Spirodecospora (Xylariaceae)

a new genus for Western Europe, characterised by spores with spiralling ornamentation

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Abstract

Spirodecospora is a xylariaceous genus occurring on bamboos, characterised by minute, discrete, deeply immersed, nonstromatic ascomata yielding fairly large, distinctive ascospores with a pigmented, spirally ornamented wall. Its known distribution so far is temperate (Japan) to tropical (Hong Kong). A pyrenomycete collected on *Arundinaria* sticks in Devon (UK) proved to match this morphological definition of *Spirodecospora* in all respects. A detailed morphological description of this collection is provided. An ITS sequence obtained from this material supported this view by showing 99.8% similarity to *S. melnikii*, a species known from Japan and Far East Russia on *Sasa*. Our results therefore considerably expand the known geographic range of *Spirodecospora*.

This collection is herein assigned to *S. melnikii*, which may be a synonym of the type of *Spirodecospora*, *S. bambusicola*; DNA data from the type specimen of *S. bambusicola* is not yet available. To explain the unexpected presence of *S. melnikii* in Western Europe, its endophytic origin from live bamboo material imported from Asia is considered.

Keywords: *Ascomycota*, bambusicolous fungi, endophytic fungi.

Introduction

On 03 March 2025 a pyrenomycete fungus was collected from a detached dead culm of the bamboo *Phyllostachys aurea* from the ground at Exmoor Zoological & Conservation Centre, Bratton Fleming, Devon, U.K. (see Fig 1). *Phyllostachys aurea* Rivière & Rivière is also known as Fishpole Bamboo and is native to China. The preliminary microscopy results were shared with J. Fournier, (France), who was able to identify an association with the genus *Spirodecospora* B.S. Lu, K.D. Hyde & W.H. Ho. The material was found to be in the early stages of growth and in good condition and sections were subsequently shared with J. Fournier.

A detailed morphological characterisation of the collection quickly confirmed the generic placement

Fig. 1. *Phyllostachys aurea* present at the host site within Exmoor Zoological Centre. Photo © T. Hardware.

and oriented our first investigation towards *S. bambusicola* B.S. Lu, K. D. Hyde & W. H. Ho, the type and then only species of *Spirodecospora* (Lu *et al.* 1998). Mel'nik & Hyde (2003) replaced this name with their new combination *S. melnikii* (Lar.N. Vassiljeva) K.D. Hyde & Mel'nik, based on the previously published name *Anthostomella melnikii* Lar.N. Vassiljeva (1990). Our collection appears to be the first reported record of *Spirodecospora* in western Europe with all other records of this genus recorded in China (Lu *et al.*, 1998, Liu *et al.* 2025), Japan (Sugita *et al.* 2022) or Far Eastern Russia (Vassiljeva 1990; Mel'nik & Hyde 2003). Sugita *et al.* (2022) suggested that the two taxa were not synonymous, but there are no DNA data available for *S. bambusicola* and the morphological evidence they gave is not convincing. As DNA from our sample closely

matched that of several collections of *S. melnikii* and the two host genera (*Arundinaria* and *Sasa*) are quite closely related, we are content to use that name for the British collection.

Based on molecular phylogenetic analyses of DNA sequence data of three regions (ITS, LSU and *rpb2*), Sugita *et al.* (2022) established the new family *Spirodecosporaceae* R. Sugita & Kaz. Tanaka within *Xylariaceae*, provided sequence data for *S. melnikii* and recognised *S. paramelnikii* R. Sugita & Kaz. Tanaka and *S. paulospiralis* R. Sugita & Kaz. Tanaka as distinct species based on both molecular and morphological evidence. Four further species were added from Chinese collections by Liu *et al.* (2025), though regrettably none of the host species were identified.

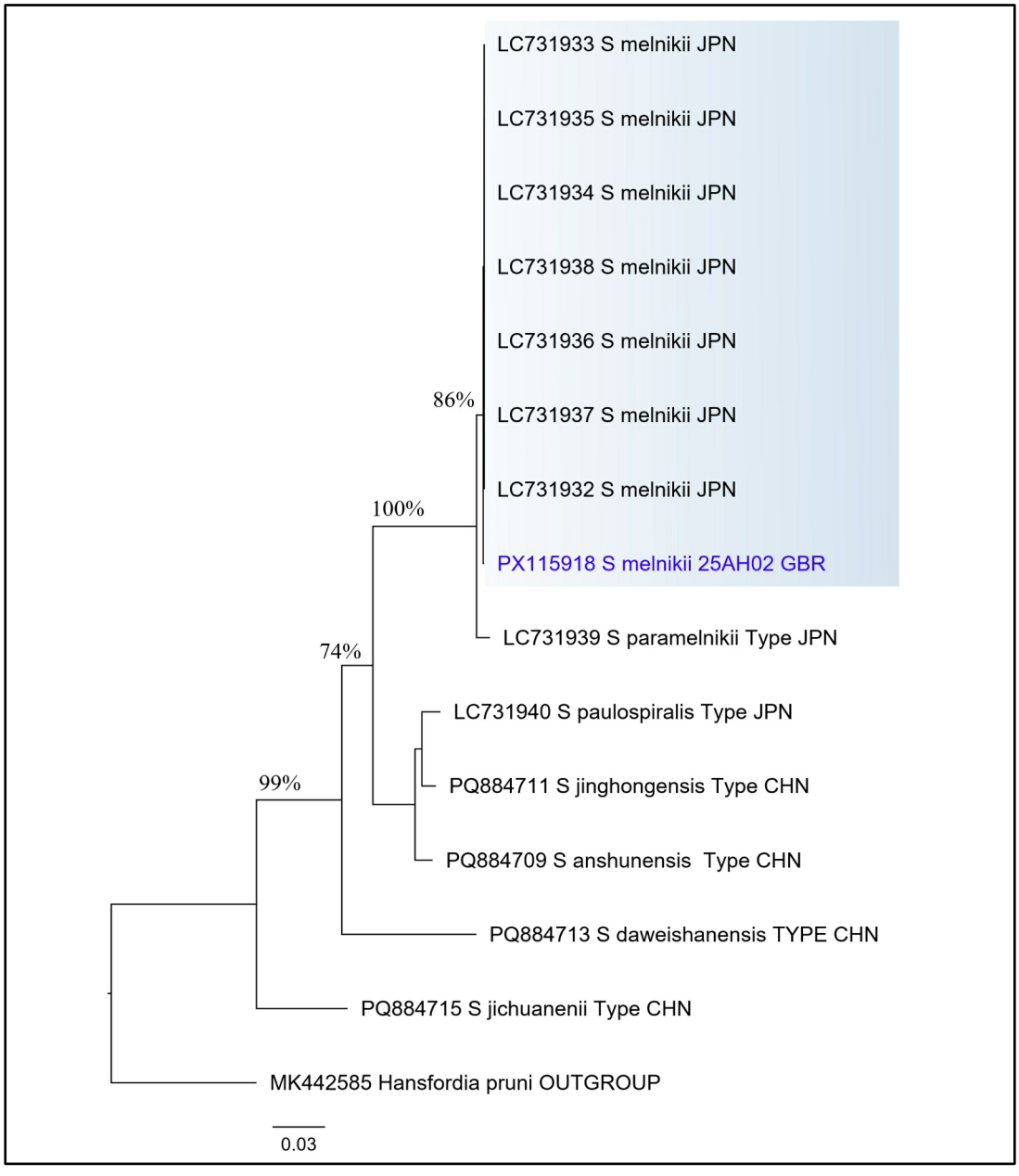

Fig. 2. Phylogenetic tree of sequences published on GenBank. Three-letter ISO codes are used to indicate country of collection.

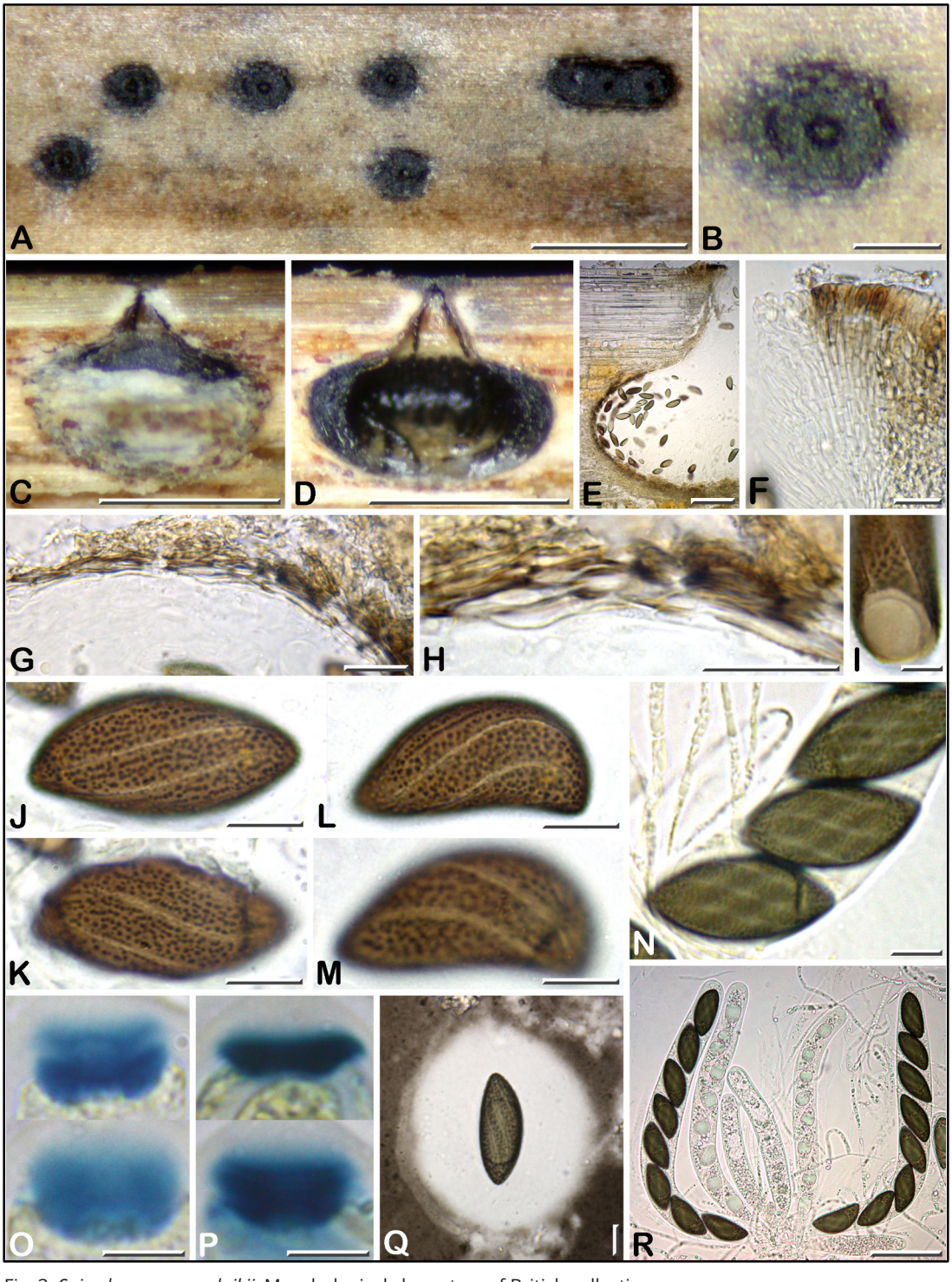

Fig. 3. *Spirodecospora melnikii*. Morphological characters of British collection.

A-R: K-M001445782. **A:** Ostiolar discs on host surface, separate or occasionally in contact; **B**: Ostiolar disc in close-up showing a central pore; **C**: Immersed ascoma visible after splitting of the substrate, showing necrotic fibres around its lower half; **D**: Ascoma in vertical section, note the bleached wood around the neck; **E**: Ascoma in vertical section showing a thin peridium; **F**: Ostiolar region in vertical section showing periphyses lining the canal (left) and palisadic hyphae with thick-walled brown cells forming the superficial disc;
cont. p.135 ...

Materials and methods

Morphological characterisation

The general protocols regarding macro- and microscopic observations, ascospore measurements, photography and illustrations follow Fournier *et al.* (2018). In addition, ascospore ornamentation was studied after mounting in heated chloral-lactophenol and Indian ink to show a gelatinous sheath. Spore illustration includes showing upper and lower spore sides to prove the existence of fully spiralling linear crests and granular bands around each spore. Subapical apparati are shown using Melzer's reagent and separately using Lugol's solution.

Voucher material has been deposited in the Fungarium of the Royal Botanic Gardens, Kew under the specimen number K-M001445782.

Phylogenetic methods and results

A portion of the original collection of host material was forwarded to David Harries for sequencing through the British Mycological Society (BMS) DNA barcoding programme.

DNA extraction, PCR amplification and sequencing

A single ascoma was excised from the substrate and DNA extraction performed using an alkaline-PEG200 method (Chomczynski & Rymaszewski, 2006). The molecular marker region (ITS1-5.8S-ITS2) was amplified using primers ITS1F and ITS4 (Gardes & Bruns, 1993) using a Bento Lab thermal cycler (Bento Bioworks Ltd, London, UK). The PCR product was forwarded to Aberystwyth University for Sanger sequencing at the IBERS Genomics Facility.

A BLAST search was performed on the sequence using the GenBank database (https://www.ncbi.nlm.nih.gov/genbank/) and gave a 99.8% match to a series of sequences named *S. melnikii* (Lar.N. Vassiljeva) K.D. Hyde & Melnik, 2003.

A maximum likelihood phylogenetic tree (Fig. 2) was constructed based on the ITS sequences listed in Sugita *et al.* (2022) together with additional sequences published on GenBank and the subject sequence, GenBank PX115918.

Taxonomic part

Class: *Sordariomycetes*

Order: *Xylariales*

Family: *Xylariaceae*

Genus: *Spirodecospora*

Spirodecospora melnikii (Lar.N. Vassiljeva) K.D. Hyde & Mel'nik (2003)

≡ *Anthostomella melnikii* Lar.N. Vassiljeva (1990)

?= *Spirodecospora bambusicola* B.S. Lu, K.D. Hyde & W.H. Ho (1998)

Ascomata perithecial, non-stromatic, deeply immersed, appearing on host surface as small loosely scattered black dots, separate or rarely in contact, flush with the surface. Perithecia subglobose to depressed-spherical, 420–550 µm high including a conical neck 200–240 µm high and a venter 200–260 µm high, 450–620 µm diam. Peridium 11–18 µm thick, brown, comprised of 3–4 layers of flattened, thin-walled cells textura prismatica 7–9 µm long, 2.5–3.8 µm wide, inwardly 18–20 µm long × 3–3.2 µm wide, wall 1–1.2 µm thick, irregularly pigmented; amorphous necrotic cells adherent to the lower half of the periderm, forming a whitish to light brown crust visible when splitting the substrate tangentially to a perithecium. Ostiolar neck broadly to narrowly conical, thin-walled, periphysate, the surrounding host tissue bleached in the upper half beneath the surface. Ostioles discoid, black, 170–180 µm diam. not prominent above host surface, pierced by a minute central pore, composed by palisadic hyphae ending into dark brown, tightly packed, slightly swollen cells.

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cont. from p.134... **G, H**: Fusiform and flattened, irregularly pigmented and thin-walled cells of the lateral peridium; **I**: Obliquely cut ascospore showing superficial warts and linear crests (E-I all in heated chloral-lactophenol); **J, K**: Same ascospore with focus on upper side (J) and lower side (K) showing the ornamentation fully spiralling around the spore axis; **L, M**: Same ascospore in side view, with focus on upper side (L) and lower side (M) showing the ornamentation fully spiralling around the spore axis; **N**: Submature ascospores with intermediate focus showing both upper and lower spiralling pale crests (note the guttulate paraphyses); **O**: Subapical apparati (J-O all in Melzer's reagent); **P**: Subapical apparati in Lugol solution; **Q**: Ascospore featuring a wide gelatinous sheath, in Indian ink; **R**: Mature and immature subsessile asci, in 1% sodium dodecyl sulphate.

Scale bars: A, C, D = 0.5 mm; B, E = 100 µm; F, G, H = 20 µm; I, O, P = 5 µm; J-N, Q = 10 µm; R = 50 µm. Plate © J. Fournier.

Dichotomous key to known *Spirodecospora* taxa (to facilitate their comparison, ascospore dimensions are given as mean values)

1– Ascospores non-verrucose, narrowly fusiform with a single, straight, short, central linear ridge, 21.7 × 6.8 µm	*S. jichuanenii*
1–Ascospores verrucose, broadly ellipsoid-inequilateral, with 3 almost straight to spiralling long ridges	2
2–Ascospores with almost straight to faintly spiral ornamentation	3
2– Ascospores with spirally arranged ornamentation	4
3–Ascospores 19.2 × 10.5 µm	*S. jinghongensis*
3–Ascospores 31.6 × 12.5 µm	*S. paulospiralis*
4– Ascospores lacking a gelatinous sheath, 30.7 × 15.3 µm	*S. anshunensis*
4– Ascospores featuring a conspicuous gelatinous sheath	5
5–Ascospores 61.8 × 26.1 µm	*S. daweishanensis*
5– Ascospores significantly smaller, less than 40.2 × 16.4 µm	6
6–Ascospores 40.2 × 16.4 µm	*S. paramelnikii*
6–Ascospores slightly smaller, less than 36.5 µm long	7
7–Described from Far East Russia and Japan on *Sasa* and on *Bambusa* in UK	*S. melnikii*
7–Described from Hong Kong on *Bambusa* and possibly different	*S. bambusicola*

	Host	**Geographic origin and climate**	**Authors**	**Extreme values (µm(**	**Mean values (µm)**
S. bambusicola holotype	*Bambusa*	Hong Kong tropical	Lu *et al.* 1998	28–45 × 11–15	36 × 14
S. melnikii K-M001445782	*Arundinaria*	Devon (UK) temperate	Present study	33.1–38.7 × 13.8–15.6	35.5 × 14.8
Anthostomella melnikii holotype	*Sasa*	Far East Russia temperate	Vassiljeva 1990 (in Mel'nik & Hyde 2003)	(30–)33–36(–39.6) × 14–16.5	34.5 × 15.3
S. melnikii LE212430	*Sasa*	Far East Russia temperate	Mel'nik & Hyde 2003	32–38(–42) × 12.5–15	35 × 13.8
S. melnikii	*Sasa*	Japan temperate	Sugita *et al.* 2022	30–36.5 × 12–17	33.9 × 13.7

Table. 1. Synopsis of ascospore dimensions from known collections of *S. melnikii* and *S. bambusicola* reported in literature, in correlation with their host affiliation, geographic origin and climate (adapted from Mel'nik & Hyde, 2003).

Paraphyses copious, filiform, 2–2.8 µm wide, sparingly septate, simple, hyaline, minutely guttulate with refractive content, longer than asci.

Asci unitunicate, cylindrical, short-stipitate to subsessile, (6–)8-spored, 210–256 × 20.5 × 28.4 µm (N = 10), with a massive subapical ring wider than high, varying from wedge-shaped with a flat base to basally convex, bluing more strongly in Lugol's solution than in Melzer's reagent, also varying in dimension and shape depending on the medium, 4.1–5.7 × 7.2–9.4 µm (Me = 5.1 × 8.5 µm, N = 22) in Melzer's reagent, 3.3–5.3 × 7.1–8.7 µm (Me = 4.4 × 7.9 µm, N = 25) in Lugol's solution.

Ascospores: (31.7–)33.1–38.7(–40.7) × (12.7–)13.8–15.6(–16.3) µm, Q = (2.1–)2.2–2.7(–2.9); N = 60 (Me = 35.5 × 14.8 µm; Qe = 2.4), ellipsoid-inequilateral to slightly fusiform, with mostly narrowly rounded to subacute ends, olivaceous brown in the fresh state, turning medium to dark brown upon drying, the wall conspicuously ornamented by minute dark brown warts densely distributed around two to mostly three whitish narrow parallel ridges arranged in a spiral configuration, continuous and extending over the entire ascospore; surrounded by a wide mucilaginous sheath 14–19 µm best seen by contrast in Indian ink and lacking polar appendages.

The distribution pattern of the warty ornamentation and linear whitish ridges is the key characteristic of the genus *Spirodecospora* but was perhaps not fully understood. Microscopic investigations carried out in Melzer's reagent to provide clearest images showed that, by combining focusing on the upper side and on the lower side (Fig. 3 J–M) or focusing on the intermediate zone, bands of warts and whitish ridges are continuous all around the spore and cross each other at stable angles forming a strikingly regular and most unusual pattern (Fig. 3 N). See also the illustrations of ascospores of *S. daweishanensis* in Liu *et al.* (2025: 62).

Discussion

Taxonomic status

Assessing the taxonomic status of our collection was facilitated by the distinctive and unique morphology of ascospores quickly leading us to the genus *Spirodecospora* after consultation of Lu & Hyde's world monograph of *Anthostomella* (Lu & Hyde, 2000) and checking its original description in Lu *et al.* (1998). At this time and until the first revision of the genus by Sugita *et al.* (2022), the genus was monotypic and represented by *S. bambusicola*, the type species (Lu *et al.*, 1998).

When aware of a collection on *Sasa* from Kunashir island in Far East Russia, published by Vassiljeva (1990) under the name *Anthostomella melnikii* (Lar.N. Vassiljeva), K.D. Hyde & Mel'nik (2003) assessed it was not an *Anthostomella* Sacc. but could not be morphologically distinguished from *S. bambusicola*. They became therefore synonyms but the epithet *melnikii* having priority, they proposed the new combination *S. melnikii* (Lar.N. Vassiljeva), K.D. Hyde & Mel'nik (2003) to name the type species of *Spirodecospora*.

Sugita *et al.* (2022) interpreted differently the minor morphological differences between collections on *Bambusa* and *Sasa* listed by Mel'nik & Hyde (2003), assessed them as significant and emphasised the importance of host affiliation and geographic origin as good separators setting *S. melnikii* apart from *S. bambusicola* as a distinct species. Oddly enough, the status of *S. melnikii* in MycoBank changed very recently from synonym of *S. bambusicola* to *S. melnikii* replacing *S. bambusicola*. However, the type species of *Spirodecospora* is still *S. bambusicola* in MycoBank (accessed 10/09/2025) and according to the curator, K. Bensch, the update of *S. melnikii* was made based on Mel'nik & Hyde (2003) and Sugita *et al.* (2022) papers but both interpretations remain possible until sequence data become available (pers. comm. 01/09/2025). *Spirodecospora bambusicola* is likewise still accepted as the type species by Index Fungorum where no synonymy with *S. melnikii* is suggested (accessed 10/09/2025).

We do agree that sequence data are required to clearly evaluate whether *S. melnikii* is distinct from *S. bambusicola* but the status of both species as distinct is challenged by the observations made during this study. Sugita *et al.* (2022) stated: "We identified our specimens collected on *Sasa* spp. as *S. melnikii* based on the smaller ascospore size and the host plant". We summarised in Table 1 available information on ascospore dimensions reported by different authors for collections assigned either to *S. melnikii* or *S. bambusicola*. This shows a fairly wide variation range of extreme and mean values which, due to a wide overlap, does not clearly show significant differences and appears uncorrelated with host, location or climate. For example, our collection from UK having an ITS sequence with 99.8% similarity to *S. melnikii* is on *Bambusa*, not *Sasa*, which contradicts the taxonomic importance of

host affiliation put forward to support the separation of these two species.

We therefore assign our collection to *S. melnikii* in agreement with Mel'nik & Hyde (2003) but with reservations about its taxonomic difference from *S. bambusicola* defended by Sugita *et al*. (2022).

Supposed endophytic origin

With the highly disjunct distribution of *S. melnikii* revealed by our finding, ranging from South East Asia to Western Europe, some questions naturally may arise about how this could happen. Numerous examples can be found in literature about macrobasidiomycetes featuring a widely disjunct distribution, usually explained by ectomycorrhizal species having followed their host through the soil embedding their roots and successfully transplanted in a suitable environment.

The ecology of pyrenomycetous microfungi is radically different in relying on the presence of fungal mycelium within live host tissues without damaging them. This is termed endophytism and is well documented in all ecosystems and plants worldwide, including bamboos, e.g. Giba *et al*. (2020). It seems therefore reasonable to explain the presence of this exotic fungus by its presence as an endophyte within the bamboo material imported from Asia (most often China and India) and naturally developing with its host in this suitable part of UK enjoying mild and rainy winters. Asian bambusicolous pyrenomycetes are countless and one can predict numerous discoveries of interest on these hosts in the future in this region.

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