Characterization of Three Species of Sordariomycetes Isolated from Freshwater and Soil Samples in Korea

Seo Hee Lee, Hyo Sun Park, Thuong T. T. Nguyen and Hyang Burm Lee

Division of Food Technology, Biotechnology and Agrochemistry, College of Agriculture and Life Sciences, Chonnam National University, Gwangju, Korea

1. Introduction

Sordariomycetes is the second largest class of the division Ascomycota, and it is typically characterized by non-lichenized, perithecial (flask-shaped) ascomata and inoperculate unitunicate asci [1–4]. Members of Sordariomycetes are found in different niches including terrestrial and freshwater habitats [5–7]. Some species are pathogens and endophytes of various plants, whereas others cause diseases in arthropods and mammals [3,8,9]. Many species are saprobes involved in decomposition and nutrient cycling [10], and some species are fungicolous [11].

The classification of Sordariomycetes has changed significantly in the past few decades [12–16]. Recently, Maharachchikumbura et al. [3] introduced 3 new subclasses on the basis of the morphology and combined analysis of 28S large subunit rDNA (LSU), 18S small subunit rDNA (SSU), translation elongation factor 1-alpha gene (TEF), and RNA polymerase II second largest subunit gene sequences. On the basis of their morphology and phylogeny, CNUFC-KMHY6-1, CNUFC-MSW24-2-11, and CNUFC-GW2S-4 isolates were identified as Arcopilus aureus, Memnoniella echinata, and Stachybotrys sansevieriae, respectively. To the best of our knowledge, Ar. aureus and M. echinata have not been previously recorded in Korea, and this is the first report of S. sansevieriae from freshwater niche.

ABSTRACT

During a survey of fungal diversity in the class Sordariomycetes, 3 fungal strains, CNUFC-KMHY6-1, CNUFC-MSW24-2-11, and CNUFC-GW2S-4 were isolated from soil and freshwater samples, respectively in Korea. The strains were analyzed both morphologically and phylogenetically on the basis of internal transcribed spacer and RNA polymerase II second largest subunit gene sequences. On the basis of their morphology and phylogeny, CNUFC-KMHY6-1, CNUFC-MSW24-2-11, and CNUFC-GW2S-4 isolates were identified as Arcopilus aureus, Memnoniella echinata, and Stachybotrys sansevieriae, respectively. To the best of our knowledge, Ar. aureus and M. echinata have not been previously recorded in Korea, and this is the first report of S. sansevieriae from freshwater niche.

KEYWORDS

Arcopilus aureus; Memnoniella echinata; Stachybotrys sansevieriae; Sordariomycetes

ARTICLE HISTORY

Received 7 August 2018
Revised 1 December 2018
Accepted 18 January 2019

CONTACT Hyang Burm Lee hblee@jnu.ac.kr

© 2019 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group on behalf of the Korean Society of Mycology. This is an Open Access article distributed under the terms of the Creative Commons Attribution-NonCommercial License (http://creativecommons.org/licenses/by-nc/4.0/), which permits unrestricted non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.
Stachybotryaceae. These 2 genera have similar morphological characteristics. The only difference between these 2 genera is that Memnoniella species have long and dry chains of conidia, whereas Stachybotrys species have single-celled conidia aggregated in slimy heads [19,20]. Some authors have considered this is insufficient to distinguish between these genera and have suggested that the 2 genera should be combined under the older name of Stachybotrys [21,22]. This is supported by the molecular results based on the ITS phylogenetic analysis of Haugland et al. [23]. However, Lombard et al. [24] performed multi-locus sequence analysis of the family Stachybotriaceae and showed that the Memnoniella species grouped in a well-supported clade distinct from the Stachybotrys clade. Currently, the genus Memnoniella is composed of 11 species, and more than 50 species of Stachybotrys are accepted.

To date, Arcopilus and Memnoniella species have not been described in Korea. The aim of the present study was to perform morphological and molecular analyses to characterize 3 ascomycetes species in Korea: Ar. aureus, M. echinata, and S. sansevieriae.

2. Materials and methods

2.1 Isolation of fungal strains from freshwater and soil samples

In 2017, freshwater samples were collected from the Wonhyo Valley located at Mudeung Mt., Gwangju, and Geum River located in Gongju, Korea. The samples were transferred to sterile 50-mL conical tubes (SPL Life Sciences Co., Pocheon, Korea) and stored at 4°C until examination. In 2017, soil samples were collected from Geumgol Mountain located in Jindo Island, Korea. These samples were transported in sterile 50-mL Falcon tubes and stored at 4°C, until examination. Fungi were isolated using the serial dilution plating technique. Briefly, 1 mL of water or 1 g of soil was mixed with 9 mL of sterile distilled water, shaken for 7-10 min, and serially diluted from 10^{-1} to 10^{-4}. An aliquot of 0.1 mL from each dilution was transferred to potato dextrose agar (PDA) and oatmeal agar (OA; 30 g of oatmeal and 20 g of agar in 1 L of deionized water), and potato carrot agar (PCA; 20 g of potato, 20 g of carrot, and 20 g of agar in 1 L of deionized water). The plates were incubated at 15, 25, and 35°C in the dark for 14 days. The samples were mounted in distilled water or lactophenol solution (Junsei Chemical Co. Ltd., Tokyo, Japan) and observed using an Olympus BX51 microscope with differential interference contrast optics (Olympus, Tokyo, Japan).

2.2. Morphological studies

For detailed morphological studies, CNUFC-MSW24-2-11 and CNUFC-GW2S-5 strains were cultured on PDA, corn meal agar (CMA; 2 g of cornmeal and 2 g of agar in 1 L of deionized water), and oatmeal agar (OA; 30 g of oatmeal and 20 g of agar in 1 L of deionized water). CNUFC-KMHY6-1 strain was cultured on PDA, OA, and potato carrot agar (PCA; 20 g of potato, 20 g of carrot, and 20 g of agar in 1 L of deionized water). The plates were incubated at 15, 25, and 35°C in the dark for 14 days. The samples were mounted in distilled water or lactophenol solution (Junsei Chemical Co. Ltd., Tokyo, Japan) and observed using an Olympus BX51 microscope with differential interference contrast optics (Olympus, Tokyo, Japan).

2.3. DNA extraction, PCR, and sequencing

Genomic DNA was extracted directly from the mycelia of the fungal isolates by using the Solgent Genomic DNA prep Kit (Solgent Co. Ltd., Daejeon, Korea). The ITS region and RPB2 were amplified with the primer pairs ITS4 and ITS5 [25], and fRPB2-5F and fRPB2-7cR [26], respectively. The PCR amplification mixture (total volume, 20 μL) contained fungal DNA template, 5 pmol/μL of each primer, and Accupower PCR Premix (Bioneer Corp., Daejeon, Korea). The PCR products were purified using the Accuprep PCR Purification Kit (Bioneer Corp., Daejeon, Korea), according to the manufacturer’s instructions. DNA sequencing was performed with an ABI 3700 Automated DNA sequencer (Applied Biosystems Inc., Foster City, CA).

2.4. Phylogenetic analysis

The fungal sequences obtained from the GenBank database (Table 1) were aligned using Clustal_X v. 2.0 [27] and edited with Bioedit v. 7.2.5 software [28]. Phylogenetic analyses were performed using MEGA 6 software [29], and maximum likelihood was constructed by Kimura’s two-parameter correction method. The reliability of internal branches was assessed using the p-distance substitution model with 1000 bootstrap replications.
Table 1. Taxa, collection numbers, sequences, and GenBank accession numbers used in this study.

| Taxon name                          | Collection No. (Isolate No.) | GenBank accession No. |
|-------------------------------------|------------------------------|-----------------------|
|                                     |                              | ITS                   |
| Achaetomium globosum                | CBS 332.67                   | KX976570              |
| A. luteum                           | CBS 618.68                   | KX976571              |
| A. macrosporum                      | CBS 152.97                   | KX976573              |
| Ar. aureus                          | CBS 153.52                   | KX976582              |
| Ar. aureus                          | CNUF-C-182-1                 | MH685565              |
| Ar. aureus                          | CNUF-C-182-2                 | MH685566              |
| Ar. aureus                          | CBS 560.80                   | KX976584              |
| Ar. flavigenus                      | CBS 337.67                   | KX976571              |
| Ar. fusiformis                      | CBS 484.85                   | KX976585              |
| Ar. turgidipilosus                  | CBS 169.52                   | KX976588              |
| Cymostachys coffeicola              | CBS 252.76                   | KU846052              |
| C. fabispora                        | CBS 136180                   | KU846054              |
| Memnoniella brunneoconidiophora     | CBS 109477                   | KU846138              |
| M. dichroa                          | CBS 526.50                   | KU846140              |
| M. echinata                         | CBS 216.32                   | KU846142              |
| M. echinata                         | CBS 343.50                   | KU846144              |
| M. echinata                         | CBS 627.66                   | KU846147              |
| M. echinata                         | DAOM 235365                  | KU846149              |
| M. echinata                         | CNUF-C-182-1                 | MH685569              |
| M. echinata                         | CNUF-C-182-2                 | MH685570              |
| M. humicola                         | CBS 463.74                   | KU846154              |
| M. oenanthes                        | CBS 388.73                   | KU846156              |
| M. puteofolia                       | CBS 101177                   | KU846158              |
| Ovatospora unipora                  | CBS 109.83                   | KX976689              |
| O. medusarum                        | CBS 148.67                   | KX976684              |
| Stachybotrys chartarum              | CBS 136161                   | KU846702              |
| Helminthosporidium echinatum        | CBS 109285                   | KU846261              |
| S. limonispora                      | CBS 128809                   | KU846735              |
| S. sansevieriae                     | HGUP 0103                    | JX998165              |
| S. sansevieriae                     | KN16-141                     | KY587783              |
| S. sansevieriae                     | CNUF-C-182-5                 | MH685568              |
| S. sansevieriae                     | CNUF-C-182-1                 | MH685567              |
| S. subcylinodospora                 | HGUP 0201                    | KX998163              |
| Striatibotrys rhobodora             | CBS 528.80                   | KU846760              |
| St. atypica                         | CBS 141059                   | KU846753              |
| Lasiosphaeria ovinia                | SMH4605                      | KU846793              |
| Peethambara sundara                 | CBS 521.96                   | KU846470              |

Bold letters indicate isolates and accession numbers determined in our study.

ITS: internal transcribed spacer; RP2B: RNA polymerase II second largest subunit; CBS: Centraalbureau voor Schimmelcultures, Utrecht, The Netherlands; CNUFC: Chonnam National University Fungal Collection, Gwangju, South Korea; DAOM: Canadian Collection of Fungal Cultures, Agriculture and Agri-Food Canada, Ottawa, Canada; HGUP: Herbarium of Guizhou University, Plant Pathology, China.

Figure 1. Phylogenetic tree based on neighbor-joining analysis of internal transcribed rDNA sequences for Ar. aureus CNUF-C-182-1 and Ar. aureus CNUF-C-182-2. Lasiosphaeria ovinia was used as the outgroup. Bootstrap support values of >50% are indicated at the nodes. The bar indicates the number of substitutions per position. Ex-type strains are in bold.
Figure 2. Phylogenetic tree based on neighbor-joining analysis of RNA polymerase II second largest subunit (RPB2) sequences for *Arcopilus aureus* CNUFC-KMHY6-1 and *Arcopilus aureus* CNUFC-KMHY6-2. *Lasiosphaeria ovina* was used as the outgroup. Bootstrap support values of >50% are indicated at the nodes. The bar indicates the number of substitutions per position. Ex-type strains are in bold.

Figure 3. Phylogenetic tree based on neighbor-joining analysis of internal transcribed rDNA sequences for *Memnoniella echinata* CNUFC-MSW24-2-11, *Memnoniella echinata* CNUFC-MSW24-2-12, *Stachybotrys sansevieriae* CNUFC-GW2S-4, and *Stachybotrys sansevieriae* CNUFC-GW2S-5. *Peethambara sundara* was used as the outgroup. Bootstrap support values of >50% are indicated at the nodes. The bar indicates the number of substitutions per position. Ex-type and epi-type strains are in bold.
3. Results

3.1. Phylogenetic analysis

The phylogenetic analyses of the 2 sequence datasets (ITS and RPB2) showed that the strains CNUFC-KMHY6-1, CNUFC-KMHY6-2, CNUFC-MSW24-2-11, CNUFC-MSW24-2-12, CNUFC-GW2S-4, and CNUFC-GW2S-5 were placed within the same clade with species of Arcopilus, Memnoniella, and Stachybotrys (Figures 1–4).

In BLASTn for the ITS sequences, CNUFC-KMHY6-1, CNUFC-MSW24-2-11, and CNUFC-GW2S-4 showed 100% (500/500 bp), 100% (663/663 bp), and 100% (513/513 bp) sequence identity values with *Ar. aureus* (GenBank accession No. KX976582), *M. echinata* (GenBank accession No. KU846149), and *S. sansevieriae* (GenBank accession No. JX987249), respectively.

In BLASTn for the RPB2 sequences, CNUFC-KMHY6-1, CNUFC-MSW24-2-11, and CNUFC-GW2S-4 strains showed 99.8% (495/496 bp), 100% (526/526 bp), and 100% (743/743 bp) identity values with *Ar. aureus* (GenBank accession No. KX976806), *M. echinata* (GenBank accession No. KU846196), and *S. sansevieriae* (GenBank accession No. JX987249), respectively.

3.2. Taxonomy

3.2.1. Taxonomy of CNUFC-KMHY6-1

*Arcopilus aureus* (Chivers) X. Wei Wang & Samson, Stud. Mycol. 84: 217 (2016) (Table 2, Figure 5).

≡*Chaetomium aureum* Chivers, Proc. Amer. Acad. Arts & Sci. 48: 86 (1912).

**Description:** Colonies grew moderately at 25°C on PDA, reaching 66 mm in diameter after 15 days at 25°C. The colony color was initially white-to-orange, later greenish. The colony reverse was reddish purple. Ascomata were superficial, globose or oval, 76.3–157.8 x 96.7–165.8 μm. Lateral hairs were apically incurved. Terminal hairs were brown, mostly hook shape, verrucose, arcuate, slightly circinate to coiled.

![Figure 4. Phylogenetic tree based on neighbor-joining analysis of RNA polymerase II second largest subunit (RPB2) sequences for Memnoniella echinata CNUFC-MSW24-2-11, Memnoniella echinata CNUFC-MSW24-2-12, Stachybotrys sansevieriae CNUFC-GW2S-4, and Stachybotrys sansevieriae CNUFC-GW2S-5. Peethambara sundara was used as the outgroup. Bootstrap support values of >50% are indicated at the nodes. The bar indicates the number of substitutions per position. Ex-type and epitype strains are in bold.](image-url)
### Table 2. Morphological characteristics of CNUFC-KMHY6-1 and the reference species Arcopilus aureus (≡C. aureum).

| Characteristics          | CNUFC-KMHY6-1                                      | Arcopilus aureus (≡C. aureum) |
|--------------------------|----------------------------------------------------|--------------------------------|
| Colony color             | Initially white-to-orange, later greenish, reverse reddish purple | First gray, pale olive then yellow |
| Ascomata                 | Superficial, globose or oval, 76.3–157.8 × 96.7–165.8 μm | Minute, globose or subglobose, 127 × 115 μm (110–140 × 105–123 μm) |
| Lateral hairs            | Apically incurved                                   | Numerous, slender, straight or flexed |
| Terminal hairs           | Mostly hook shape, verrucose, arcuate, slightly circinate to coiled | Minutely roughened, straight or slightly recurved |
| Asci                     | Fasciculate, clavate, with 8 biseriate or irregularly arranged ascospores, 24.9–41.5 × 7.3–12.8 μm | Club-shaped, 8-spored, 42 × 10 μm |
| Ascospore                | Brown when mature, 9.2–11.5 × 4.5–6.5 μm, sometimes irregular, fusiform, limoniform, lunate, with one or two apical germ pores | Irregularly ovate, apiculate at both ends, 9.8 × 5.4 μm (9.4–11 × 4.7–5.6 μm) |

*From the description by Wang et al. [18] and Chivers [30].

---

**Figure 5.** Morphology of Arcopilus aureus CNUFC-KMHY6-1. A) and D) Colony on potato dextrose agar (PDA); B) and E) Colony on potato carrot agar (PCA); C) and F) Colony on oatmeal agar (OA) (A)-C) top view, D)–F) reverse view); G) and O) Ascomata; H) and Q) Ascomatal hair; I) and P) Structure and surface of ascomatal wall; J)–L) Asci and ascospores; M), N), and R) Ascospores (Scale bars: G), H), and O) = 50 μm; I), K), and L) = 20 μm; J) = 40 μm; M) and N) = 5 μm; P) and Q) = 2.5 μm; R) = 5 μm).
Asci were fasciculate, clavate, with 8 biseriate or irregularly arranged ascospores, 24.9–41.5 × 7.3–12.8 µm. Ascospores were brown when mature, 9.2–11.5 × 4.5–6.5 µm, sometimes irregular, fusiform, limoniform, lunate, with one or two apical germ pores. The optimal growth temperature was 35°C.

### 3.2.2. Taxonomy of CNUFC-MSW24-2-11

#### Memnoniella echinata
(Riv.) Galloway, Trans. Brit. Mycol. Soc. 18: 165 (1933) ([Table 3, Figure 6](#)).

| Characteristics                  | CNUFC-MSW24-2-11 | Memnoniella echinata<sup>a</sup> |
|----------------------------------|------------------|---------------------------------|
| Colony color                     | Amber            | Amber to Sienna                 |
| Conidiophore                     | Straight to slightly flexuous, smooth to slightly verrucose, unbranched, septate, 2.7–3.6 µm in width, variable in length | Simple, macroconidiate, mononematous, single, thick-walled, unbranched, erect, straight to slightly flexuous, septate, smooth to slightly verrucose, 40–100 × 4–6 µm, bearing 6–10 conidiogenous cells |
| Conidiogenous cell               | Phialidic, clavate, smooth, 7.3–11.0 × 3.3–4.2 µm | Phialidic, clavate to subcilindrical, smooth, 7–10 × 2–5 µm, with conspicuous collarettes |
| Conidia                          | Globose to subglobose, verrucose, aseptate, 5.3–6.3 × 4.5–6.2 µm, formed in long dry chains | Acrogenous, aseptate, globose, verrucose, thick-walled, 3–6 × 3–5 µm (average, 5 × 4 µm), formed in long dry chains |

<sup>a</sup>From the description by Lombard et al. [24].

#### Description
Colonies grew slowly on OA, reaching 23.5 mm diameter after 15 days at 25°C. The colony color was brown to dark Sepia. The conidiophore was straight, unbranched, with septate, cylindrical, 28.1–73.8 µm in length, and 2.4–8.5 µm in width. Conidigenous cells were phialidic, obovate, smooth, 8.3–12.5 × 3.5–6.1 µm. Conidia were ellipsoidal, unicellular, 5.4–10.1 × 3.5–6.9 µm. On PDA, growth was slower than on OA and CMA, and abundant sporulation was observed when grown on OA and CMA.

### 4. Discussion

In this study, two species of *Ar. aureus* and *M. echinata* were isolated from soil samples and one species of *S. sansevieriae* from freshwater samples in Korea. *Ar. aureus* and *M. echinata* have been recorded for the first time in Korea, and *S. sansevieriae* is the first report from freshwater niche in Korea.

In previous studies, SSU, LSU, TEF, and RPB2 sequence data have been used for phylogeny of the class Sordariomycetes [2,17]. In the present study, the phylogenetic trees for selected genera within the family Chaetomiaceae and Stachybotryaceae were inferred from ITS and RPB2 sequence data and provided to infer the phylogenetic position of the 3 species.

Our analyses of ITS and RPB2 sequences showed that strains CNUFC-KMHY6-1 and CNUFC-KMHY6-2 were clustered with other *Ar. aureus* species in a well-supported clade with high bootstrap values ([Figures 1 and 2](#)). The morphological features of our isolate were generally similar to the description of *C. aureum* (=*Ar. aureus*) by Chivers et al. [30]. Many *Chaetomium*-like fungi produce secondary metabolites with different biological activities. Interestingly, Dwibedi and Saxena [31] have reported that *Ar. aureus* produces resveratrol. Resveratrol is a polyphenolic flavonoid and widely used as a therapeutic moiety as well as a pharmacophore for the development of novel drugs because of its various beneficial effects [31]. It has been

### Table 3. Morphological characteristics of CNUFC-MSW24-2-11 and the reference species Memnoniella echinata.

| Characteristics                  | CNUFC-MSW24-2-11 | Memnoniella echinata<sup>a</sup> |
|----------------------------------|------------------|---------------------------------|
| Colony color                     | Amber            | Amber to Sienna                 |
| Conidiophore                     | Straight to slightly flexuous, smooth to slightly verrucose, unbranched, septate, 2.7–3.6 µm in width, variable in length | Simple, macroconidiate, mononematous, single, thick-walled, unbranched, erect, straight to slightly flexuous, septate, smooth to slightly verrucose, 40–100 × 4–6 µm, bearing 6–10 conidiogenous cells |
| Conidiogenous cell               | Phialidic, clavate, smooth, 7.3–11.0 × 3.3–4.2 µm | Phialidic, clavate to subcilindrical, smooth, 7–10 × 2–5 µm, with conspicuous collarettes |
| Conidia                          | Globose to subglobose, verrucose, aseptate, 5.3–6.3 × 4.5–6.2 µm, formed in long dry chains | Acrogenous, aseptate, globose, verrucose, thick-walled, 3–6 × 3–5 µm (average, 5 × 4 µm), formed in long dry chains |

<sup>a</sup>From the description by Lombard et al. [24].

### Stachybotrys sansevieriae
G.P. Agarwal & N.D. Sharma, J. Indian Bot. Soc. 53: 78 (1974) ([Table 4, Figure 7](#)).

=Stachybotrys indica P.C. Misra, Mycotaxon 2: 107 (1975).

**Description:** Colonies grew slowly on PDA, reaching 23.5 mm diameter after 15 days at 25°C. The colony color was brown to dark Sepia. The conidiophore was straight, unbranched, with septate, cylindrical, 28.1–73.8 µm in length, and 2.4–8.5 µm in width. Conidigenous cells were phialidic, obovate, smooth, 8.3–12.5 × 3.5–6.1 µm. Conidia were ellipsoidal, unicellular, 5.4–10.1 × 3.5–6.9 µm. On PDA, growth was slower than on OA and CMA, and abundant sporulation was observed when grown on OA and CMA.
reported to have beneficial effects in the treatment of neurological diseases like Alzheimer’s, dementia, and Parkinson’s diseases [32,33]. This finding suggests that the strain CNUFC-KMHY6-1 is a potentially useful source for medical and biotechnological applications and needs to be investigated further.

In the phylogenetic trees based on ITS and RPB2 sequences, the 2 investigated strains CNUFC-MSW24-2-11 and CNUFC-MSW24-2-12 were clustered with other *M. echinata* species in a well-supported clade with high bootstrap values (Figures 3 and 4). The morphological features of our isolate...
Table 4. Morphological characteristics of CNUFC-GW2S-4 and the reference species Stachybotrys sansevieriae.

| Character          | CNUFC-GW2S-4                                      | Stachybotrys sansevieriae* |
|--------------------|---------------------------------------------------|-----------------------------|
| Colony color       | Brown to dark sepia                               | NA                          |
| Conidiophore       | Macronematous, mononematous, erected, straight, unbranched, septae, cylindrical, 28.1–73.8 × 2.4–5.5 μm | Subhyaline to pale brown, up to 60 μm long |
| Conidiogenous cell | Phialidic, obovate, smooth, 8.3–12.5 × 3.5–6.1 μm | 8–13 × 3–4 μm               |
| Conidia            | Ellipsoidal, unicellular, 5.4–10.1 × 3.5–6.9 μm    | Navicular, dark brown, 6–9 × 3–4 μm |

*aFrom the description by Pinruan et al. [19].
NA: not available.

Figure 7. Morphology of Stachybotrys sansevieriae CNUFC-GW2S-4. A) and D) Colony on potato dextrose agar (PDA); B) and E) Colony on oatmeal agar (OA); C) and F) Colony on corn meal agar (CMA) (A)–(C) top view, D)–(F) reverse view; G)–J), L), and M)–O) Conidiophores and phialides; K) and P) Conidia (Scale bars: G)–M) = 20 μm, N) = 5 μm, O) = 10 μm, P) = 2 μm).
were consistent with the description of *M. echinata* by Lombard et al. [24]. However, the size of the conidia was 5.3–6.3 × 4.5–6.2 μm, which was slightly larger than the conidia (3–6 × 3–5 μm) for *M. echinata* described by Lombard et al. [24].

In the ITS phylogenetic tree, the strains CNUFC-GW2S-4 and CNUFC-GW2S-5 were clustered in the same clade with *S. limonispora* CBS 128809, *S. sansevieriae* HGUP 0103, *S. sansevieriae* KNU16-141, and *S. subcylinodrospora* HGUP 0201 (Figure 3). However, the RPB2 sequences of CNUFC-GW2S-4 and CNUFC-GW2S-5 were easily distinguishable and were well separated in the phylogeny (Figure 4).

In 2017, the species of *S. sansevieriae* was isolated from field soils in Korea by Adhikari et al. [34] without detailed description such as the size of conidiophores, conidiogenous cells, and conidia. There was no any detailed phylogenetic analysis of the species in the family Stachybotriaceae.

Morphologically, *S. sansevieriae* reported here had a close similarity with the description by Pinruan et al. [19], although slight differences in the size of the conidia were noted. In comparison with other related species, our *S. sansevieriae* isolate presented ellipsoidal conidia (5.4–10.1 × 3.5–6.9 μm) that were larger than the ellipsoidal to limoniform conidia of *S. limonispora* ((5–9) – (6–16.5–7.5) × (3–4) μm) [24] and smaller than the cylindrical to subcylindrical conidia of *S. subcylinodrospora* ((9.7) – (11.6–13.8) – (2.9) – (3.8–4.6) – (5) μm) [35]. Furthermore, in the phylogenetic tree based on RPB2 sequence data, our strains formed a separate branch from *S. limonispora* CBS 128809 and *S. subcylinodrospora* HGUP 0201.

Among species of the genus Stachybotrys, *S. chartarum* is known to produce mycotoxins, including the macrocyclic trichothecenes [36], as well as diverse immunosuppressant agents [37,38]. Our newly recorded isolate *M. echinata* is closely related to *S. chartarum*. According to Jarvis et al. [39,40], *M. echinata* produces mycotoxins, including cytotoxic trichothecenes, as well as several griseofulvins. Our findings contribute to the understanding of three Sordariomycetes genera *Arcopilus*, *Memnoniella*, and *Stachybotrys* and increase the number of undiscovered species from freshwater and soil in Korea. Further studies on these 3 newly reported fungal isolates from Korea need to be performed.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

**Funding**

This work was in part supported by the Graduate Program for the Undiscovered Taxa of Korea, and in part by the Project on Survey and Discovery of Indigenous Fungal Species of Korea funded by NIBR and Project on Discovery of Fungi from Freshwater and Collection of Fungarium funded by NNIBR of the Ministry of Environment (MOE), and in part carried out with the support of Cooperative Research Program for Agriculture Science and Technology Development [PJ013744], Rural Development Administration, Republic of Korea. This work was in part supported by the BK21 plus program through the National Research Foundation (NRF) funded by the Ministry of Education of Korea.

**References**

[1] Lumbsch HT. Phylogeny of filamentous ascomycetes. Naturwissenschaften. 2000;87:335–342.
[2] Zhang N, Castlebury LA, Miller AN, et al. An overview of the systematics of the Sordariomycetes based on a four-gene phylogeny. Mycologia. 2006;98:1076–1087.
[3] Maharachchikumbura SSN, Hyde KD, Jones EBG, et al. Towards a natural classification and backbone tree for Sordariomycetes. Fungal Divers. 2015;72:199–301.
[4] Maharachchikumbura SSN, Hyde KD, Jones EBG, et al. Families of Sordariomycetes. Fungal Divers. 2016;79:1–317.
[5] Ho WH, Hyde KD, Hodgkiss IJ. Fungal communities on submerged wood from streams in Brunei, Hong Kong and Malaysia. Mycol Res. 2001;105:1492–1501.
[6] Cai L, Tsui CKM, Zhang KQ, et al. Aquatic fungi from Lake Fuxian, Yunnan, China. Fungal Divers. 2002;9:57–70.
[7] Jones EBG, Suetrong S, Sakayaroj J, et al. Classification of marine Ascomycota, Basidiomycota, Blastocladiomycota and Chytridiomycota. Fungal Divers. 2015;73:1–72.
[8] Sung GH, Hywel-Jones NL, Sung JM, et al. Phylogenetic classification of Cordyceps and the clavicipitaceous fungi. Stud Mycol. 2007;57:5–59.
[9] Hyde KD, Hongsanan S, Jeewon R, et al. Fungal diversity notes 367–491: taxonomic and phylogenetic contributions to fungal taxa. Fungal Divers. 2016;80:1–270.
[10] Jaklitsch WM, Voglmaier H. Phylogenetic relationships of five genera of Xylariales and Rosaphæria gen. nov. (Hypocreales). Fungal Divers. 2012;52:75–98.
[11] PeiGui L, DoiY X, Hua W, et al. The Hypocreaceae of China III. Some fungicolous species of the genus Hypocreia. Mycosystema. 2000;19:317–327.
[12] Barr ME. The ascomycetes connection. Mycologia. 1983;75:1–13.
[13] Barr ME. Prodromus to class Loculoascomycetes. Massachusetts: Amherst; 1987.
[14] Barr ME. Prodromus to nonlichenized, pyrenomycetous members of class Hymenoascomycetes. Mycotaxon. 1990;39:43–184.
Eriksson O, Hawksworth DL. Outline of the Ascomycetes—1993. Syst Ascomycetum. 1993;12:1–257.

Alexopoulos CJ, Mims CW, Blackwell M. Introductory mycology. New York: Wiley; 1996.

Hongsanan S, Maharachchikumbura SSN, Hyde KD, et al. An updated phylogeny of Sordariomycetes based on phylogenetic and molecular clock evidence. Fungal Divers. 2017;84:25–41.

Wang XW, Houbraken J, Groenewald JZ, et al. Diversity and taxonomy of Chaetomium and chaetomium-like fungi from indoor environments. Stud Mycol. 2016;84:145–224.

Pinruan U, McKenzie EHC, Jones EBG, et al. Two new species of Stachybotrys, and a key to the genus. Fungal Divers. 2004;17:145–157.

Wang Y, Hyde KD, McKenzie EHC, et al. Overview of Stachybotrys (Memnoniella) and current species status. Fungal Divers. 2015;71:17–83.

Smith G. Some new and interesting species of micro-fungi. III. Trans Br Mycol Soc. 1962;45:387–394.

Carmichael JW, Kendrick WB, Conners IL, et al. Genera of hyphomycetes. Edmonto: University Alberta Press; 1980.

Haugland RA, Vesper SJ, Harmon SM. Phylogenetic relationships of Memnoniella and Stachybotrys species and evaluation of morphological features for Memnoniella species identification. Mycologia. 2001;93:54–65.

Lombard L, Houbraken J, Decock C, et al. Generic hyper-diversity in Stachybotriaceae. Persoonia. 2016;36:156–246.

White TJ, Bruns T, Lee S, et al. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky JJ, White TJ, editors. PCR protocols: a guide to methods and applications. San Diego, CA: Academic Press; 1990. p. 315–322.

Liu YJ, Whelen S, Hall BD. Phylogenetic relationships among ascomycetes: evidence from an RNA polymerase II subunit. Mol Biol Evol. 1999;16:1799–1808.

Thompson JD, Gibson TJ, Plewniak F, et al. The CLUSTAL_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. Nucleic Acids Res. 1997;25:4876–4882.

Hall TA. BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symp Ser. 1999;41:95–98.

Tamura K, Stecher G, Peterson D, et al. MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. Mol Biol Evol. 2013;30:2725–2729.

Chivers AH. A monograph of the genera Chaetomium and Asperochitra. Mem Torrey Bot Club. 1915;14:155–240.

Dwivedi V, Saxena S. Arcopilus aureus, a resveratrol-producing endophyte from Vitis vinifera. Appl Biochem Biotechnol. 2018;186:476–495.

Li F, Gong Q, Dong H, et al. Resveratrol, a neuroprotective supplement for Alzheimer’s disease. Curr Pharm Des. 2012;18:27–33.

Lange KW, Li S. Resveratrol, pterostilbene, and dementia. Biofactors. 2018;44:83–90.

Adhikari M, Gurung SM, Bazie S, et al. Seven unrecorded fungal species from field soils in Korea. Kor J Mycol. 2018;46:9–21.

Jie CY, Geng K, Jiang YL, et al. Stachybotrys from soil in China, identified by morphology and molecular phylogeny. Mycol Progress. 2013;12:693–698.

Jarvis BB. Macrocyclic trichothecenes. In: Sharma RP, Salunkhe DK, editors. Mycotoxins and phytalexins in human and animal health. Boca Raton, FL: CRC Press; 1991. p. 361–421.

Roggo B, Petersen F, Sills M, et al. Novel spirodihydrobenzofuranlactams as antagonists of endothelin and as inhibitors of HIV-1 protease produced by Stachybotrys sp. I. Fermentation, isolation and biological activity. J Antibiot. 1996;49:13–19.

Roggo BE, Hug P, Moss S, et al. Novel spirodihydrobenzofuranlactams as antagonists of endothelin and as inhibitors of HIV-1 protease produced by Stachybotrys sp. II. Structure determination. J Antibiot. 1996;49:374–379.

Jarvis BB, Sorenson WG, Hintikka EL, et al. Study of toxin production by isolates of Stachybotrys chartarum and Memnoniella echinata isolated during a study of pulmonary hemosiderosis in infants. Appl Environ Microbiol. 1998;64:3620–3625.

Jarvis BB, Zhou Y, Wang S, et al. Toxicigenic molds in water-damaged buildings: dechlorogriseofulvins from Memnoniella echinata. J Nat Prod. 1996;59:553–554.