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# Article

Mycosphere Online Edition

Doi 10.5943/mycosphere/5/3/3

# A new species, Lophiostoma versicolor, from Japan (Pleosporales, Dothideomycetes)

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Hirayama K, Hashimoto A, Tanaka K 2014 – A new species, *Lophiostoma versicolor*, from Japan (Pleosporales, Dothideomycetes). Mycosphere 5(3), 411–417, Doi 10.5943/mycosphere/5/3/3

#### **Abstract**

Lophiostoma versicolor sp. nov. was found on Acer sp. in Japan. This species is characterized by ascomata with a laterally compressed apex; clavate, 2(-4)-spored asci with a long stipe; and verruculose, 3-septate, versicolored ascospores without a sheath or appendages. Phylogenetic analyses based on LSU nrDNA sequences supported the generic placement and species validity of L. versicolor.

**Key words** – ITS – Lophiostomataceae – *Lophiotrema* – LSU nrDNA – Pleosporomycetidae – Systematics – Taxonomy

#### Introduction

During an investigation of bitunicate ascomycetes in Japan, an unidentified fungus was found on dead twigs of *Acer* sp. The morphological characteristics of the fungus, such as the presence of ascomata with a compressed beak and clavate asci, recall those of *Lophiostoma* (Hirayama & Tanaka 2011) belonging to the Lophiostomataceae. This fungus, however, is different from any of the existing species of the genus because it possesses 2(–4)-spored asci and verruculose, 3-septate, versicolored ascospores without a sheath or appendages.

As a generic placement of our obtained fungus, *Lophiotrema* was also considered. This genus is morphologically similar to *Lophiostoma*. For example, they share several characteristics including their carbonaceous ascomata with a laterally compressed apex (termed as a crest-like beak with a slit-like ostiole), fissitunicate asci, and hyaline to dark brown, uni- to multiseptate ascospores (Holm & Holm 1988). Some authors treated *Lophiotrema* as a synonym of the older genus *Lophiostoma* (Chesters & Bell 1970, Leuchtmann 1985), whereas most authors regarded them as distinct but closely related genera within Lophiostomataceae on the basis of morphological observations (Barr 1992, Yuan & Zhao 1994, Tanaka & Harada 2003a, b).

Hirayama & Tanaka (2011) revealed that *Lophiostoma* and *Lophiotrema* are distinct genera belonging to Lophiostomataceae and Lophiotremataceae, respectively, based on phylogenetic analyses of small subunit (SSU) and large subunit (LSU) nuclear ribosomal DNA (nrDNA) sequences. They concluded that the ascus shape including the length of the ascus stipe is the most important morphological criterion to delineate both genera. In *Lophiostoma*, the asci are clavate

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with a relatively long stipe [mostly  $(10-)15-30 \mu m \log$ ], whereas in *Lophiotrema*, the asci are cylindrical with a short stipe (up to 15  $\mu m \log$ ; Hirayama & Tanaka 2011). According to these generic circumscriptions, the collected fungus might appear to be a member of *Lophiostoma* because it has clavate asci with a relatively long stipe.

The objectives of this study were to evaluate the taxonomic significance of ascus shape and ascus stipe length which were used to distinguish both genera (Hirayama & Tanaka 2011) using the newly obtained fungus and to confirm its species validity based on phylogenetic analyses of LSU sequences.

#### **Materials & Methods**

# **Isolates and morphology**

The methods for microscopy and single spore isolation followed those described by Hirayama et al. (2010). For the ascospore septum position, the decimal system (Shoemaker 1984) was used. The holotype specimen was deposited in the Herbarium of Hirosaki University (HHUF). The growth rate and colony characteristics were recorded from cultures grown on corn meal agar (CMA, Difco), malt extract agar (MEA, Difco), and potato dextrose agar (PDA, Difco) after 3 weeks at 20 °C in the dark. Colors were designated as described by Kornerup & Wanscher (1978). To validate isolations, sporulation was promoted by placing a small piece of mycelial culture on rice straw agar (RSA; Tanaka & Harada 2003a). The utilized fungal culture was deposited in the National Institute of Agrobiological Sciences (MAFF).

# Phylogenetic analyses

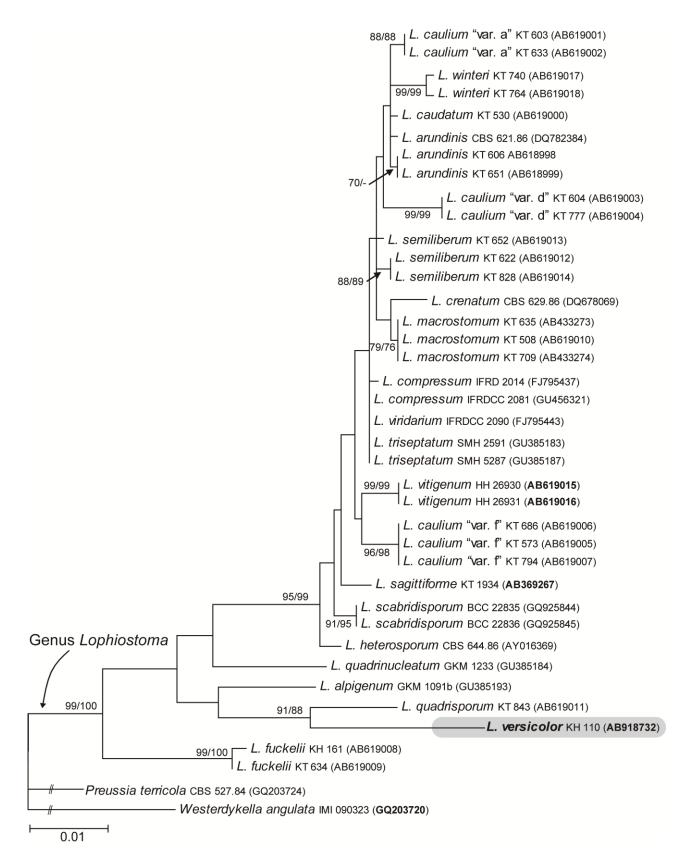
The detailed methods of DNA extraction and polymerase chain reaction (PCR) amplification were as those described by Tanaka et al. (2009). Partial LSU nrDNA and complete internally transcribed spacers (ITS) of nrDNA were amplified by PCR using the primer pairs LR0R–LR7 for LSU (Rehner & Samuels 1994) and ITS1–ITS4 for ITS (White et al. 1990). Newly obtained sequences were deposited in GenBank.

A BLAST search using the LSU sequence of the newly obtained taxon suggested that it is a member of Lophiostoma rather than Lophiotrema. Therefore, phylogenetic analyses of the collected fungus (Lophiostoma versicolor) with other Lophiostoma spp. were performed. The obtained LSU sequence of L. versicolor was manually aligned along with published sequences of Lophiostoma (e.g., Tanaka & Hosoya 2008, Mugambi & Huhndorf 2009, Suetrong et al. 2009, Zhang et al. 2009a, b, Hirayama & Tanaka 2011) in GenBank using the MUSCLE algorithm implemented in the program Molecular Evolutionary Genetic Analysis (MEGA) v5 (Tamura et al. 2011). Sequences of *Preussia terricola* and *Westerdykella angulata*, both members of Sporormiaceae (Kruys & Wedin 2009), were used as outgroup taxa. The aligned dataset was subjected to two phylogenetic analyses involving maximum likelihood (ML) and maximum parsimony (MP) using MEGA 5. Based on the Bayesian information criterion of MEGA 5, Kimura 2-parameter model with gamma distribution (K2 + G) was selected for the ML analysis. The ML tree was obtained using the default settings with "use all site" for gaps/missing data treatment. MP tree was generated using the close-neighbor-interchange heuristic search (level 1), the initial tree by random addition sequence (100 replicates), and the "use all site" option. The confidence in topologies was assessed using a bootstrap (BS) test involving 1000 replicates. The ITS sequence of L. versicolor was also obtained as a DNA barcode maker (Schoch et al. 2012), and it was not used for phylogenetic analysis.

#### **Results**

#### Phylogenetic analyses

A total of 37 LSU sequences of *Lophiostoma* spp. were aligned with outgroup taxa. Of 1228 characters, 143 (11.6%) were variable and 100 (8.1%) were parsimony-informative. The ML tree



**Fig. 1** – The ML tree of *Lophiostoma* spp. with the highest log likelihood (–3081.8178) based on the LSU dataset (1228 positions). ML and MP BS values greater than 70% are indicated at the nodes. A hyphen indicates BS values lower than 70%. The isolate number and GenBank accession number (in parentheses) are noted after the species name. Sequence derived from the type is shown in bold. The tree was rooted with *Preussia terricola* and *Westerdykella angulata* (Sporormiaceae).

with the highest log likelihood (-3081.8178) is shown in Fig. 1. The topology of the MP tree was almost identical to that of the ML tree. The newly obtained fungus (*L. versicolor*) nested within the strongly supported clade of *Lophiostoma*, which had high BS values (99% in ML, 100% in MP; Fig. 1). Phylogenetically, *L. versicolor* was most closely related to *L. quadrisporum*, and their relationship was moderately supported (91% in ML, 88% in MP; Fig. 1). These two species were sister taxa to *L. alpigenum*, but without support.

# **Taxonomy**

Lophiostoma versicolor K. Hiray. & Kaz. Tanaka, sp. nov.

Figs. 2–18

MycoBank: MB 808363.

Etymology – in reference to the versicolored ascospores.

Holotype: HHUF 30448.

Ascomata 330–350 µm high, 360–400 µm diam., scattered, immersed, erumpent at beak, subglobose, black. Beak 170 µm wide, crest-like, composed of globose, 2–4 µm diam., thick-walled cells, with a slit-like ostiole. Ascomatal wall 20–27.5 µm thick at sides, composed of 5–7 layers of rectangular, 7–10  $\times$  2.5–6 µm, thin-walled cells, poorly developed at the base. Pseudoparaphyses numerous, 1–2 µm wide, septate, hyaline, branched and anastomosed, associated with gelatinous material. Asci 60–67.5(–77.5)  $\times$  10–12.5(–15) µm, fissitunicate, clavate, with a stalk of 12.5–22.5(–27.5) µm long, rounded at the apex, with an ocular chamber, with 2(–4) overlapping uni- or bi-seriate ascospores. Ascospores 18–23  $\times$  6–9 µm (mean 20.2  $\times$  7.7 µm, n = 30), L/W 2.3–2.9 (mean 2.6, n = 30), broadly fusiform, straight, with a primary septum median to submedian (0.50–0.55; mean 0.51, n = 30), 3-septate, constricted at primary septum, versicolored, brown to reddish brown except pale end cells, verruculose, guttulate, without sheath or appendage.

Colonies on CMA 13 mm after 3 weeks at 20 °C in the dark, Pastel Gray (1C1: Kornerup & Wanscher 1978), reverse Olive Gray (2F2). On MEA 11 mm, Olive Gray (2E2), reverse Olive Gray (1F2). On PDA 15 mm, Medium Gray (1D1) reverse Pastel Gray (1C1). No pigment was produced on these media. On RSA ascomatal state almost identical with those on the natural specimen was observed. Ascospores  $19–22\times6–7~\mu m$  (mean  $20.8\times6.5~\mu m$ , n=50), L/W 2.9–3.7 (mean 3.2, n=50).

Asexual state – unknown.

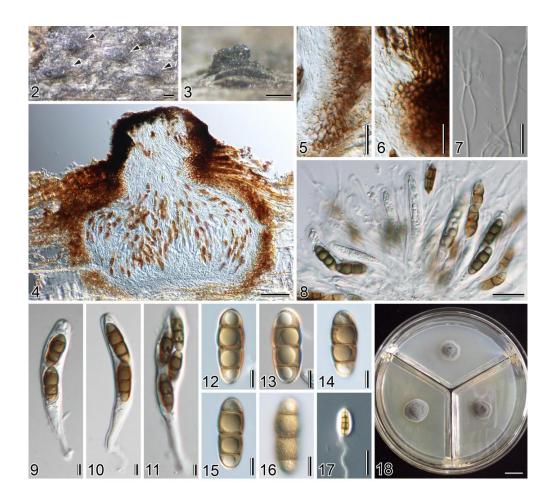
Known distribution – Japan.

Material examined – Japan, Mie, Tsu, Campus of Mie Univ., on twigs of *Acer* sp., 30 May 2008, coll. K. Tanaka and H. Yonezawa, KH 110 (HHUF 30448 holotype designated here) – extype culture MAFF 244508.

nrDNA sequences – AB918731 (ITS), AB918732 (LSU).

### **Discussion**

Lophiostoma, typified by L. macrostomum, belongs to Lophiostomataceae, Pleosporales, Dothideomycetes (Kirk et al. 2008, Zhang et al. 2012, Hyde et al. 2013). Species of this genus are found on various plants, e.g. woody plants, reeds, palms and bamboo, they and are inhabitants of terrestrial, freshwater and marine environments. This genus is characterized by ascomata with a laterally compressed apex, fissitunicate asci, and hyaline to dark brown, uni- to multiseptate ascospores (Holm & Holm 1988, Hirayama & Tanaka 2011). These ecological and morphological features are similar to those of Lophiotrema. Therefore, they have been considered as closely related genera belonging to the same family (Barr 1992) or congeneric (Chesters & Bell 1970). Recently, a molecular study of Lophiostoma and Lophiotrema revealed that they are phylogenetically distinct genera, and Lophiotrema is related to Testudinaceae rather than Lophiostomataceae (Zhang et al. 2009a, b). More recently, Hirayama & Tanaka (2011) concluded that these genera can be mainly distinguished by ascus shape including its stipe length, for example, clavate asci with a relatively long stipe [mostly (10–)15–30 µm] in Lophiostoma and cylindrical



**Figs 2–18** – *Lophiostoma versicolor* (2–17 from HHUF 30448. 18 from MAFF 244508). 2 Ascomata on host surface. 3 Compressed beak of ascoma, 4 Longitudinal section of ascoma. 5 Ascomatal wall at side. 6 Wall of beak. 7 Pseudoparaphyses. 8 Pseudoparaphyses and asci. 9–11 Asci. 12–16 Ascospores (16 Ascospore with verruculose ornamentation). 17 Germinating ascospore. 18 Colonies on CMA (upper), PDA (left) and MEA (right) after 3 weeks at 20 °C in the dark. – Bars 2,  $3 = 200 \, \mu m$ .  $4 = 50 \, \mu m$ . 5-8,  $17 = 20 \, \mu m$ .  $9-16 = 5 \, \mu m$ .  $18 = 1 \, cm$ .

asci with a short stipe (up to 15  $\mu$ m) in *Lophiotrema*, and they established a new family Lophiotremataceae for *Lophiotrema*.

The collected fungus from *Acer* sp. has ascomata with a laterally compressed beak with a slit-like ostiole and clavate asci with a long stipe (Figs. 2, 3, 8). These morphological characteristics of this fungus suggest that it is a member of *Lophiostoma*, but it also has unusual features for the genus. For example, 2(–4)-spored asci and verruculose, 3-septate, versicolored ascospores without a sheath or appendages (Figs. 9–16) are atypical for this genus and there are no species with these characteristics in the monographs of *Lophiostoma* (e.g., Lehmann 1886, Berlese 1894, Chesters & Bell 1970, Holm & Holm 1988, Barr 1992, Yuan & Zhao 1994, Tanaka & Harada 2003a). *Lophiotrema*, morphologically closest genus to *Lophiostoma*, was also considered as a generic placement of the fungus. Therefore, molecular studies were conducted to confirm the generic classification of the collected fungus.

Preliminary analysis based on a BLAST search using LSU sequences, as well as those of ITS obtained for barcoding, suggested that the new species belongs to *Lophiostoma* rather than *Lophiotrema*. Subsequent phylogenetic analyses based on LSU nrDNA sequences for the obtained fungus (*L. versicolor*) and *Lophiostoma* spp. clearly indicated that *L. versicolor* is a member of *Lophiostoma* (Fig. 1). The characteristic versicolored ascospores observed in *L. versicolor* are known in *Byssothecium* (Boise 1983) and in *Passeriniella* (Berlese 1894), but these genera belong to the Massarinaceae (Zhang et al. 2012, Hyde et al. 2013) and to an unknown lineage comprising

marine fungi (Suetrong et al. 2009), respectively. *Lophiostoma* species including *L. versicolor* formed a monophyletic clade supported by strong BS values (99–100%; Fig. 1). *Lophiostoma versicolor* was most close to *L. quadrisporum* (similarity 978/1009 = 96.9% in LSU), and their relationship had moderate BS support (88–91%; Fig. 1). These results reconfirmed that the ascus shape including the length of ascus stipe, which was previously proposed for differentiating *Lophiostoma* and *Lophiotrema* (Hirayama & Tanaka 2011), is a reliable taxonomic indicator for distinguishing these genera.

Lophiostoma versicolor has several unique characteristics such as 2(-4)-spored asci and verruculose, versicolored ascospores (Figs. 8–16). Versicolored ascospores similar to those of *L. versicolor* are known to be present in *L. pileatum*, but this species differs from *L. versicolor* in having 8-spored asci and 6–10-septate, larger ascospores  $[(35-)40-60(-67)\times12-30~\mu m;$  Chesters & Bell 1970]. Most species of *Lophiostoma* have 8-spored asci, whereas species that have 2- or 4-spored asci are extremely rare. *Lophiostoma quadrisporum*, which is phylogenetically close to *L. versicolor* (Fig. 1), has 4-spored asci, but it has 1-septate, smooth, hyaline ascospores (Tanaka & Harada 2003b, misidentified as *L. nucula*, see also Hirayama & Tanaka 2011). The asci of *L. macrostomoides* and *L. mucosum* are (4-)8-spored, but the former has (4-)5-7(-8)-septate ascospores (Mathiassen 1993) and the latter has more large-sized ascospores,  $(27.5-)30.5-40(-46.5)\times(5.5-)7-10.5(-12)~\mu m$  (Tanaka & Harada 2003a), as compared to those of *L. versicolor*. Generally, the number of ascospores per ascus is considered as an important character for species discrimination (Voglmayr & Jaklitsch 2011). Therefore, we described here the fungus as a new species of *Lophiostoma*, *L. versicolor*.

# Acknowledgements

This work was partially supported by funding from the Japan Society for the Promotion of Science (JSPS, 25440199) and a Hirosaki University Grant for Exploratory Research by Young Scientists (2008–2013). We thank H. Yonezawa for helping with the collection of fungal specimen.

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