright © Guizhou Academy of Agricultural Sciences

***Kavinia chacoserrana* sp. nov. (Gomphales, Basidiomycota): a new species from South America based on morphological and molecular data**

Robledo GL^{1,2*} and Urcelay C¹

¹Instituto Multidisciplinario de Biología Vegetal, Universidad Nacional de Córdoba, C.C.495, 5000, Córdoba, Argentina.

²Fundación FungiCosmos, Av. General Paz 154, 4°, Of. 4, CP 5000, Córdoba, Argentina.

Robledo GL, Urcelay C 2017 – *Kavinia chacoserrana* sp. nov. (Gomphales, Basidiomycota): a new species from South America based on morphological and molecular data. Mycosphe 8(8), 1028–1034, Doi 10.5943/mycosphe/8/6/3

Abstract

Kavinia chacoserrana is described as a new species based on morphological data and molecular evidence. The species is characterized by its white to pale yellowish hydroid hymenophore and cylindrical to fusiform basidiospores measured as 10–12 × 3–4 μm. Phylogenetic analysis provide evidence suggesting that, as currently accepted, *Kavinia alboviridis* is a species complex.

Key words – Argentina – Chaco – corticioid fungi – neotropical fungi – phylogeny – taxonomy

Introduction

Kavinia Pilát is a small genus belonging to the Gomphales (Giachini et al. 2010) typified by *K. sajanensis* (Pilát) Pilát (= *Kavinia alboviridis* (Morgan) Gilb. & Budington). Up to now includes four species characterized by annual resupinate and hydroid basidiocarps, a monomitic hyphal structure with clamp connections, and oblong, subcylindrical or fusiform and non-amyloid basidiospores bearing cyanophilous warts (Eriksson & Ryvar den 1976, Boidin & Gilles 2000).

Three species are known from only from their type locations, all in the tropics: *Kavinia globispora* Natarajan & Koland. from southern India (Natarajan & Kolandavelu 1985), *K. salmonea* Boidin & Gilles from the Reunion Island in the pacific (Boidin & Gilles 2000), and *K. vivantii* Boidin & Gilles in Marie Galante Island in the Caribe (Boidin & Gilles 2000). In notorious contrast, the fourth species of *Kavinia*, *K. alboviridis*, is widely distributed in both hemispheres, mainly in temperate regions such as North America (e.g. Gilbertson & Budington 1970), Europe (e.g. Eriksson & Ryvar den 1976, Boidin & Gilles 2000, Kout & Hajšmanová 2015), Turkey (Doğan 2009), central China (Maekawa & Zang 2002, Dai 2011), Northern India (Rattan 1977) and southern South America (Greslebin 2002), but also in some tropical regions such as Ethiopia in Africa (Bitew & Ryvar den 2011). Despite its wide distribution, *K. alboviridis* is not a common species and it has been suggested that more than one species is involved under this name (Kout & Hajšmanová 2015).

Here we describe a new species from central Argentina, subtropical Chaquean region in South America based on morphological and molecular evidence, and provide phylogenetic evidence that, as currently accepted, *Kavinia alboviridis* is a complex of species.

Materials & Methods

Morphological studies

The studied specimens were deposited in the herbarium CORD. Herbarium acronyms follow Thiers (2017). Basidiomata sections were examined in Melzer's reagent, KOH 3-5% plus phloxine 1%. Microscopic measurements of basidiospores ($n = 40$) were made in Melzer's reagent, 5% of the measurements were excluded from each end and are given in parentheses. The following abbreviations are used for basidiospores measurements: \bar{X} = arithmetic average, Q = ratio length/width, \bar{Q} = arithmetic average of Q .

DNA extraction and sequencing

DNA was extracted from dry basidiomata tissue using the CTAB method described in Ferreira-Lopes et al. (2016). Primer pairs ITS8-F / ITS6-R (Dentinger et al. 2010) to amplify ITS rDNA. PCR conditions were as described in Gómez-Montoya et al. (2017). Sequencing reactions were performed with the same primers pairs.

Phylogenetic analyses

Sequences of nrITS of Gomphales were selected following reference phylogenetic works (Giachini et al. 2010, Chen et al. 2015), retrieved from GenBank (NCBI) and combined to construct a dataset matrix (Table 1). The dataset was aligned using MAFFT v.7 (Kato & Standley 2013), under the G-INS-1 or Q-INS-i criteria. The alignment obtained, was then manually inspected using MEGA v.6 (Tamura et al. 2013), and then deposited at TreeBase (Submission ID 21247). The best-fit model of nucleotide evolution to the dataset was selected by AIC (Akaike Information Criterion) using jModelTest2 v.1.6 (Darriba et al. 2012). Bayesian Inference (BI) was performed using MrBayes 3.1.2 (Ronquist et al. 2011) with two independent runs, each one beginning from random trees with four simultaneous independent chains, performing 1×10^7 replications, sampling one tree every 1×10^3 th generation. The first 2500 sampled trees were discarded as burn-in and checked by the convergence criterion (frequencies of average standard deviation of split < 0.01), while the remaining ones were used to reconstruct a 50% majority-rule consensus tree and calculate Bayesian posterior probabilities (BPP) of the clades. Nodes showing $BPP \geq 0.95$ was considered to be strongly supported, while those with values $BPP \geq 0.85$ were considered moderately supported.

Table 1 List of taxa, specimens and sequences used in the phylogenetic analysis. **O** = outgroup.

<i>Species</i>	<i>Voucher reference - Origin</i>	<i>ITS Genbank Accesion N°</i>
<i>Ramaria suecica</i> (O)		
	OSC 115933-USA: OR, Linn County	KP658148
	OSC 134634-USA: OR	JX310417
<i>Clavariadelphus occidentalis</i>		
	OSC 114281, USA	EU846242
	OSC 104664, USA	EU669308
	H21536, Tunisia	KU973835
<i>Clavariadelphus pistillaris</i>		
	3894, Canada, Quebec	KM248917
<i>Clavariadelphus truncatus</i>		
	SMI278, Canada, British Columbia	HQ650728
<i>Lentaria bambusina</i>		
	MHHNU 7302, Liuyang, Hunan, China	KU324496
	MHHNU 6794, Sangzhi, Hunan, China	KU870448
<i>Lentaria byssisseda</i>		

TENN61159, USA, TN	FJ596785
<i>Lentaria. aff. micheneri</i>	
MA-Fungi 48116 Equatorial Guinea	AJ292289
<i>Lentaria patouillardii</i>	
MHHNU 7829, China: Baihaba, Xinjiang	KU324498
HMJAU:26892, China: Inner Mongolia	KU870449
MA-Fungi 48032, Spain	AJ292290
<i>Lentaria surculus</i>	
PDD 95856, Mid Canterbury, New Zealand	HQ533048
MHHNU 8721 Xishuangbanna, Yunnan, China	KU870450
FHMU 880 Dinghushan, Guangdong, China	KU870451
<i>Hydnocristella himantia</i>	
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
<i>Hydnocristella latihpha</i>	
He 20120911-3 China, Jiuzhaigou Nature Reserve	KM489521
He 20120914-4 China, Jiuzhaigou Nature Reserve	KM489522
<i>Kavinia alboviridis</i>	
KM82737, England	GQ981505
KM141510, England	GQ981506
UC2022816, USA: AK	KP814530
<i>Kavinia chacoserrana</i>	
Robledo 2516, Argentina	MF377531
<i>Ramaria rubella</i>	
OSC 115946, USA	EU669317
OSC 140659, USA	JX310405
AFTOL-ID 724	NR119527
<i>Ramaria pinicola</i>	
TENN 29617, USA: ID, Upper Priest River County	KX574473
139.1, USA	DQ365649
<i>Ramaria sp.</i>	
OSC 65995, USA	DQ365600
<i>Ramaria stricta</i>	
OUC97191, Canada?	DQ367910

Results

Phylogenetic analyses

The final nrITS dataset included sequences from 35 specimens, with 621 characters including gaps, of which 270 are conserved and 286 parsimony informative. The evolutionary model selected for nrITS dataset was GTR+I+G.

Our analysis (Fig. 1) recovered *Kavinia* as a well-supported clade (BS = 1) where *Kavinia chacoserrana* emerged a distinct lineage. *Kavinia chacoserrana* grouped with a specimen identified as *Kavinia aff. alboviridis* in a moderately supported clade (BS = 0.87). Two specimens identified as *K. alboviridis*, the type species of *Kavinia*, appear as a third taxon integrating the clade.

Kavinia chacoserrana Robledo & Urcelay, sp. nov.

Mycobank: MB821874; Facesoffungi number: FoF03450

Figs 2–5

Type – 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 a.s.l., 28 Apr 2012 *Robledo 2516* (CORD holotype, ITS MF377531).

Etymology – Referring to the ecoregion where it was collected, Chaco Serrano.

Basidiomata seasonal, resupinate, loosely attached, arising from the substrate in several surrounding points and then confluent with development. Hymenophore hydroid, with spines up to 10 mm long, about 3 mm diam at the base slimming gradually to end in a sharp apex, white when immature, pale yellowish at maturity. Margin sterile, whitish, myceliar, with rizhomorphic strands. Subiculum whitish, loose, extremely thin. Hyphal system monomitic. Generative hyphae with clamps, ampuliform clamps occasionally observed, hyaline and thin-walled to very slightly thick-walled, up to 5 µm diam; hyphae parallel ordered and compact in the trama of spines, loosely interwoven in the subiculum. Cystidia absent. Basidia clavate, 30–40 long, 5–6 (–12) µm in the apex with four sterigmata and 2–3 µm at the base where present a basal clamp. Hymenium not reaching the apex of the spine which is sterile. Basidiospores cylindrical to fusiform in side view, with a distinctly supra-apicular concavity and a tapering to rounded apex (Fig. 5); in dorsi-ventral view cylindrical to subcylindrical and then ovoid to slightly ellipsoid (Fig. 5), (9.0–)10.0–12.0(–13.0) × (2.5–)3.0–4.0(–4.0) µm, (\bar{X} = 10.7 × 3.3 µm), Q = 2.5–4.2, (\bar{Q} = 3.3), slightly thick-walled, hyaline to pale yellowish, warted, IKI–, CB–; commonly grouped in tetrads (Fig. 5 black arrows).

Known distribution – So far known only from the type locality.

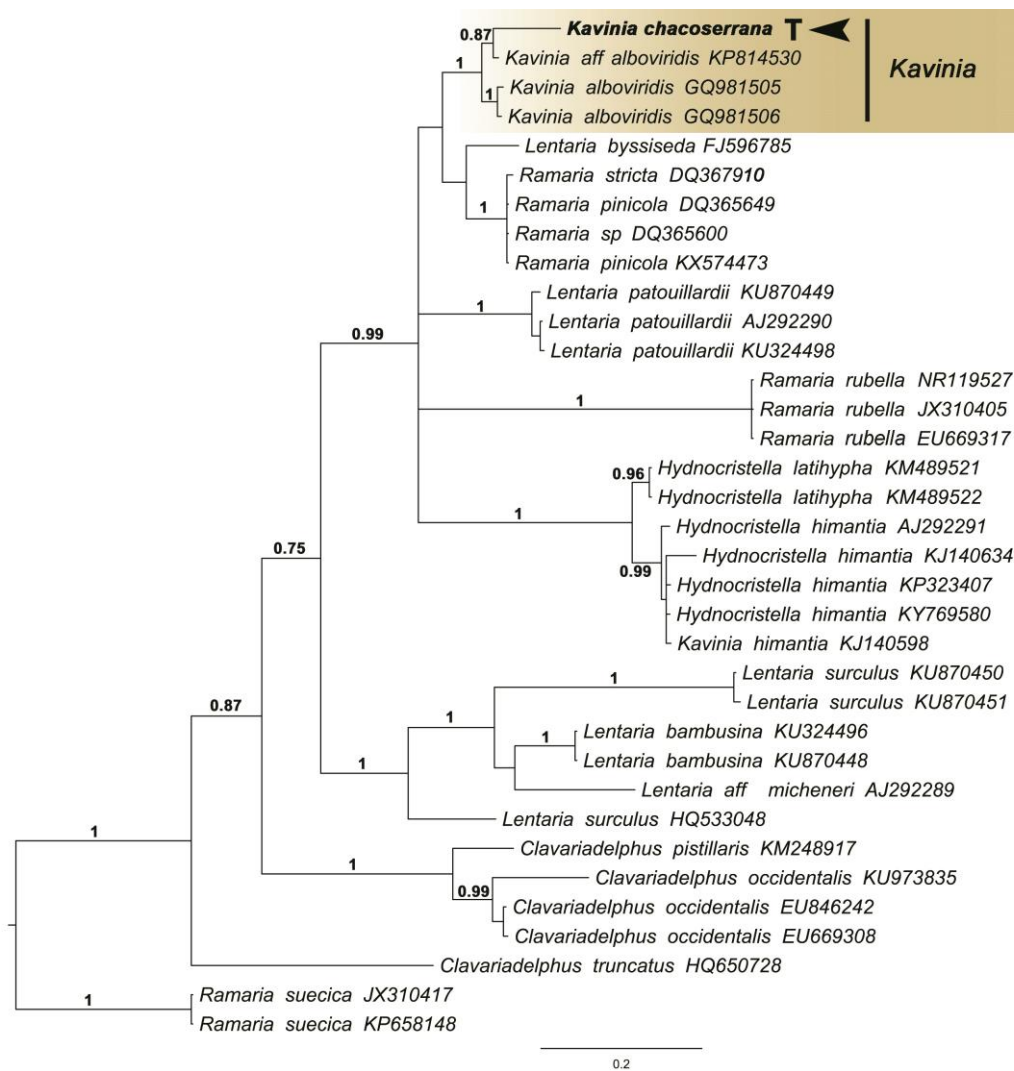
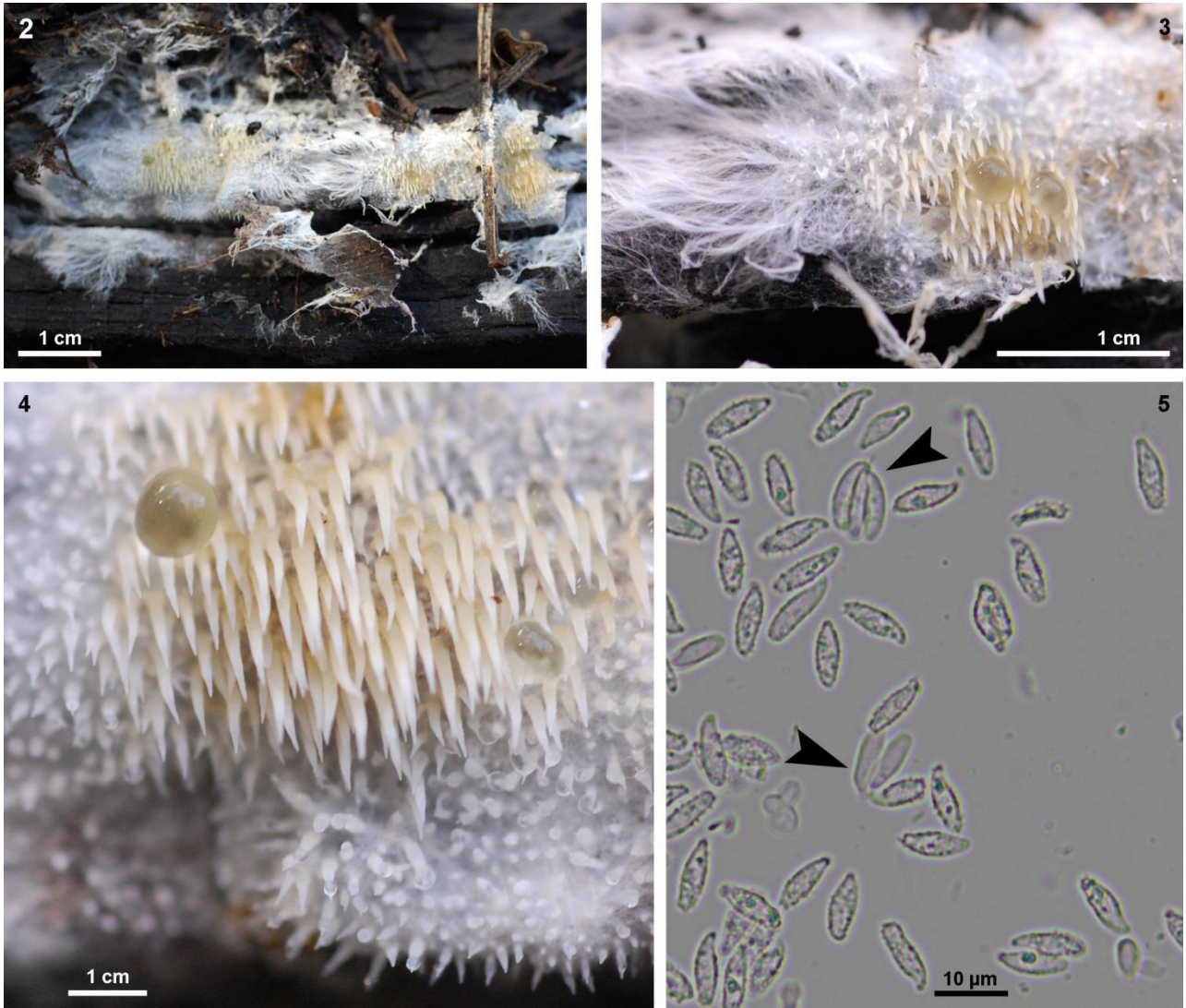


Figure 1 – Strict consensus tree from Bayesian inference of the combined ITS dataset. T◀= type specimen.



Figures 2–5 – *Kavinia chacoserrana* (Robledo 2516 CORD Holotype). 2–4 Macromorphological characters. 2 General view *in situ*. 3 Close-up of margin showing rhizomorphs. 4 Detail of the spiny hymenophore. 5 Basidiospores. Black arrows (◄) indicate tetrads of basidiospores. These pictures are copyright of Gerardo Robledo.

Annotated Key to *Kavinia* and *Hydnocristella* species

- | | |
|--|-------------------------|
| 1. Basidiospores smooth, CB–..... | 2 <i>Hydnocristella</i> |
| 1'. Basidiospores verrucose, CB + | 3 <i>Kavinia</i> |
| 2. Basidiospores 8–10 µm long | <i>H. hymantia</i> |
| 2'. Basidiospores 10–12 µm long | <i>H. latihypha</i> |
| 3. Basidiospores fusiform | 4 |
| 3'. Basidiospores globose to ellipsoid | 5 |
| 4. Basidiospores 8–9 × 3.5–4.5 µm; hymenophore typically olive green | <i>K. albo-viridis</i> |
| 4'. Basidiospores 10–12 × 3–4 µm; hymenophore white to pale yellowish..... | <i>K. chacoserrana</i> |
| 5. Basidiospores globose to subglobose | <i>K. globispora</i> |
| 5'. Basidiospores ellipsoid or subamygdalyform | 6 |
| 6. Basidiospores ellipsoid | <i>K. salmonea</i> |
| 6'. Basidiospores subamygdalyform | <i>K. vivanii</i> |

Discussion

Macroscopically *Kavinia chacoserrana* differs from the other species in the genus by developing resupinate basidiomata with a white to pale yellowish hydroid hymenophore. Microscopically is distinguished by cylindrical to fusiform basidiospores. Morphologically, *K. chacoserrana* strongly resembles *K. alboviridis*, the only other species of the genus that has fusiform to subfusiform basidiospores, but the hymenophore is olive green in *K. alboviridis*, whereas is white to pale yellowish in *K. chacoserrana*.

Phylogenetically *Kavinia chacoserrana* is related to *K. alboviridis*, the only other species with sequences available. Our analysis showed that *K. alboviridis* seem to encompass at least two species. Two specimens coming from Europe (England) confirm a phylogenetic species. Another specimen, identified at Genbank as *K. aff. alboviridis* coming from North America, is closer related to *K. chacoserrana*. This evidence, support the idea suggested by Kout & Hajšmanová (2015) that more than one species is involved under the name.

Kavinia bourdotii (Bres.) Pilat, a species described from France with basidiospores $6-8 \times 2.75-3.5$ (Bresadola 1908) and currently under synonymy of *K. alboviridis*, is a name that could be applied to European specimens. The type specimen of *K. alboviridis* comes from Miami Valley, Ohio, USA (Morgan 1887) and is the prevailing name for specimens of North America. Further molecular evidence is desirable to resolve the taxonomical status of *K. alboviridis* and its synonyms.

Acknowledgements

Authors wish to acknowledge the assistance of the Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET) and the Universidad Nacional de Córdoba, both of which support facilities used in this project. Financial support was provided by FONCYT (PICT 1676) and Fondo IBOL Conicet to C. Urcelay; and by FONCYT (PICT-2015-0830) to G. Robledo. Agencia Cordoba Ambiente gave permissions to work in protected areas. Authors kindly acknowledged A. Bringas, curator of CORD, for providing the collections necessary for this study; Idea Wild for their support with technical equipment; and Dr. E.M. Grassi, G. Bertone, L. Caeiro and D. Franchi for their technical support

References

- Bitew A, Ryvarde L. 2011 – Preliminary check-list of wood inhabiting Basidiomycetes of Ethiopia. *Synopsis Fungorum* 29, 11–21.
- Boidin J, Gilles G. 2000 – Le genre *Kavinia* Pilat (Basidiomycotina). *Cryptogamie Mycologie* 21, 139–143.
- Bresadola G. 1908 – Fungi aliquot Gallici novi vel minus cogniti. *Annales Mycologici* 6, 37–47.
- Chen J, Shen L, Cui B. 2015 – Morphological characters and molecular data reveal a new species of *Hydnocristella* (Gomphales, Basidiomycota) from southwestern China. *Nova Hedwigia* 101, 139–146.
- Dai YC. 2011 – A revised checklist of corticioid and hydroid fungi in China for 2010. *Mycoscience* 52, 69–79.
- Darriba D, Taboada GL, Doallo R, Posada D. 2012 – jModelTest 2: more models, new heuristics and parallel computing. *Nature Methods* 9, 8–772.
- Dentinger BTM, Margaritescu S, Moncalvo JM. 2010 – Rapid and reliable high-throughput methods of DNA extraction for use in barcoding and molecular systematics of mushrooms. *Molecular Ecology Resources* 10, 628–633.
- Doğan HH. 2009 – Two new lignicolous fungi additions to turkey mycota. *SDU Journal of Science* 4, 5–39.
- Eriksson J, Ryvarde L. 1976 – The Corticiaceae of North Europe 4: *Hyphodermella* – *Mycoacia*. *Fungiflora*, Oslo, pp. 549–886.

- Ferreira-Lopes V, Robledo GL, Reck MA, Góes-Neto A., Drechsler-Santos E.R. 2016 – *Phylloporia spathulata sensu stricto* and two new South American stipitate species of *Phylloporia* (Hymenochaetaceae). *Phytotaxa* 257, 133–148.
- Giachini AJ, Hosaka K, Noura ER, Spatafora JW, Trappe JM. 2010 – Phylogenetic relationships of the Gomphales based on nuc- 25S-rDNA, mit-12S-rDNA and mit-ATPg-DNA combined sequences. *Fungal Biology* 114, 224–234.
- Gilbertson RL, Budington AB. 1970 – New records of Arizona wood-rotting fungi. *Journal of the Arizona Academy of Sciences* 6, 91–97.
- Gómez-Montoya N, Drechsler-Santos ER, Ferreira Lopes V, Tomšovský M et al. 2017 – New insights on *Trametopsis* Tomšovský (Polyporales Gäum) based on phylogenetic evidences and morphological analyses of neotropical species. *Phytotaxa* (In press).
- Greslebin A. 2002 – Fungi, Basidiomycota, Aphyllophorales: Coniophoraceae, Corticiaceae, Gomphaceae, Hymenochaetaceae, Lachnocladiaceae, Stereaceae, Thelephoraceae. Tulasnellales: Tulasnellaceae. *Flora Criptogámica de Tierra del Fuego* 11(4). pp. 1–212.
- Katoh K, Standley DM. 2013 – MAFFT. Multiple sequence alignment software 7: improvements in performance and usability. *Molecular Biology and Evolution* 30, 772–780.
- Kout J, Hajšmanová P. 2015 – *Kavinia alboviridis* in the Czech Republic. *Czech Mycology* 67, 59–67.
- Maekawa N, Yang ZL, Zang M. 2002 – Corticioid fungi (Basidiomycetes) collected in Sichuan Province, China. *Mycotaxon* 83, 81–95.
- Morgan AP. 1887 – The mycologic flora of the Miami Valley, Ohio. *Journal of the Cincinnati Society of Natural History* 10, 7–18.
- Natarajan K; Kolandavelu K. 1985 – *Kavinia globispora* sp. nov. *Transactions of the British Mycological Society* 84, 362–363.
- Rattan S. 1977 – The resupinate Aphyllophorales of the North-Western Himalayas. *Bibliotheca Mycologica* 60. Ed. J. Cramer, Vaduz. pp. 1–427.
- Ronquist F, Teslenko M, Van der Mark P, Ayres DL et al. 2011 – MRBAYES 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. *Systematic Biology* 61, 539–542.
- Tamura K, Stecher G, Peterson D, Filipski A, Kumar S. 2013 – MEGA 6: Molecular Evolutionary Genetics Analysis Version 6.0. *Molecular Biology and Evolution* 30: 2725–2729.
- Thiers B. 2017 – (continuously updated). Index Herbariorum: a global directory of public herbaria and associated staff. New York Garden's Virtual Herbarium. In: New York Garden's Virtual Herbarium. Available from <http://sweetgum.nybg.org/ih/> (accessed 24 Jun 2017).