



Article

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## *Xylaria spinulosa* sp. nov. and *X. atosphaerica* from southern China

Li QR<sup>1,2</sup>, Liu LL<sup>2</sup>, Zhang X<sup>2</sup>, Shen XC<sup>2</sup> and Kang JC<sup>1\*</sup>

<sup>1</sup>The Engineering and Research Center for Southwest Bio-Pharmaceutical Resources of National Education Ministry of China, Guizhou University Guiyang 550025, People's Republic of China

<sup>2</sup>The High Educational Key Laboratory of Guizhou Province for Natural Medicinal Pharmacology and Druggability, Guizhou Medical University, Huaxi University Town, Guian new district 550025, Guizhou, People's Republic of China

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### Abstract

Two species of *Xylaria* collected from southern China are reported. *Xylaria spinulosa* sp. nov. is introduced as a new species based on morphology and sequence data analysis. *Xylaria spinulosa* differs from other species in the genus mainly by its long spines covering the surface of the stroma. *Xylaria atosphaerica* is a new record for China. Descriptions and illustrations for both species are provided in this paper.

**Key words** – morphology – new species – phylogeny – taxonomy – Xylariales

### Introduction

*Xylaria* belongs in the subclass *Xylariomycetidae* in the order Xylariales, a group which is presently undergoing considerable revision (Daranagama et al. 2015, 2016). It is not presently clear how many families will be accepted in the genus, but *Xylaria* Hill ex Schrank is the largest genus in the family with species having been recorded in most countries worldwide (Læssøe 1987, 1999, Ju & Hsieh 2007, Ju et al. 2009, Liu et al. 2015, Hongsanan et al. 2017). Currently, nearly 300 estimated species are thought to belong in *Xylaria* (Kirk et al. 2008). *Xylaria* differs from other genera in Xylariaceae by producing upright, cylindrical to clavate, multi-peritheciate stromata (Maharachchikumbura et al. 2016). Most *Xylaria* species produce stromata on decayed dicotyledonous wood (Hsieh et al. 2010).

Species of *Xylaria* are difficult to identify and classify especially as stroma of a given species often varies greatly in colour, size and sometimes in general shape (Whalley 1996). Species have mainly been resolved on the basis of morphological characteristics. These characteristics are not suitable for differentiating closely related species of *Xylaria*, due to lack of differentiating characteristics. The genus *Xylaria* has great variation in morphology and may be polyphyletic. Few phylogenetic studies have been conducted to infer the relationships of the taxa of *Xylaria* and there is a need for a comprehensive monograph. ITS sequence data have been used to infer phylogenetic relationships among species of *Xylaria* by Lee et al. (2000). Hsieh et al. (2010) analyzed 114 species of *Xylariaceae*, based on  $\alpha$ -actin,  $\beta$ -tubulin and rpb2 sequence data and stated that *Xylaria* is a paraphyletic genus. Hsieh et al. (2010) made an important step to resolve closely related species of *Xylaria*.

Although there has been a high interest in *Xylaria* over the last 30 years (Smith et al. 2003, Tang et al. 2009, Daranagama et al. 2015, 2016, Hashemi et al. 2015, Karun & Sridhar 2015, Srihanant et al. 2015, Kim et al. 2016), these have generally not incorporated molecular data and

have rarely looked at type species. There have been very few reports on the genus from the Chinese mainland (Chou 1935, Tai 1979, Abe & Liu 1995, Ma et al. 2011, Huang et al. 2014a, b). Therefore, the diversity of *Xylaria* in China is still underrepresented and needs further investigation (Ma et al. 2011). In the present paper, we have collected *Xylaria* species from China and introduce *Xylaria spinulosa* sp. nov. and provide a description of *X. atosphaerica* which is a new record for China.

## Materials & Methods

### Isolation and morphology

The fungal materials were collected in the forest from Hainan and Guizhou provinces in China. The methodology used for morphological examination of fungi followed that used by Stadler et al. (2004). Materials were mounted in water and Melzer's iodine reagent for examination. Asci and ascospores were examined by light microscopy (BX41, Olympus). Cultures were obtained by placing tissue of freshly collected stromata on Oatmeal agar (Ju et al. 2009). Total DNA extraction and sequencing of ITS rDNA,  $\alpha$ -actin gene (act) and RNA polymerase II second largest subunit genes (rpb2) follow Ju & Hsieh (2007). For PCR amplification of  $\beta$ -tubulin gene (tub2), primers T1/T2, Bt2a/Bt2b were used (Ju & Hsieh 2007). The herbarium and living culture are deposited in the Collection of Guizhou University (GZUCC) and Kunming Institute of Botany (KUN), Chinese Academy of Sciences.

### Phylogenetic analyses

All sequences used in this paper were gained from recent publications and are listed in Table 1. The alignments are available in TreeBASE ([www.treebase.org/treebase-web/home.html](http://www.treebase.org/treebase-web/home.html)) under ID15112 for ITS alignment and ID 20686 for act-rpb2-tub2 alignment.  $\alpha$ -actin,  $\beta$ -tubulin and rpb2 sequence data were assembled using the alignment program BioEdit (Hall 1999) and ClustalX (Thompson et al. 1997). Alignment was manually adjusted to achieve the maximum alignment and to minimize gaps. Maximum parsimony was applied to the act-tub2-rpb2 dataset. All characters were assessed as independent, unordered, and equally weighted. Gaps were treated as missing characters. *Biscogniauxia arima* was used as the outgroup taxon (Hsieh et al. 2010). Maximum parsimony analysis was performed using PAUP (Phylogenetic Analysis Using Parsimony) v.4.0b10 (Felsenstein 1985, Swofford 2002).

## Results

Using ITS rDNA sequences, our initial BLAST searches suggested that our sequences were most closely related to those of the taxa in *Xylaria polymorpha* complex (Hsieh et al. 2010). Act, Rpb2 and tub2 genes sequences were used to identify those species.

### Phylogenetic analyses

A phylogenetic study using three combined loci (Rpb2, act and tub2) was conducted. All characters and gaps have equal weight. A total of 47 taxa were included in the analysis. Total length of the alignment had 1892 characters, in which 144 of those characters were variable, 935 characters were constant, 813 parsimony-informative characters.

The result of the phylogenetic analysis is shown in Fig. 1. The appearance of *Xylaria spinulosa* (100% BS) was reasonably well-supported as sister clade of *X. haemorrhoidalis* Berk. & Broome. The closest relatives to *X. spinulosa*, clustered basal to this subclade, were *X. scruposa* (Fr.: Fr.) Fr., *X. atosphaerica* (Cooke & Masee) Callan & J. D. Rogers, *X. polymorpha* (Pers.: Fr.) Grev., *X. cf. glebulosa* (Ces.) Y.-M. Ju & J. D. Rogers, *X. ophiopoda* Sacc. *X. schweinitzii* Berk. & M. A. Curtis, *X. globosa* (Spreng. ex Fr.: Fr.) Mont. and the earliest diverging lineage is represented by *Xylaria enterogena* (Mont.) Fr. and *X. telfairii* (Berk.) Fr. supported by the bootstrap analysis (100% BS). *Xylaria atosphaerica* GZUCC14028 and *X. atosphaerica* 91111214 HAST clustered at a short branch with high bootstrap support (100%

**Table 1** Strains used in phylogenetic analyses and their corresponding GenBank accession numbers.

Taxon	Origin and strains	GenBank accession number			References
		Rpb2	$\alpha$ -actin	$\beta$ -tubulin	
<i>Amphirosellinia fushanensis</i>	Taiwan, 91111209 HAST	GQ848339	GQ452360	GQ495950	Ju et al. 2004
<i>A. nigrospora</i>	Taiwan, 91092308 HAST	GQ848340	GQ452361	GQ495951	Ju et al. 2004
<i>Astrocystis bambusae</i>	Taiwan, 89021904 HAST	GQ844836	GQ449239	GQ495942	Hsieh et al. 2010
<i>As. mirabilis</i>	Taiwan, 94070803 HAST	GQ844835	GQ449238	GQ495941	Hsieh et al. 2010
<i>As. sublimbata</i>	Taiwan, 89032207 HAST	GQ844834	GQ449236	GQ495940	Hsieh et al. 2010
<i>Biscogniauxia arima</i>	Mexico, YMJ 122	GQ304736	AY951784	AY951672	Ju et al. 1998; Hsieh et al. 2005
<i>Discoxylaria myrmecophila</i>	Mexico, 169 HAST	GQ844819	GQ438747	GQ487710	Rogers et al. 1995
<i>Stilbohypoxyton elaeicola</i>	Taiwan, 94082615 HAST	GQ844827	GQ438754	GQ495933	Hsieh et al. 2010
<i>S. quisquiliarum</i>	French Guiana, 91111209 HAST	GQ853020	EF025590	EF025605	Rogers & Ju, 1997; Ju et al. 2007
<i>S. quisquiliarum</i>	Taiwan, YMJ 172	GQ853021	EF025591	EF025606	Ju et al. 2007
<i>Xylaria allantoidea</i>	Taiwan, 94042903 HAST	GQ848356	GQ452377	GQ502692	Hsieh et al. 2010
<i>X. apoda</i>	Taiwan, 90080804 HAST	GQ844823	GQ438751	GQ495930	Hsieh et al. 2010
<i>X. atosphaerica</i>	Taiwan, 91111214 HAST	GQ848342	GQ452363	GQ495953	Hsieh et al. 2010
<i>X. badia</i>	Taiwan, 95070101 HAST	GQ844833	GQ449235	GQ495939	Hsieh et al. 2010
<i>X. berteri</i>	Taiwan, YMJ 90112623	GQ848362	AY951874	AY951763	Hsieh et al. 2005
<i>X. castorea</i>	New Zealand, PDD 47417	GQ853018	GQ455447	GQ502703	Hsieh et al. 2010
<i>X. cf. castorea</i>	Taiwan, 91092303 HAST	GQ853019	GQ455448	GQ502704	Hsieh et al. 2010
<i>X. cf. glebulosa</i>	French West Indies, 431 HAST	GQ848345	GQ452366	GQ495956	Hsieh et al. 2010
<i>X. cf. heliscus</i>	Taiwan, 88113010 HAST	GQ848355	GQ452376	GQ502691	Hsieh et al. 2010
<i>X. crozonensis</i>	France, 398 HAST	GQ848361	GQ455441	GQ502697	Hsieh et al. 2010
<i>X. cubensis</i>	Papua New Guinea, 860 JDR	GQ853017	GQ455446	GQ502702	Gucht, 1995
<i>X. culleniae</i>	Thailand, 189 JDR	GQ844829	GQ438756	GQ495935	Hsieh et al. 2010
<i>X. curta</i>	French West Indies, 494 HAST	GQ844831	GQ449233	GQ495937	Hsieh et al. 2010
<i>X. digitata</i>	Ukraine, 919 HAST	GQ848338	GQ449245	GQ495949	Hsieh et al. 2010
<i>X. enterogena</i>	French Guiana, 785 HAST	GQ848349	GQ452370	GQ502685	Hsieh et al. 2010
<i>X. feejeensis</i>	Taiwan, 92092013 HAST	GQ848336	GQ449243	GQ495947	Hsieh et al. 2010
<i>X. feejeensis</i>	Thailand, 180 JDR	GQ848335	GQ449242	GQ495946	Hsieh et al. 2010
<i>X. frustulosa</i>	Taiwan, 92092010 HAST	GQ844838	GQ449240	GQ495944	Hsieh et al. 2010

**Table 1** Strains used in phylogenetic analyses and their corresponding GenBank accession numbers.

Taxon	Origin and strains	GenBank accession number			References
		Rpb2	$\alpha$ -actin	$\beta$ -tubulin	
<i>X. globosa</i>	French West Indies, 775 HAST	GQ848348	GQ452369	GQ502684	Hsieh et al. 2010
<i>X. haemorrhoidalis</i>	Taiwan, 89041207 HAST	GQ848347	GQ452368	GQ502683	Hsieh et al. 2010
<i>X. ianthinovelutina</i>	French West Indies, 553 HAST	GQ844828	GQ438755	GQ495934	Hsieh et al. 2010
<i>X. intracolorata</i>	Taiwan, 90080402 HAST	GQ502690	GQ452375	GQ502690	Hsieh et al. 2010
<i>X. juruensis</i>	Taiwan, 92042501 HAST	GQ844825	GQ438753	GQ495932	Hsieh et al. 2010
<i>X. laevis</i>	French West Indies, 419 HAST	GQ848359	GQ455439	GQ502695	Hsieh et al. 2010
<i>X. luteostromata</i> var. <i>macrospora</i>	French West Indies, 508 HAST	GQ848352	GQ452373	GQ502688	Hsieh et al. 2010
<i>X. ophiopoda</i>	Taiwan, 93082805 HAST	GQ848344	GQ452365	GQ495955	Hsieh et al. 2010
<i>X. oxyacanthae</i>	USA, 93082805 HAST	GQ844820	GQ438748	GQ495927	Hsieh et al. 2010
<i>X. palmicola</i>	New Zealand, 604 PDD	GQ844822	GQ438750	GQ495929	Hsieh et al. 2010
<i>X. phyllocharis</i>	French West Indies, 528 HAST	GQ844832	GQ449234	GQ495938	Hsieh et al. 2010
<i>X. plebeja</i>	Taiwan, 91122401 HAST	GQ848353	GQ452374	GQ502689	Hsieh et al. 2010
<i>X. polymorpha</i>	USA, 1012 JDR	GQ848343	GQ452364	GQ495954	Hsieh et al. 2010
<i>X. regalis</i>	Taiwan, 92072001 HAST	GQ848357	GQ452378	GQ502693	Hsieh et al. 2010
<i>X. schweinitzii</i>	Taiwan, 92092023 HAST	GQ848346	GQ452367	GQ495957	Hsieh et al. 2010
<i>X. scruposa</i>	French West Indies, 497 HAST	GQ848341	GQ452362	GQ495952	Hsieh et al. 2010
<i>X. telfairii</i>	French West Indies, 421 HAST	GQ848350	GQ452371	GQ502686	Hsieh et al. 2010
<i>X. spinulosa</i>	Hainan, China, GZUCC13016	KM236098	KM236097	KM236099	This study
<i>X. atrosphaerica</i>	Guizhou, China, GZUCC14028	KY677915	KY677916	KY677917	This study

**JDR:** Herbarium of Jack D. Rogers; **HAST:** Herbarium, Research Center for Biodiversity, Academia Sinica, Taipei; **YMJ:** Herbarium of Yu-Min Ju; **PDD:** Landcare Research

## Taxonomy

*Xylaria spinulosa* Q.R. Li & J.C. Kang, *sp. nov.*

(Figs 2, 3)

MycoBank – MB513099; Facesoffungi number – FoF 03180

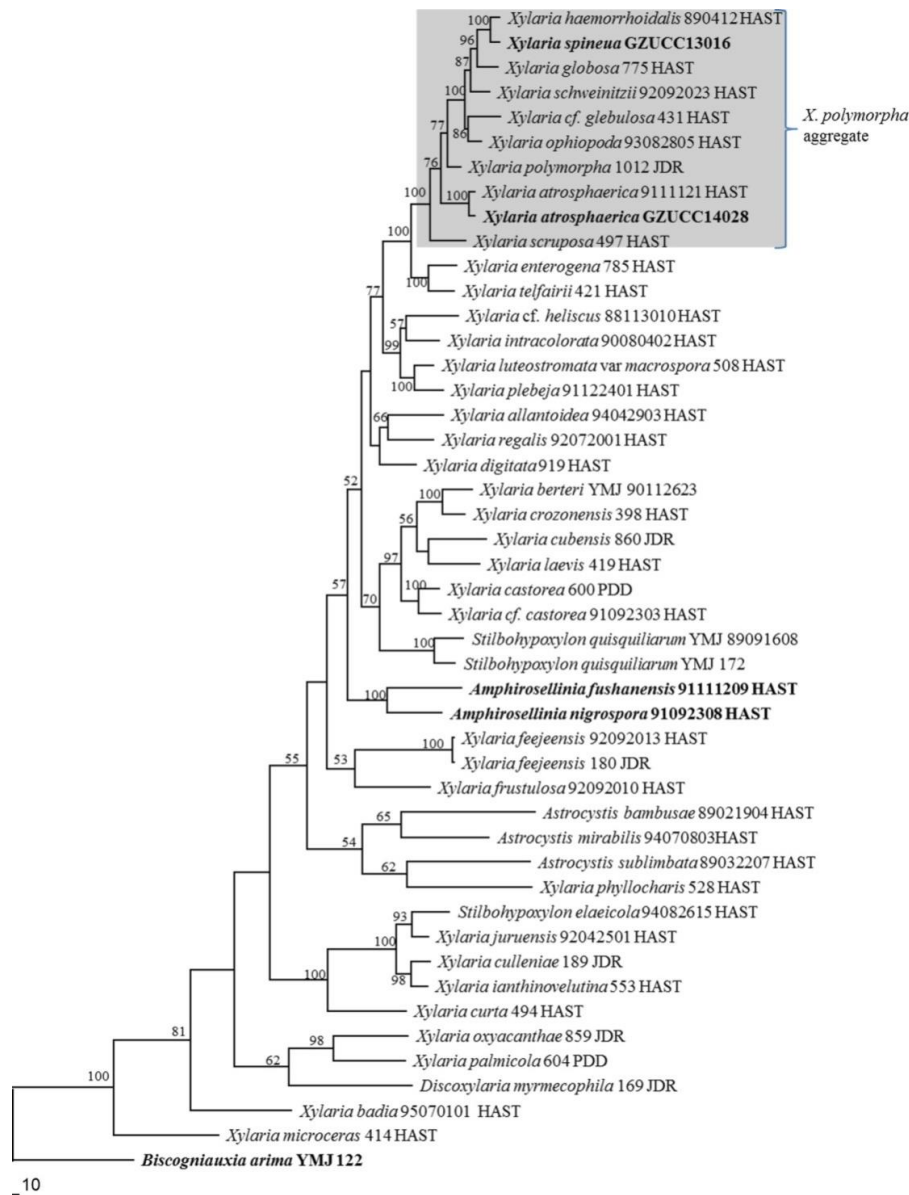
Etymology – in reference to the long thorns covering the stromatal surface.

Holotype – GZUH13016

*Saprobic* on dead tree trunk, forming on the host surface. **Sexual morph:** *Stromata* upright, usually solitary, unbranched, cylindrical or clavate, fertile at apex, texture soft, internally white, whole stromata up to 1.8–2.5 cm long  $\times$  0.3–0.5 cm broad, 0.5–1 cm long at stipes. Surface of stromata black, covered with long soft hairs. Stalk well defined and easy to distinguish. *Perithecia* 0.3–0.5 mm diam., spherical, embedded, closely arranged. Ostioles inconspicuous, not clear. *Asci* 80–214  $\times$  8–12  $\mu$ m (157  $\times$  10.2  $\mu$ m, n=20), unitunicate, 8-spored, cylindrical, long-stipitate, the spore-bearing part 60–170  $\mu$ m long. *Apical ring* 8.5–11.5  $\mu$ m high  $\times$  5–6  $\mu$ m broad, blue in Melzer's reagent, urn-shaped, 8.5–11.5  $\mu$ m high  $\times$  5–6  $\mu$ m broad. *Ascospores* 19–23  $\times$  6.5–8.5  $\mu$ m (21.3  $\times$  7.6  $\mu$ m, n=30), dark brown to black, unicellular, ellipsoid to inequilateral, with broadly

rounded ends, smooth-walled. Germ slit half spore-length, oblique to sigmoid, lacking sheath and appendage. **Asexual morph:** Undetermined.

Culture characteristics – Colonies on OA (Fig. 3) cover a 9-cm plate in 3–4 weeks. Mycelia white at first, velvety, soon becoming grey and finally become to black and developing a secondary, aerial mycelium, reverse of cultures a little black.



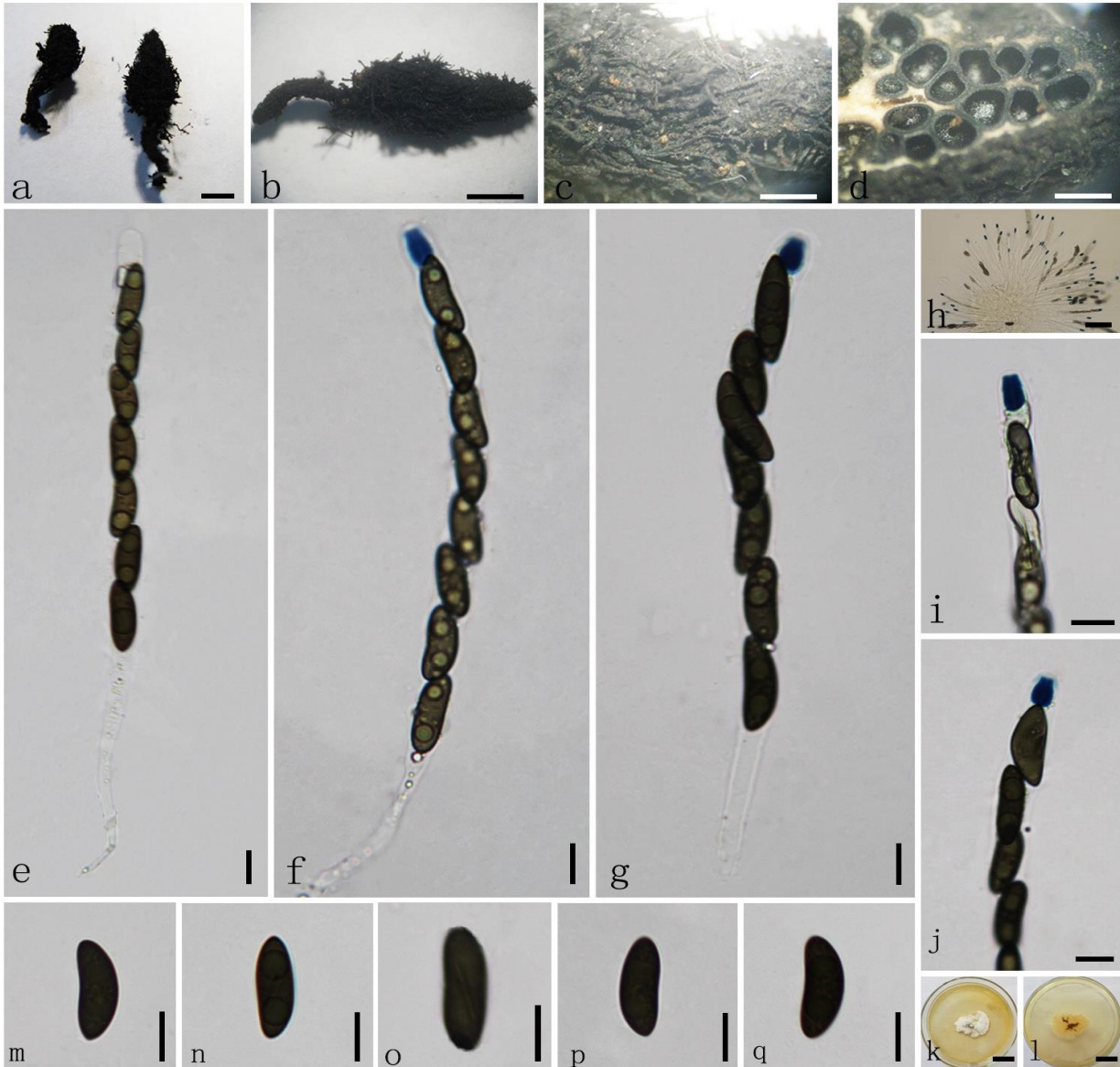
**Fig. 1** – MP tree inferred from the analysis of act, rpb2 and tub2 genes sequences. CI=0.319, RI=0.481, RC=0.154, HI=0.681. Bootstrap support values based on 1000 replicates are indicated (above 50%) at the branches at nodes. Sequences labelled in bold were type and our cultures. The tree was rooted to *Biscogniauxia arima* YMJ 122.

No pigments were observed. Stromata arising after 3 weeks of incubation, cylindrical, unbranched, up to 3 cm high and 2 mm diam.

Material examined – CHINA, Hainan Province, Wuzhishan City, Wuzhishan Nature Reserve, on deadwood of unknown plant, March 2013, Q.R. Li, WZS3 (GZUH 13016, holotype; HKAS 99544, isotype); ex-type living culture, GZUCC 13016.

*Xylaria atrosphaerica* (Cooke & Masee) Callan & J.D. Rogers, Mycotaxon 36 (2): 349 (1990).  
(Fig. 4) MycoBank MB 127393

*Saprobic* on dead tree trunk, forming on the host surface. **Sexual morph:** Stromata semiglobular or irregularly globose, pulvinate, 0.5–1.5 mm high × 1.5–3 mm diam., with flattened or slightly convex top, grey dark to black, internally white. Surface cracked into small plates and perithecial mounds inconspicuous.



**Fig. 2** – *Xylaria spinulosa* (GZUH13016, holotype). **a–c.** Stromata. **d.** Perithecia. **e–h.** Asci. **i, j.** Ascus apical apparatus (stained in Melzer’s reagent). **m–q.** Ascospore. **k, l.** Culture on PDA. Scale bars: a,b = 3 mm, c = 1 mm, d = 500  $\mu$ m, e–g = 10  $\mu$ m, h = 50  $\mu$ m, i–q = 10  $\mu$ m, k, l = 20 mm.

*Perithecia* 0.2–0.5 mm diam., completely immersed, sphaerical. *Ostioles* inconspicuous. *Asci* 142–215 × 12.5–18.5  $\mu$ m (188 × 15.5  $\mu$ m, n=30), unitunicate, 8-spored, cylindrical, long-stipitate, the spore-bearing part 120–170  $\mu$ m long. *Apical ring* bluing in Melzer’s iodine reagent, urn-shaped, 7.5–9  $\mu$ m high × 5–6.5  $\mu$ m broad. *Ascospores* 18.5–24 × 6.5–9.5  $\mu$ m (22.5 × 8  $\mu$ m, n=30), dark brown to black, unicellular, ellipsoid-inequilateral or crescent to navicular, with ends slightly pinched, smooth, with oblique to spiral germ slit, nearly 1/2 spore-length, lacking sheath and appendage. **Asexual morph:** Undetermined.

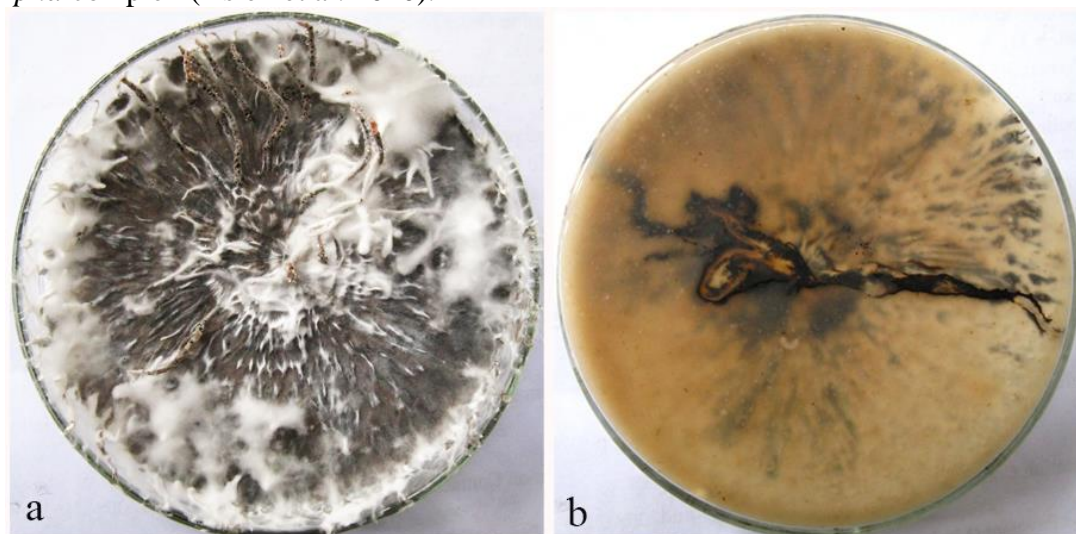
**Habitat/Distribution** – Known from Guiana, Indonesia and China.

**Material examined** – CHINA. Guizhou Province, Tongren City, Fanjingshan Nature Reserve, on deadwood of unknown plant, July 2014, Q.R. Li, FJS 19 (GZUH14028, HKAS 99545);

living culture, GZUCC14028.

## Discussion

Phylogenetic analysis (Fig. 1) showed that *X. spinulosa* clustered with species in the *X. polymorpha* complex (Hsieh et al. 2010).



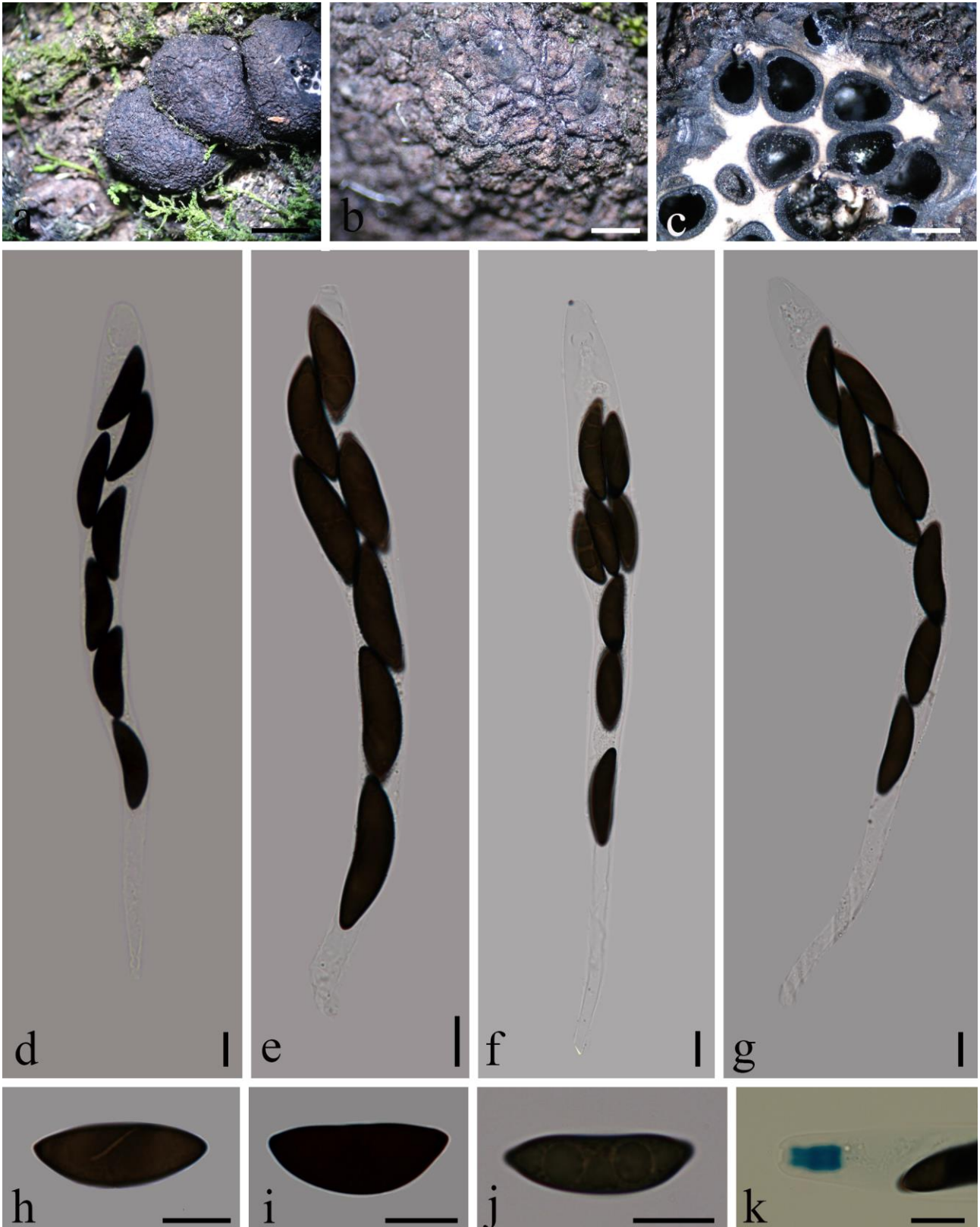
**Fig. 3** – Culture of *Xylaria spinulosa* on OA after 4 weeks. a. Culture from above. b. Culture from below.

Taxa within the *X. polymorpha* complex formed a monophyletic group with high bootstrap support. The species were discriminated from the most common known representatives of *Xylaria*. *Xylaria spinulosa* is most closely related to *X. haemorrhoidalis* Berk. & Broome according to the best-scoring maximum parsimony tree (Fig. 1). Morphologically, *X. haemorrhoidalis* Berk. & Broome has subglobose stromata, and stromatal surface cracked into fine scales without long thorns. *Xylaria spinulosa* has upright, stipitate, woody to leathery stromata. Ascomata of *X. spinulosa* are embedded immediately beneath the surface. Species of *X. polymorpha* complex have a stromatal surface cracked into fine scales and 20–30  $\mu\text{m}$  long ascospores (Ju et al. 2009). *Xylaria spinulosa*, however, differs from other species of the *X. polymorpha* complex in having long thorns on the surface of clavate stromata (Hsieh et al. 2010). Ascospores with half spore-length long germ slit from *X. spinulosa* also separates from other species in the *X. polymorpha* complex which are characterized by bearing a less than spore length germ slit (Rogers and Callan 1986).

The asexual morph of *Penzigia atosphaerica* collected from Indonesia was described by Rogers et al. (1987). Based on primarily on the nature of cultures, Callan and Rogers (1990) asserted that most species should be accommodated in *Xylaria* and *Hypoxyylon* and placed this species in the genus *Xylaria*. GZUCC14028 indicated a rather close relationship to the other sequences included *X. polymorpha* complex. Phylogenetic analysis (Fig. 1) showed GZUCC14028 is much closer to *Xylaria atosphaerica* 91111214 HAST. Morphologically, our species has same characters with *X. atosphaerica* and is a new record from China. *Xylaria atosphaerica* was described from Guiana, Indonesia.

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**Fig. 4** – *Xylaria atosphaerica* (GZUH14028). a, b. Stromata on the host. c. Vertical section of stroma. d–g. Asci with ascospores. h–j. Ascospores. k. Ascus apical apparatus and ascospores. – Scale bars: a = 3 mm, b, c = 200  $\mu$ m, d–k = 10  $\mu$ m.

#### References

Abe Y, Liu Z. 1995 – An annotated list of xylariaceous and diatrypaceous fungi collected from Mt. Fengyangshan and Mt. Baishanzu, Zhejiang Prov. in East China. Bulletin of the National



- Science Museum, Tokyo, Series B 21, 75–86.
- Callan BE, Rogers JD. 1990 – Teleomorph-anamorph connections and correlations in some *Xylaria* species. *Mycotaxon* 36, 343–369.
- Chou ZH. 1935 – Notes on some fungi from Kweichow. *Bulletin of the Fan Memorial Institute of Biology (Botany)* 6, 161–166.
- Daranagama DA, Camporesi E, Liu XZ, Bhat DJ et al. 2016 – *Tristratiperidium microsporium*, gen. et sp. nov. (Xylariales) on dead leaves of *Arundo plinii*. *Mycological Progress* 15, 8.
- Daranagama DA, Camporesi E, Tian Q, Liu XZ et al. 2015 – *Anthostomella* is polyphyletic comprising several genera in Xylariaceae. *Fungal Diversity* 73, 203–238.
- Felsenstein J. 1985 – Confidence intervals on phylogenetics: an approach using bootstrap. *Evolution* 39, 783–791.
- Gucht KVD. 1995 – Illustrations and descriptions of xylariaceous fungi collected in Papua New Guinea. *Bulletin du Jardin Botanique National de Belgique* 64, 219–403.
- 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.
- Hashemi SA, Zare R, Khodaparast SA, Elahinia SA. 2015 – A new *Xylaria* species from Iran. *Mycologia Iranica* 2, 1–10.
- Hsieh HM, Ju YM, Rogers JD. 2005 – Molecular phylogeny of *Hypoxylon* and closely related genera. *Mycologia* 97, 914–923.
- Hsieh HM, Lin CR, Fang MJ, Rogers JD et al. 2010 – Phylogenetic status of *Xylaria* subgenus *Pseudoxylaria* among taxa of the subfamily Xylarioideae (Xylariaceae) and phylogeny of the taxa involved in the subfamily. *Molecular Phylogenetics and Evolution* 54, 957–969.
- Huang G, Guo L, Liu N. 2014a – Two new species of *Xylaria* and *X. diminuta* new to China. *Mycotaxon* 129, 149–152.
- Huang G, Guo L, Liu N. 2014b – *Xylaria byttneriae* sp. nov. from Yunnan Province in China. *Mycosystema* 33, 567–570.
- Ju YM, Hsieh HM. 2007 – *Xylaria* species associated with nests of *Odontotermes formosanus* in Taiwan. *Mycologia* 99, 936–957.
- Ju YM, Hsieh HM, Ho MC, Szu DH et al. 2007 – *Theissenia rogersii* sp. nov. and phylogenetic position of *Theissenia*. *Mycologia* 99, 612–621.
- Ju YM, Hsieh HM, Vasilyeva L, Akulov A. 2009 – Three new *Xylaria* species from Russian Far East. *Mycologia* 101, 548–553.
- Ju YM, Rogers JD, Hsieh HM. 2004 – *Amphirosellinia* gen. nov. and a new species of *Entoleuca*. *Mycologia* 96, 1393–1402.
- Ju YM, Rogers JD, San Martín F, Granmo A. 1998 – The genus *Biscogniauxia*. *Mycotaxon* 66, 1–98.
- Karun NC, Sridhar KR. 2015 – *Xylaria* complex in the South-Western India. *Plant Pathology & Quarantine* 5, 83–96.
- Kim CS, Jo JW, Kwag YN, Oh SO et al. 2016 – New Records of *Xylaria* Species in Korea: *X. ripicola* sp. nov. and *X. tentaculata*. *Mycobiology* 44, 21–28.
- Kirk PF, Cannon PF, Minter DW, Stalpers JA, (eds). 2008 – *Dictionary of the fungi*, 10th edn. CABI, Egham CABI Bioscience, CBS, Landcare Research.
- Læssøe T. 1987 – *Xylaria corniformis* reconsidered. *Mycotaxon* 30, 81–85.
- Læssøe T. 1999 – The *Xylaria comosa* complex. *Kew Bulletin* 54, 605–619.
- Lee JS, Ko KS, Jung HS. 2000 – Phylogenetic analysis of *Xylaria* based on nuclear ribosomal ITS1–5.8S–ITS2 sequences. *FEMS Microbiology Letters* 187, 89–93.
- Liu JK, Hyde KD, Jones EBG, Ariyawansa HA et al. 2015 – Fungal diversity notes 1–110: taxonomic and phylogenetic contributions to fungal species. *Fungal Diversity* 72, 1–197.
- Maharachchikumbura SSN, Hyde KD, Jones EBG, McKenzie EHC et al. 2016 – Families of Sordariomycetes. *Fungal Diversity* 79, 1–317.
- Ma HX, Vasilyeva L, Li Y. 2011 – A new species of *Xylaria* from China. *Mycotaxon* 116, 151–155.
- Rogers JD, Callan BE. 1986 – *Xylaria polymorpha* and its allies in continental United States.

- Mycologia 78, 391–400.
- Rogers JD, Callan BE, Samuels GJ. 1987 – The Xylariaceae of the rain forests of north Sulawesi (Indonesia). *Mycotaxon* 29, 113–172.
- Rogers JD, Ju YM. 1997 – The genus *Stilbohypoxylon*. *Mycological Research* 101: 135–138.
- Rogers JD, Ju YM, San MGF. 1995 – *Discoxylaria myrmecophila* and its *Hypocreodendron* anamorph. *Mycologia* 87, 41–45.
- Smith GJD, Liew ECY, Hyde KD. 2003 – The Xylariales: A monophyletic order containing 7 families. *Fungal Diversity* 13, 175–208.
- Srihanant N, Petcharat V, Vasilyeva LN. 2015 – *Xylaria thailandica* – a new species from southern Thailand. *Mycotaxon* 130, 227–231.
- Stadler M, Wollweber H, Jäger W, Brieger M et al. 2004 – Cryptic species related to *Daldinia concentrica* and *D. eschscholzii*, with notes on *D. bakeri*. *Mycological Research* 108, 257–273.
- Swofford DL. 2002 – PAUP: Phylogenetic analysis using parsimony. Version 4.0 b10, Sinauer Associates, Sunderland.
- Tai FL. 1979 – *Sylloge fungorum Sinicorum*. Science Press, Peking. 1527.
- Tang A, Jeewon R, Hyde KD. 2009 – A re-evaluation of the evolutionary relationships within the Xylariaceae based on ribosomal and protein-coding gene sequences. *Fungal Diversity* 34, 127–155.
- Thompson JD, Gibson TJ, Plewniak F, Jeanmougin F et al. 1997 – The ClustalX Windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Research* 24, 4876–4882.
- Whalley AJS. 1996 – The xylariaceous way of life. *Mycological Research* 100, 897–922.