Four Newly Recorded *Amanita* Species in Korea: *Amanita* sect. *Amanita* and sect. *Vaginatae*

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Abstract We collected nearly 70 specimens of *Amanita* species during a diversity study of Korean mushrooms conducted in 2012. In this study, we primarily investigated 23 *Amanita* specimens belonging to sections *Amanita* and *Vaginatae*. Based on sequence data of the internal transcribed spacers and partial large subunit of ribosomal RNA and morphological characteristics, we identified the following 15 phylogenetic species: *A. alboflavescens*, *A. ceciliae*, *A. farinosa*, *A. fulva*, *A. griseofolia*, *A. ibotengutake*, *A. melleiceps*, *A. orientifulva*, *A. pantherina*, *A. rubrovolvata*, *A. sinensis*, *A. subglobosa*, *A. vaginata*, *A. cf. vaginata* f. *alba*, and an undescribed *Amanita* species. In this study, four of the identified *Amanita* species (*A. griseofolia*, *A. ibotengutake*, *A. orientifulva*, and *A. sinensis*) were reported for the first time in Korea.

Keywords *Amanita* sect. *Amanita*, *Amanita* sect. *Vaginatae*, ITS, Morphology, nLSU, Phylogeny

Amanita Pers. comprises both edible and poisonous mushrooms that exhibit worldwide distribution, usually as mycorrhizal symbionts with plants [1, 2]. Infrageneric classification, which is based mainly on the morphological characteristics of the fruit body, has divided this genus into two subgenera [subgen. *Amanita* Pers. (having inamyloid spores) and subgen. *Lepidella* (E. J. Gilbert) Veselý emend. Corner & Bas (having amyloid spores)] and seven sections [*Amanita* Pers., *Caesareae* Singer, *Vaginatae* (Fr.) Quél., *Amidella* (E. J. Gilbert) Konrad & Maubl., *Lepidella* (E. J. Gilbert) Corner & Bas, *Phalloideae* (Fr.) Quél., and *Validae* (Fr.) Quél.] [1]. *Amanita muscaria* (L.) Lam., the type species of the genus, consists of several varieties with different color forms, such as *A. muscaria* var. *muscaria*

(L.) Lam. (red pileus and white stem and warts), *A. muscaria* var. *alba* Peck (white-to-tan pileus, warts, and stem), *A. muscaria* var. *flavivolvata* (Singer) D. T. Jenkins (orange-to-red pileus, tannish-yellow warts, and white-to-cream stem), *A. muscaria* var. *formosa* Pers. (orange-to-yellow pileus and yellowish-to-tannish warts and stem), *A. muscaria* var. *persicina* D. T. Jenkins (melon pileus and tannish-to-yellowish warts), and *A. muscaria* var. *regalis* (Fr.) Sacc. [now *A. regalis* (Fr.) Michael] (brown pileus and tannish-to-yellowish warts) [3, 4].

While nearly 500 *Amanita* species have been described, molecular studies are required to confirm and verify morphology-based identifications because some *Amanita* species are morphologically identical [1, 5, 6]. In addition, some *Amanita* species represent the most-poisonous higher fungi, which makes accurate identification of morphologically similar species especially important [7, 8]. This situation has prompted many mycologists to investigate the DNA-based phylogenies of *Amanita* species [1-3, 9-13]. Most reports on *Amanita* species in Korea only include short morphological descriptions or their sequences have not been deposited in GenBank [7, 14, 15].

We conducted a preliminary investigation of the taxonomy of *Amanita* species. We collected 70 specimens of *Amanita* species during a diversity study of Korean mushrooms conducted in 2012 and preserved them in the herbarium of the Korea National Arboretum (KA), Gwangneung Forest, Pocheon-si, Gyeonggi Pref., Korea. For the current study, we selected 23 of these specimens belonging to the

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Amanita sect. *Amanita* and *Amanita* sect. *Vaginatae*. The goal of the present study was to clarify the phylogenetic positions of *Amanita* species collected during the survey conducted in 2012 based on sequence data of the internal transcribed spacers (ITS) and partial large subunit (nLSU) of ribosomal RNA. In addition, we describe four *Amanita* species that have not been previously reported in Korea, and designate them with Korean names.

MATERIALS AND METHODS

Specimens and morphological observations. The 23 *Amanita* specimens used in the present study are listed in Table 1 and the dried specimens were deposited in the KA herbarium. Reliable DNA sequence data for other reported *Amanita* species were obtained from GenBank for the phylogenetic analyses. Macro-morphological descriptions were based on field notes and color photographs of basidiomata. Micro-morphological data were obtained from the dried specimens with the aid of a light microscope after sectioning and rehydration in 3% KOH solution. Descriptions of spore shapes are based on the study reported by Bas [16].

PCR amplification and sequencing. DNA was isolated from fresh fruit bodies (approximately 0.1 g) using a modified version of the CTAB procedure reported by Doyle and Doyle [17]. Two primer sets were used for

amplification of the ITS regions and partial LSUs of ribosomal RNA: ITS5 and ITS4 [18], and LR0R and LR5 [19]. PCR mixtures contained 0.5 pmol of each primer, 0.25 mM dNTPs, 10 mM Tris-HCl, 50 mM KCl, 1.5 mM MgCl₂, 2.5 U of Taq DNA polymerase, and 15 ng of template DNA. The PCR conditions for ITS and nLSU were as follows: an initial denaturation step at 94°C for 4 min, followed by 34 cycles of 94°C for 40 sec, 52°C for 40 sec, and 72°C for 60 sec, and a final elongation step at 72°C for 8 min. PCR products were purified using an ExoSAP kit (USB, Cleveland, OH, USA). The purified double-stranded PCR fragments were directly sequenced using a BigDye Terminator Cycle Sequencing Kit (Applied Biosystems, Foster City, CA, USA) following the manufacturer's instructions. The same primer sets used for amplification of ITS and nLSU were employed for sequencing. Capillary electrophoresis and data collection were performed on an ABI Prism 310 Genetic Analyzer (Applied Biosystems). Sequence data were submitted to GenBank (Table 1).

Phylogenetic analyses. Raw sequences were proofread, edited, and assembled into contigs using PHYDIT 3.2 [20]. DNA sequences were aligned using ClustalX 1.81 [21], and then manually adjusted using PHYDIT. Ambiguously aligned regions were excluded from subsequent analyses.

To determine the phylogenetic positions of the sampled specimens, datasets were analyzed using maximum parsimony (MP) in PAUP version 4.0b10 [22] and Bayesian inference

Table 1. Information on the *Amanita* species used in this study

Species	Specimens ^a	Locality	Collection date	GenBank accession Nos.	
				ITS	nLSU
<i>A. alboflavescens</i>	KA12-0970	Gwangneung forest, Pocheon-si, Gyeonggi	9 Aug 2012	KF017928	KF021667
<i>A. ceciliae</i>	KA12-0758	Mt. Seodae, Geumsan-gun, Chungnam	18 Jul 2012	KF017929	KF021668
	KA12-0916	Gwangneung forest, Pocheon-si, Gyeonggi	27 Jul 2012	KF017930	KF021669
<i>A. farinosa</i>	KA12-0783	Mt. Geumjeok, Boeun-gun, Chungbuk	19 Jul 2012	KF017931	KF021670
	KA12-1009	Gwangneung forest, Pocheon-si, Gyeonggi	9 Aug 2012	KF017932	KF021671
<i>A. fulva</i>	KA12-1406	Mt. Seonginbong, Ulleung-gun, Gyeongbuk	6 Sep 2012	KF017933	KF021672
<i>A. griseofolia</i>	KA12-0818	Gwangneung forest, Pocheon-si, Gyeonggi	26 Jul 2012	KF017934	KF021673
	KA12-0994	Gwangneung forest, Pocheon-si, Gyeonggi	9 Aug 2012	KF017935	KF021674
	KA12-1454	Gwangneung forest, Pocheon-si, Gyeonggi	12 Sep 2012	KF017936	KF021675
<i>A. ibotengutake</i>	KA12-1339	Nari Basin, Ulleung-gun, Gyeongbuk	5 Sep 2012	KF017937	KF021676
<i>Amanita</i> sp.	KA12-1175	Mt. Jinak, Geumsan-gun, Chungnam	28 Aug 2012	KF017938	KF021677
<i>A. melleiceps</i>	KA12-1213	Mt. Seodae, Geumsan-gun, Chungnam	29 Aug 2012	KF017939	KF021678
<i>A. orientifulva</i>	KA12-0642	Mt. Minjuji, Yeongdong-gun, Chungbuk	16 Jul 2012	KF017940	KF021679
	KA12-1596	Mt. Geumjeok, Boeun-gun, Chungbuk	27 Sep 2012	KF017941	KF021680
	KA12-0932	Gwangneung forest, Pocheon-si, Gyeonggi	8 Aug 2012	KF017942	KF021681
<i>A. pantherina</i>	KA12-1225	Mt. Seodae, Geumsan-gun, Chungnam	29 Aug 2012	KF017943	KF021682
	KA12-1393	Nari Basin, Ulleung-gun, Gyeongbuk	6 Sep 2012	KF017944	KF021683
	KA12-1023	Mt. Sokri, Boeun-gun, Chungbuk	16 Aug 2012	KF017945	KF021684
<i>A. rubrovolvata</i>	KA12-1023	Mt. Sokri, Boeun-gun, Chungbuk	16 Aug 2012	KF017945	KF021684
<i>A. sinensis</i>	KA12-1555	Mt. Jinak, Geumsan-gun, Chungnam	25 Sep 2012	KF017946	KF021685
<i>A. subglobosa</i>	KA12-0848	Gwangneung forest, Pocheon-si, Gyeonggi	26 Jul 2012	KF017947	KF021686
<i>A. vaginata</i>	KA12-0665	Mt. Minjuji, Yeongdong-gun, Chungbuk	16 Jul 2012	KF017948	KF021687
	KA12-1190	Mt. Jinak, Geumsan-gun, Chungnam	28 Aug 2012	KF017949	KF021688
<i>A. cf. vaginata</i> f. <i>alba</i>	KA12-0962	Gwangneung forest, Pocheon-si, Gyeonggi	8 Aug 2012	KF017950	KF021689

^aThe herbarium of the Korea National Arboretum (KA). Bold-letters indicate the newly recorded *Amanita* species in Korea.

in MrBayes 3.1.2 [23]. Parsimony analysis was performed using a heuristic search with 1,000 random additional replicates and tree bisection-reconnection branch swapping. MP bootstrap support values (MPBSs) for internal nodes were calculated from 1,000 replicates of the MP analysis. Posterior probability (PP) was estimated using the metropolis-coupled Markov-chain Monte Carlo method. Two parallel runs were performed using one cold and three heated chains for 5 million (ITS) and 10 million (nLSU) generations, respectively, starting with a random tree. The trees were sampled every 100 generations. We considered that two independent runs had converged when the average standard deviation (SD) of the split frequencies dropped below 0.01. The trees obtained before the convergence were discarded using the burn-in command, and the remaining trees were used for calculation of a 50% majority consensus tree and for estimation of the PP. PPs below 0.95 were not considered significant, with values below 0.9 being indicated on the resulting phylograms.

RESULTS AND DISCUSSION

Phylogenetic analyses of ITS and nLSU sequences.

The ITS dataset included 51 taxa and 601 characters, of which 261 were parsimony-informative. The MP tree was 858 steps long and had a consistency index (CI) of 0.6119, a retention index (RI) of 0.8208, and a homoplasy index (HI) of 0.3881. Bayesian analysis used a GTR + I + G model, and the first 12,500 trees were discarded as burn-in (with a “burninfrac” value of 0.25). For the nLSU dataset, 52 taxa and 567 characters were included, of which 147 characters were parsimony-informative. The MP tree was 451 steps long with CI of 0.5499, RI of 0.8450, and HI of 0.4501. In the Bayesian analysis, the first 35,000 trees using a GTR + I + G model were discarded as burn-in (burninfrac = 0.35).

The specimens used in phylogenetic analyses were divided into two sections—sect. *Amanita* and sect. *Vaginatae*—with high support values (Figs. 1 and 2). The phylogenetic positions of *Amanita* species in our study were generally consistent with the findings reported by Zhang *et al.* [1] and Moreno *et al.* [2]. We identified the following 15 phylogenetic species: *Amanita alboflavescens* Hongo, *A. ceciliae* (Berk. & Broome) Bas, *A. farinosa* Schwein, *A. fulva* Fr., *A. griseofolia* Zhu L. Yang, *A. ibotengutake* T. Oda, C. Tanaka & Tsuda, *A. melleiceps* Hongo, *A. orientifulva* Zhu L. Yang, M. Weiss, & F. Oberwinkler, *A. pantherina* (DC.) Krombh., *A. rubrovolvata* S. Imai, *A. sinensis* Zhu L. Yang, *A. subglobosa* Zhu L. Yang, *A. vaginata* (Bull.) Lam., *A. cf. vaginata* f. *alba* (Sacc.) Romagn., and one undescribed *Amanita* species. Most of these species formed a group with high support values (MPBS > 70%, PP > 0.95) in the ITS tree (Fig. 1). However, *A. pantherina* formed a group with moderate support values [MPBS/PP = 64/0.91 in the ITS tree (Fig. 1) and MPBS/PP = 63/0.96 in the nLSU tree (Fig. 2)] and was closely related to *A. subglobosa*.

Previously reported *Amanita* species in Korea. The ITS and nLSU sequences of *A. subglobosa* (HKAS56893 and HKAS58837—deposited in the Cryptogamic Herbarium of the Kunming Institute of Botany, Chinese Academy of Sciences; KA12-0848) and *A. pantherina* (LEM960235—deposited in the Herbarium, Laboratory of Environmental Mycoscience, Faculty of Agriculture, Kyoto University; KA12-0932, KA12-1225, and KA12-1393) were virtually identical, differing in only one nucleotide. Although the overall morphological features of *A. subglobosa* and *A. pantherina* are very similar, according to Yang [24] and Sanmee *et al.* [25], they can be distinguished based on the existence of clamps at the bases of basidia. Clamps were not found on *A. pantherina* but were found on *A. subglobosa* at the bases of basidia, along with a difference in the size of the basidia [24, 25]. Based on the morphological and molecular evidence, we identified specimen KA12-0848 as *A. subglobosa*, and specimens KA12-0932, KA12-1225, and KA12-1393 as *A. pantherina*. *Amanita ceciliae* was closely related to *A. griseofolia* both morphologically and phylogenetically, with differences in the color of the fruit body and in the thickness and structure of the stipe [26].

Amanita vaginata, which comprises several varieties and formae (Index Fungorum, <http://www.indexfungorum.org/Names/Names.asp>), belongs to a group of *Amanita* species with colors ranging from white to gray to brown-capped [27]. Our two specimens, designated as KA12-0665 and KA12-1190, were grouped with *A. vaginata* CUB: Microbiology MN18 (sequences submitted to GenBank, but unpublished; Department of Microbiology, Chulalongkorn University, Phayathai, Bangkok, Thailand) with strong support in the ITS tree, however, they formed an independent group with weak support in the nLSU tree (Figs. 1 and 2). In our analyses, although the *A. vaginata* specimens did not represent a monophyletic group, we tentatively assigned these two specimens as members of an *A. vaginata* complex. One of the specimens, KA12-0962, has morphological similarity to *A. vaginata* f. *alba*; however, unfortunately, no reliable sequences of *A. vaginata* f. *alba* have been deposited in GenBank. Therefore, we could not confidently conclude that KA12-0962 is *A. vaginata* f. *alba*. The previously reported species (i.e., *A. alboflavescens*, *A. farinosa*, *A. fulva*, *A. melleiceps*, and *A. rubrovolvata*) were clearly consistent with those of previous taxonomical descriptions (detailed descriptions of each species are available at <http://www.amanitaceae.org/>), and phylogenetically grouped with the deposited sequences in GenBank (Figs. 1 and 2).

Four newly recorded *Amanita* species in Korea and an undescribed *Amanita* species.

In the present study, we reported four newly recorded *Amanita* species that have not been previously reported in Korea are as follows: *A. griseofolia*, *A. ibotengutake*, *A. orientifulva*, and *A. sinensis*. *Amanita griseofolia* is closely related to *A. ceciliae* (originally described from Europe) in terms of both morphology and

Fig. 1. One of the 105 most-parsimonious trees from a heuristic analysis of the internal transcribed spacer sequences. Thick black branches indicate maximum parsimony bootstrap value (MPBS) > 50% and Bayesian posterior probability (PP) > 0.95. Thick gray branches indicate MPBS > 50% and $0.89 < PP < 0.95$. Only MPBSs > 50% are shown above or below branches. Section *Caesareae* was used as the outgroup. ITS, internal transcribed spacer; CI, consistency index; RI, retention index; HI, homoplasy index.

phylogeny (Figs. 1~3) [1]. However, the original description of *Amanita griseofolia* was originally described from southwestern China [28] and is characterized by a much more robust fruit body, a thicker stipe, and production of more filamentous hyphae in the volval remnants than *A. ceciliae* [1, 26]. In the present study, the differences in these morphological features are consistent with their phylogenetic positions being separated at the trees of the ITS and nLSU sequences (Figs. 1 and 2).

Amanita ibotengutake is a poisonous fungus originally reported from Japan [11]. This species produces the toxic substances ibotenic acid and muscimol, which cause Pantherina syndrome [11]. We confirmed that one of our specimens (KA12-1339—collected from Nari Basin, Ulleung-gun, Korea) could be assigned as *A. ibotengutake* based on its morphology and phylogeny (Figs. 1~3). In our phylogenetic analyses, *Amanita orientifulva* was closely related to *A. fulva* (Figs. 1 and 2); however, these two species can be

Fig. 2. One of the 32 most-parsimonious trees from a heuristic analysis of partial large subunit sequences. Thick black branches indicate maximum parsimony bootstrap value (MPBS) > 50% and posterior probability (PP) > 0.95. Thick gray branches indicate MPBS > 50% and 0.89 < PP < 0.95. Only MPBSs > 50% are shown above or below branches. Section *Caesareae* was used as the outgroup. nLSU, partial large subunit; CI, consistency index; RI, retention index; HI, homoplasy index.

distinguished based on the volval structure and size of basidiocarps, because *A. orientifulva* generally possess larger basidiocarps, as indicated by the phylogenetic analyses of ITS and nLSU sequences (Figs. 1 and 2) [26]. *Amanita sinensis*, which was originally described in a report from China, is found in mixed forests with broad-leaved trees and conifers [24]. Specimen KA12-1555 was grouped with *A. sinensis* LEM960225 in the ITS tree, and its morphological characteristics were identical to those in the original

descriptions of *A. sinensis* (Figs. 1 and 2). The undescribed *Amanita* sp. KA12-1175 is included in sect. *Vaginatae* of the ITS and nLSU trees (Figs. 1 and 2). *Amanita* sp. KA12-1175 possesses distinguishing morphological features of sect. *Vaginatae*, which can be characterized by the presence of clamp connections at the bases of basidia and the absence of an annulus [28]. In future studies, its morphological features should be carefully compared with those typical of the species belonging to sect. *Vaginatae*.

Fig. 3. Fruit bodies of *Amanita* species. A, B, *A. griseofolia* (KA12-0818); C, *A. ibotengutake* (KA12-1339); D, *A. orientifulva* (KA12-0642); E, F, *A. sinensis* (KA12-1555); G, H, *Amanita* sp. KA12-1175; I, *A. cf. vaginata* f. *alba* (KA12-0962) (scale bars: A~I = 5 cm).

Taxonomical remarks on four newly recorded *Amanita* species in Korea. Here, we have briefly shown the taxonomic remarks on four newly recorded *Amanita* species in Korea, (e.g., *Amanita griseofolia*, *A. ibotengutake*, *A. orientifulva*, and *A. sinensis*).

Amanita griseofolia Zhu L. Yang, *Frontiers in Basidiomycote Mycology*: 315 (2004); Section *Vaginatae*.

Specimens examined: Korea, Gyeonggi Pref., Pocheon-si, Gwangneung Forest, collected on 26 Jul 2012 (KA12-0818), 9 Aug 2012 (KA12-0994), and 12 Sep 2012 (KA12-1457) by Han *et al.*

Remarks: *Amanita griseofolia* is similar to *A. ceciliae*. KA12-0818 and KA12-0994 were regarded as *A. ceciliae* by S. K. Han in 2012. However, *A. ceciliae* differs from *A. griseofolia* by having a more robust fruit body with a yellow-brown or reddish-brown-to-gray-brown pileus covered with

lighter colored volval remnants, white lamellae with white edges, and a thicker stipe [28]. The basidiospores of *A. ceciliae* are slightly larger than those of *A. griseofolia* [29].

Amanita ibotengutake T. Oda, C. Tanaka, & Tsuda, *Mycol. Prog.* 1: 360 (2002); Section *Amanita*.

Specimen examined: Korea, Gyeongbuk Pref., Ulleung-gun, Nari Basin, collected on 5 Sep 2012 (KA12-1339) by Han *et al.*

Remarks: Unfortunately, specimen KA12-1339 was immature, therefore, we did not observe basidiospores. However, based on macroscopic features and the results of phylogenetic analyses, we confirmed that our specimen is *A. ibotengutake*. This species was originally reported from Japan in a mixed forest of *Quercus serrata* and *Pinus densiflora*. However, we found this specimen in Nari Basin on Ulleung Island in a mixed forest of *Fagus engleriana*

and *Acer okamotoanum*.

Amanita orientifulva Zhu L. Yang, M. Weiss, & F. Oberwinkler, Mycologia 96: 643 (2004); Section *Vaginatae*.

Specimens examined: Korea, Chungbuk Pref., Yeongdong-gun, Mt. Minjuji, collected on 16 Jul 2012 (KA12-0642) by Han *et al.*; Korea, Chungbuk Pref., Boeun-gun, Mt. Geumjeok, collected on 27 Sep 2012 (KA12-1596) by Han *et al.*

Remarks: *Amanita orientifulva* is very similar to *A. fulva*. Specimens KA12-0642 and KA12-1596 were identified as *A. fulva* by S. K. Han in 2012. However, they have distinct basidiocarp sizes and volval structures. The basidiocarp of *A. orientifulva* (pileus diameter ca. 10 cm, stipe ca. 15 × 2 cm) is generally larger than that of *A. fulva* (pileus diameter ca. 5~7 cm, stipe ca. 9~12 × 1~1.5 cm). The inner layer of the volval limb of *A. orientifulva* has a more compact arrangement. In addition, this species is characterized by its filamentous hyphae mixed with fewer inflated cells and scattered to locally conspicuous vascular hyphae [26].

Amanita sinensis Zhu L. Yang, Bibl. Mycol. 170: 23 (1997); Section *Amanita*.

Specimen examined: Korea, Chungnam Pref., Geumsan-gun, Mt. Jinak, collected on 25 Sep 2012 (KA12-1555) by Han *et al.*

Remarks: In this study, we identified this species based on phylogeny and morphology. *Amanita sinensis* is recorded in southwestern China, and Oda *et al.* [30] and Sanmee *et al.* [25] reported this species in Japan, Nepal, and Northern Thailand. Spore measurements from the protolog are provided for comparative purposes: basidiospores of size 11.1~16.3 × 6.9~10.3 μm ($Q = 1.36\text{--}1.70$, $Q = 1.51 \pm 0.06$, mean ± SD), ellipsoid, inamyloid, colorless, hyaline, thin-walled, and smooth. The length and Q value of basidiospores are somewhat larger for the Korean specimens than for the Chinese specimens, but are similar to those of Japanese and Nepalese specimens.

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REFERENCES

- Zhang L, Yang J, Yang Z. Molecular phylogeny of eastern Asian species of *Amanita* (Agaricales, Basidiomycota): taxonomic and biogeographic implications. *Fungal Divers* 2004;17:219-38.
- Moreno G, Platas G, Peláez F, Bernedo M, Vargas A, Daza A, Santamaría C, Camacho M, de la Osa LR, Manjón JL. Molecular phylogenetic analysis shows that *Amanita ponderosa* and *A. curtipes* are distinct species. *Mycol Prog* 2008;7:41-7.
- Geml J, Laursen GA, O'Neill K, Nusbaum HC, Taylor DL. Beringian origins and cryptic speciation events in the fly agaric (*Amanita muscaria*). *Mol Ecol* 2006;15:225-39.
- Jenkins DT, Petersen RH. A neotype specimen for *Amanita muscaria*. *Mycologia* 1976;68:463-9.
- Weiss M, Yang ZL, Oberwinkler F. Molecular phylogenetic studies in the genus *Amanita*. *Can J Bot* 1998;76:1170-9.
- Drehmel D, Moncalvo JM, Vilgalys R. Molecular phylogeny of *Amanita* based on large-subunit ribosomal DNA sequences: implications for taxonomy and character evolution. *Mycologia* 1999;91:610-8.
- Kim YS. The taxonomic study on the genus *Amanita* in Korea. *Kor J Mycol* 1976;4:1-10.
- Rubel W, Arora D. A study of cultural bias in field guide determinations of mushroom edibility using the iconic mushroom, *Amanita muscaria*, as an example. *Econ Bot* 2008;62:223-43.
- Oda T, Tanaka C, Tsuda M. Molecular phylogeny of Japanese *Amanita* species based on nucleotide sequences of the internal transcribed spacer region of nuclear ribosomal DNA. *Mycoscience* 1999;40:57-64.
- Moncalvo JM, Drehmel D, Vilgalys R. Variation in modes and rates of evolution in nuclear and mitochondrial ribosomal DNA in the mushroom genus *Amanita* (Agaricales, Basidiomycota): phylogenetic implications. *Mol Phylogenet Evol* 2000;16:48-63.
- Oda T, Yamazaki T, Tanaka C, Terashita T, Taniguchi N, Tsuda M. *Amanita ibotengutake* sp. nov., a poisonous fungus from Japan. *Mycol Prog* 2002;1:355-65.
- Justo A, Morgenstern I, Hallen-Adams HE, Hobbitt DS. Convergent evolution of sequestrate forms in *Amanita* under Mediterranean climate conditions. *Mycologia* 2010;102:675-88.
- Zhang P, Chen ZH, Xiao B, Tolgor B, Bao HY, Yang ZL. Lethal amanitas of East Asia characterized by morphological and molecular data. *Fungal Divers* 2010;42:119-33.
- Lee TS. Rearrangement of Korean recorded mushrooms. Namyangju: Korean Society of Forest Environment Research; 2013.
- Cho DH. Two new species of *Amanita* from Korea. *Korean J Nat Conserv* 2005;3:393-6.
- Bas C. Morphology and subdivision of *Amanita* and a monograph on its section *Lepidella*. *Persoonia* 1969;5:285-579.
- Doyle JJ, Doyle JL. A rapid DNA isolation procedure for small quantities of fresh leaf tissue. *Phytochem Bull* 1987;19:11-5.
- White TJ, Bruns T, Lee S, Taylor J. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis DH, Gelfand DH, Sninsky JJ, White TJ, editors. *PCR protocols: a guide to methods and application*. New York: Academic Press; 1990. p. 315-22.
- Hopple JS Jr, Vilgalys R. Phylogenetic relationships among coprinoid taxa and allies based on data from restriction site mapping of nuclear rDNA. *Mycologia* 1994;86:96-107.
- Chun J. Computer-assisted classification and identification of Actinomycetes [dissertation]. Newcastle upon Tyne: University of Newcastle; 1995.

21. Thompson JD, Gibson TJ, Plewniak F, Jeanmougin F, Higgins DG. The CLUSTAL_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Res* 1997;25:4876-82.
22. Swofford DL. PAUP*: phylogenetic analysis using parsimony (*and other methods). Version 4.0b10. Sunderland: Sinauer Associates; 2003.
23. Ronquist F, Huelsenbeck JP. MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics* 2003;19:1572-4.
24. Yang ZL. Die *Amanita*-Arten von Sudwestchina. *Bibl Mycol* 1997;170:1-240.
25. Sanmee R, Tulloss RE, Lumyong P, Dell B, Lumyong S. Studies on *Amanita* (Basidiomycetes: Amanitaceae) in Northern Thailand. *Fungal Divers* 2008;32:97-123.
26. Yang ZL, Weiss M, Oberwinkler F. New species of *Amanita* from the eastern Himalaya and adjacent regions. *Mycologia* 2004;96:636-46.
27. Tulloss RE. Type studies in *Amanita* section *Vaginatae* I: Some taxa described in this century (studies 1-23) with notes on description of spores and refractive hyphae in *Amanita*. *Mycotaxon* 1994;52:305-96.
28. Yang ZL. Two new species of *Amanita* (Basidiomycota) from China. In: Agerer R, Piepenbring M, Blanz P, editors. *Frontiers in Basidiomycete mycology*. Eching: IHW-Verlag und Verlagsbuchhandlung; 2004. p. 315-24.
29. Tulloss RE, Ovrebo CL, Halling RE. Studies on *Amanita* (Amanitaceae) from Andean Colombia. *Mem N Y Bot Gard* 1992;66:1-46.
30. Oda T, Tanaka C, Tsuda M. *Amanita sinensis*, new to Japan and Nepal. *Mycoscience* 2000;41:403-5.