Ascomycete Japonicae Exsiccati, Fascicle 2, Nos. 11-20

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(Received 1 May 2021; accepted 23 June 2021)

Abstract Ten sets of specimens of fungi, each composed of ten taxa were prepared to introduce fungal biodiversity to overseas herbaria including CAS, CUP, DAVFP, FH, GZU, PDD, and TUR. The specimens are accompanied with cultures deposited in a culture collection, tissue samples, and extracted DNA samples when available.

Keywords: ascomycetes, biodiversity, discomycetes, exsiccata, mycobiota.

Introduction

This is the second fascicle following the previous fascicle (Hosoya et al., 2019) of the occasional series to introduce discomycetes and other mycobiota in Japan in exsiccatae. The specimens provided here are accompanied with isolates, tissue samples, extracted DNA samples, and registered sequences whenever possible. The isolates were deposited to NITE BioResource Center (https://www.nite.go.jp/en/nbrc/cultures/index. html). Isolation, cultivation, methods for DNA extraction to sequence followed Itagaki et al. (2019). Isolates were deposited to Biological Resource Center, National Institute of Technology and Evaluation (NITE-BRC). Tissue samples and extracted DNA were deposited to Center for Molecular Biodiversity Research, National Museum of Nature and Science for collaborative research. DNA sequences were deposited to DDBJ (https://www.ddbj.nig.ac.jp/index-e.html) or UNITE (https://unite.ut.ee/). Coordinates follow WGS84 datum.

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1. Aleuria aurantia (Pers.) Fuckel

On the *Abies firma* forest floor, Yammba Nature Park, Naganohara, Agatsuma-gun, Gunma Pref. (+36.539082, +138.928146). 2020-X-12. Collected by Tsuyoshi Hosoya and Hiyori Itagaki. Identified by Tsuyoshi Hosoya. Duplicate of TNS-F-91318.

Note: This is a common species that is widely distributed in Japan. The internal transcribed spacer and 5.8S ribosomal DNA region (ITS-5.8S) sequence obtained from the present specimen (LC619223) showed >98.5% similarity with the previously registered sequences from strain or voucher specimens of *A. aurantia* (KX449456, MN992569, MK575463, DQ491495) by basic local alignment tool (BLAST) search.

2. Arachnopeziza delicatula Fuckel

On unidentified rotten wood, Atsubetsu, Atsubetsu-ku, Sapporo-shi, Hokkaido (+43.021208, +141.482246). 2020-VIII-3. Collected by Tsuyo-shi Hosoya and Hiyori Itagaki. Identified by Tsuyoshi Hosoya. Duplicate of TNS-F-86287 (culture NBRC 115014).

Note: This is a common species that mainly occurs on deciduous wood. The ITS-5.8S

sequence of this material (LC619224) was identical with that of a previously collected A. delicatula specimen (TNS-F-12770, JN033433), and showed high similarity >98.5% with other A. delicatula sequence (MT231651) cited in Kosonen et al. (2021). The species superficially resembles A. aurata in morphology (Korf, 1951), but Kosonen et al. (2021) demonstrated that the two species are phylogenetically distantly related. In Japan, we have more specimens identified as A. aurata than those identified as A. delicatula, but the former may include potential A. delicatula. There is a trend to accept Gorgoniceps delicatula (Fuckel) Höhn. as a correct name for A. delicatula (http://www.speciesfungorum. org/Names/SynSpecies.asp?RecordID=262927 (accessed on 12 March 2011), but we accept Arachnopeziza as an appropriate genus to accommodate this species based on the detailed molecular phylogenetic analysis by Kosonen et al. (2021).

3. Brunnipila clandestina (Bull.) Baral

On dead twigs of *Rubus idaeus*, Engaru-cho, Okhotsk subprefecture, Hokkaido. 2018-VII-14. Collected and identified by Yukito Tochihara. Duplicate of TNS-F-81486 (culture NBRC 113939).

Note: The present fungus was described in detail based on the present specimen in Tochihara *et al.* (2019). The ITS-5.8S sequence was registered to UNITE as UDB0779084.

4. Bulgaria inquinans (Pers.) Fr.

On *Quercus crispula* bark, Ogawa, Sekimotocho, Kita-ibaraki-shi, Ibaraki Pref. (+ 36.939483, + 140.587203). 2020-VI-10. Collected by Tsuyoshi Hosoya and Yukito Tochihara. Identified by Tsuyoshi Hosoya. Duplicate of TNS-F-223906 (culture NBRC 115011).

Note: *Bulgaria inquinans* is well-known for its characteristic morphology. The ITS-5.8S sequence of the culture from the present specimen (LC619225) showed identical sequence with voucher specimens or strains (e.g., KY633576 from DAOM 240100, KY633580 from DAOM 145165, KJ663832 from strain CBS129.58,

AY789345 from strain ZW-Geo52-Clark).

5. *Gelatinipulvinella astraeicola* Hosoya & Y.Otani

On inner surface of *Astraeus hygrometricus* cortex, Lake Shikotsu-ko, Chitose-shi, Hokkaido (+42.741878, +141.402161). 2020-VIII-4. Collected by Tsuyoshi Hosoya and Hiyori Itagaki. Identified by Tsuyoshi Hosoya. Duplicate of TNS-F-60536 (culture NBRC 115012).

Note: *Gelatinipulvinella atraeicola* is characterized by its unique fungicolous habitat and yeast-like asexual state. Since its first report (Hosoya and Otani, 1995), the occurrence has been widely known in Japan. The closest affinity with the ITS-5.8S sequence of this isolate (LC619226) was *Gelatinopsis fungicola* (Kirschst.) Baral with the similarity of 93–94% based on BLAST search. This is reasonable based on the morphological resemblance.

6. Helvella elastica Bull.

On ground, Tsukuba Botanical Garden, Tsukuba, Ibaraki Pref. (+36.100696, +140.11198). 2020-X-28. Collected by Tsuyoshi Hosoya. Identified by Tsuyoshi Hosoya. Duplicate of TNS-F-91339.

Note: *Helvella elastica* is known from a wide area in Japan, and the present specimen shows the typical morphology for the fungus recognized as *H. elastica* in Japan. However, the ITS-5.8S sequence (LC619227) showed rather low similarity with those stored in GenBank (88–90%), and only unidentified *Helvella* sequences (LC098743) showed the highest similarity of 98% as a result of BLAST search. As discussed by Skrede *et al.* (2017), ITS-5.8S region in this genus may be too diverse to define a species.

7. *Hyphopeziza pygmaea* (Mouton) J.G.Han, Hosoya & H.D.Shin

On *Quercus crispula* leaf, Kakuma, Sanadamachi, Ueda-shi, Nagano Pref. (+36.455075, +138.35878). 2015-VI-4. Collected by Tsuyoshi Hosoya. Identified by Tsuyoshi Hosoya. Duplicate of TNS-F-61910 (culture NBRC 115009).

Note: The fungus was originally described as

Hyalopeziza pygmaea by Hosoya and Otani (1997), and examined by Han *et al.* (2014) to be recognized as a member of a new monotypic genus. It is common on *Quercus crispula* in spring in Japan. The ITS-5.8S sequence from the present specimen (LC619228) showed>98.5% similarity with vouchers KUS-F51564 and TNS-F-17940, showing the conservative nature of the region for this fungus.

8. *Purpureocillium atypicola* (Yasuda) Spatafora, Hywel-Jones & Luangsa-ard

On Antrodiaetidae, Hiroshima-shi Plant Park, Kurashige, Saeki-ku, Hiroshima-shi, Hiroshima Pref. (+34.394111, +132.345167). 2011-VII-10. Collected by Toshikazu Imoto. Identified by Tsuyoshi Hosoya. Duplicate of TNS-F-39273 (culture NBRC 115008).

Note: The ITS-5.8S sequence from the isolate of the present specimen (LC619229) showed 100% match with *Cordyceps cylindrica* Petch (LC008213), regarded as the sexual state of *P. atypicola* (Spatafora *et al.*, 2015).

9. Taphrina truncicola Kusano

On *Cerasus maximowiczii* peduncle, Sugadaira Montane Research Center, Tsukuba University, Ueda-shi, Nagano Pref. (+36.524947, +138.347047). 2019-VI-9. Collected by Tsuyoshi Hosoya. Identified by Tsuyoshi Hosoya. Duplicate of TNS-F-88648 (culture NBRC 115010).

Note: The ITS-5.8S sequence obtained for this strain (LC619230) shows significant differences with sequences of other *Taphrina* species currently registered in GenBank, and justifies its specific distiction by molecular evidence.

10. Tarzetta catinus (Holmsk.) Korf & J.K.Rogers

On ground, Yamanouchi-machi, Shimotakaigun, Nagano Pref. (+36.709333, +138.49647). 2011-VI-30. Collected by Tsuyoshi Hosoya. Identified by Tsuyoshi Hosoya. Duplicate of TNS-F-91388.

Note: Although this fungus is common in the *Fagus crenata* forest in Japan, its occurrence is

not reported in academic literature in Japan. *Tarzetta catinus* is common in Europe and America and more than 2,000 occurrences has reported (GBIF.org, 29 December 2020). The ITS-5.8S sequence from the present specimen (LC619231) showed the highest similarity (99.65%) with *Tarzetta* cf. *catinus* isolate AH:53705 (MN712325), but there was no identical sequence in GenBank. Several sequences with higher similarity (>98.5%) labeled as *T. catinus* were also found.

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