**Galbinothrix**, a new monotypic genus of *Chrysotrichaceae* (*Arthoniomycetes*) lacking pulvinic acid derivatives

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**Abstract.** *Galbinothrix caesiopruinosa* is described from Japan and Korea. The new genus and species is placed in *Chrysotrichaceae* by its ascoma morphology and by a phylogenetic analysis of mtSSU and nLSU sequence data using Bayesian and maximum likelihood inference. The monotypic genus *Galbinothrix* is superficially similar to *Chrysothrix caesia* in having dark brown ascomata covered by a thin bluish grey pruina, reddish brown ascomatal pigment in the epithecium and proper exciple, the greyish green to yellowish olive thallus, and usnic acid as the main secondary thallus compound. It differs from this species and all other *Chrysotrichaceae* by its large, oblong, thick-walled ascospores with a distinct epispore, the narrowly clavate to almost tubular asci, and the never clearly granular to leprose thallus.

**Key words:** Arthoniales, Ascomycota, East Asia, taxonomy, lichenized fungi

**Introduction**

*Chrysotrichaceae* (Zahlbruckner 1905) was described as a monotypic family. *Chrysothrix* (Montagne 1852), the only genus originally included in the family, shows close affinities to *Arthoniaceae* but differs, among other characters, by the chlorococcalean instead of trentepohlioid photobionts and by the characteristic yellow pigments consisting of pulvinic acid derivatives in the ascomata and thallus (Zahlbruckner 1905; Laundon 1981; Elix 2009; Fletcher & Purvis 2009). Recent phylogenetic studies have shown that *Chrysotrichaceae* thus delimited is paraphyletic and further includes taxa lacking pulvinic acid derivatives, which were – or would have been – previously classified in the genus *Arthonia* in *Arthoniaceae* (Nelsen et al. 2009; Frisch et al. 2014). Such taxa include *Chrysothrix caesia* (Ertz & Tehler 2011), *Arthonia mediella* and the newly described *Melarthonis piceae* (Frisch et al. 2014).

In the course of recent fieldwork in Japan and Korea, we frequently collected a species of *Arthoniales* from smooth-barked deciduous trees which showed a superficial resemblance to *Chrysothrix caesia* but proved unrelated upon closer examination. Here we describe this species in its own genus as new to science, and we demonstrate its phylogenetic position relative to the other taxa lacking pulvinic acid derivatives in *Chrysotrichaceae* by Bayesian and ML analysis of mtSSU and nLSU sequence data.

**Material and methods**

Lichen sampling and investigation

Type material is deposited at the herbarium of the National Museum of Nature and Science, Tsukuba, Japan (TNS), with duplicates in the National Institute of Biological Resources, Incheon, Korea (KB), Museum of Evolution, Uppsala, Sweden (UPS), and hb Frisch. Additional specimens collected in Japan are kept in TNS, UPS and hb Frisch, while specimens from Korea are deposited at KB, UPS and hb Frisch. Morphology was examined using an Olympus SZX7 dissecting microscope. Sections for anatomical examination were cut by hand, mounted in water or lactic cotton blue (LCB), and examined with an Olympus BX51 light microscope. All measurements were made on preparations mounted in LCB.

Secondary lichen compounds were identified by TLC (Orange et al. 2010) and HPTLC (Arup et al. 1993) using solvents B’ and C. The amyloidity of the thallus and apothecia was examined using 1% aqueous iodine solution without (I) or with pre-treatment with 10% aqueous potassium hydroxide (KI). The color reaction of the thallus and apothecia was tested using 10% aqueous potassium hydroxide (K), potassium hypochlorite as...
applied in common household bleach (C), 10% aqueous potassium hydroxide followed by potassium hypochlorite (KC), and 1,4-phenyldiamine in 96% ethanol (Pd). The UV reaction of the thallus and apothecia was tested under UV365 light. Calcium oxalate crystals were identified by applying 10% sulphuric acid to squash preparations of thallus samples.

DNA extraction, PCR amplification and sequencing

Molecular work was performed in Japan at the National Museum of Nature and Science (Tsukuba) and in Korea at the National Institute of Biological Resources (Incheon). Genomic DNA was extracted using the DNEasy Plant Mini Kit following the protocol of the manufacturer. Each PCR reaction of 20 µl contained 1–3 µl DNA extract, depending on the DNA concentration in the extract, and 1 µl (mtSSU, nLSU) of each primer (10 pmol/µl). The primers used for PCR amplification were mtSSU1 and mtSSU3R for mtSSU (Zoller et al. 1999), and LIC24R and LRS for nLSU (Vilgalys & Hester 1990, Miadlikowska & Lutzoni 2000). PCR cycling conditions for mtSSU were 95°C (4 min) followed by 9 cycles of 95°C (30 sec), 62°C to 54°C (45 sec) with annealing temperatures lowered by 1°C between cycles, and 72°C (45 sec) followed by 30 cycles at 54°C annealing temperature and final extension at 72°C (7 min). For nLSU annealing temperatures started

| Species | Voucher | mtSSU | RPB2 | nLSU |
|---------|---------|-------|------|------|
| Alyxia varia | Sweden; Frisch 11/Se1 (UPS) | KJ851006 | KJ851147 | KJ851027 |
| Arthonia apatetica | Sweden; Svensson 2017 (UPS) | KJ850992 | KJ851125 | KJ851045 |
| Arthonia apotheocorium | Sweden; Frisch 11/Se23 (UPS) | KJ850970 | KJ851148 | – |
| Arthonia calcarea | France; Erz 7539 (BR) | EU704064 | EU704028 | – |
| Arthonia eos | Japan; Thor 26000 (UPS) | KJ850987 | KJ851134 | KJ851053 |
| Arthonia medulla | Sweden; Frisch 11/Se22 (UPS) | KJ851014 | KJ851133 | KJ851032 |
| Arthonia neglectula | Sweden; Frisch 10/Se90 (UPS) | KJ850989 | KJ851118 | KJ851037 |
| Arthonia punctiformis | Sweden; Thor 21658 (UPS) | KJ850973 | KJ851113 | KJ851044 |
| Arthonia radiata | Sweden; Frisch 10/Se29 (UPS) | KJ850968 | KJ851108 | – |
| Arthonia sp. (Ug10) | Uganda; Frisch 11/UG218 (UPS) | KJ850986 | KJ851131 | KJ851068 |
| Arthonia sp. (Ug9) | Uganda; Frisch 11/UG212 (UPS) | KJ850985 | KJ851129 | KJ851064 |
| Bryostigma muscigenum | Sweden; Thor 26206 (UPS) | KJ850991 | KJ851124 | KJ851052 |
| Chioecoton natalense | Uganda; Frisch 11/UG324 (UPS) | KF707647 | KF707660 | KF707641 |
| Chrysothrix caesia | USA; Amoftt (AFTOL-ID 775) | FJ469671 | FJ469670 | FJ469668 |
| Chrysothrix candelaris | Sweden; Frisch 11/Se43 (UPS) | KF707649 | KF707663 | KF707640 |
| Combea mollusca | South Africa; Teher 7725 (S) | AY751384 | DQ987862 | EFO81383 |
| Coniophorus cinnabarininum | Uganda; Frisch 11/UG297 (UPS) | KJ850977 | KJ851104 | KJ851059 |
| Dichosporidium boschianum | Fiji Islands; Lumbsch 19815a (F) | GU327692 | – | GU327716 |
| Dichosporidium brunitheri | Uganda; Frisch 11/UG8 (UPS) | KJ851011 | KJ524362 | KJ524283 |
| Dimidiographa longissima | Florida; Erz 9155 (BR) | EU704069 | EU704033 | EU704097 |
| Dothidea sambuci | AFTOL-ID 274 | AY544739 | DQ522854 | AYS44681 |
| Enterographa crassa | France; Erz 5041 (BR) | EU704056 | EU704020 | EU704088 |
| Felipes leucopelleaeus | Sweden; Frisch 10/Se34 (UPS) | KJ850984 | KJ851130 | KJ851033 |
| Fouragea filicina | Rwanda; Erz 7994 (BR) | EU704067 | EU704031 | EU704095 |
| Galbinotrix caesiopruinosus | Japan; Frisch 12/Jp282 (UPS) | MK107828 | – | – |
| Galbinotrix caesiopruinosus | Japan; Frisch 13/Jp247 (TNS) | MK107822 | – | MK107829 |
| Galbinotrix caesiopruinosus | Japan; Frisch 13/Jp235 (TNS) | MK107823 | – | MK107830 |
| Galbinotrix caesiopruinosus | Korea; Frisch 16/Kr526 (UPS) | MK107825 | – | MK107832 |
| Galbinotrix caesiopruinosus | Korea; Frisch 16/Kr527 (UPS) | MK107824 | – | MK107831 |
| Galbinotrix caesiopruinosus | Korea; Frisch 16/Kr564 (dpl. (UPS) | MK107826 | – | MK107833 |
| Galbinotrix caesiopruinosus | Korea; Frisch 16/Kr585 (UPS) | MK107827 | – | MK107834 |
| Herpotrichon rubrocinicum | Mexico; Rudolfi 5 (UPS) | KF707643 | KF707655 | – |
| Inoderma hyssaceum | Japan; Thor 25952 (UPS) | KJ850962 | KJ851089 | KJ851040 |
| Lecanactis abietina | Belgium; Erz 5068 (DUKE) | AY548813 | AY552018 | AY548812 |
| Lecanographa amylacea | Sweden; Thor 26176 (UPS) | KF707650 | KF707659 | KF707639 |
| Melaethonis piceae | Japan; Thor 25995 (UPS) | KJ851016 | – | KJ851080 |
| Nyungwea pallida | Uganda; Frisch 11/UG24 (UPS) | KJ851023 | KJ851145 | KJ851066 |
| Opegrapha vermicellifera | Belgium; Erz 7562 (BR) | EU704077 | EU704041 | EU704105 |
| Opegrapha vulgaris | Belgium; Erz 7564 (BR) | EU704080 | EU704044 | EU704108 |
| Phaeographa zwackhii | Sweden; Frisch 11/Se3 (UPS) | KJ851021 | – | KJ851048 |
| Pleospora herbarum | AFTOL-ID 940 | FJ190610 | DQ427794 | DQ427804 |
| Reichlingia leopoldi | Belgium; Erz 13294 (BR) | JF830774 | HQ45472 | HQ454582 |
| Tylophoron hibernicum | Uganda; Frisch 11/UG220 (UPS) | KJ850966 | KJ851097 | KJ851065 |
| Zwackhia viridis | Luxembourg; Erz 7619 (BR) | EU704078 | EU704042 | EU704106 |

Table 1. Vouchers used for the phylogenetic tree and the GenBank accession numbers of the sequences. New sequences are indicated in bold.
at 62°C and were lowered to 56°C. Sequencing of the PCR products was done at the National Museum of Nature and Science on a 3130xl Genetic Analyzer (Applied Biosystems) and at the National Institute of Biological Resources by Macrogen Inc., Korea.

Alignment

RPB2 sequences were added from GenBank for better backbone support of the Arthoniales tree. The sequences of the three gene loci were aligned separately using the general MAFFT settings as implemented in the Guidance Web Server (Penn et al. 2010) and manually corrected. Introns, longer insertions, and ambiguously aligned regions were excluded prior to analysis. The final concatenated alignment comprised 2654 nucleotide positions, 725 for mtSSU, 1048 for nLSU and 881 for RPB2. Of these, 1272 (mtSSU 399, nLSU 355, RPB2 518) were variable and 1061 (mtSSU 331, nLSU 255, RPB2 475) were parsimony-informative. A partitioned dataset was used for the phylogenetic analyses to enable independent parameter estimation for the three gene loci. The RPB2 dataset was further partitioned into two coding regions separated by a short intron region (369–26–486 bps, respectively). Coding regions were partitioned according to codon positions to allow for the higher evolutionary rates of the 3rd codon position.

ML and Bayesian analyses

A general-time-reversible model with a proportion of invariant sites (GTR-I-F) was found to best explain the sequence evolution for the mtSSU, nLSU and RPB2 data set using the Akaike information criterion (AIC; Akaike 1973) implemented in MEGA5 (Tamura et al. 2011). Bayesian inference (Huelsenbeck et al. 2001; Holder & Lewis 2003) and maximum likelihood (ML) were used to infer phylogenetic hypotheses. Prior to concatenation the single-gene alignments were tested for conflicting tree topologies. Serious conflict was assumed when deviant tree topologies were supported by ≥70% bootstrap values (BS) and ≥0.95 posterior probabilities (PP).

Bayesian analysis was performed with MrBayes 3.2.6 (Ronquist & Huelsenbeck 2003) implemented in the CIPRES Science Gateway (Miller et al. 2010). A GTR-I-F model of sequence evolution was applied to the partitioned dataset, and the model parameters were estimated during the run for each gene partition separately starting from a default flat Dirichlet distribution. The analysis was run for 10,000,000 generations in eight chains and every 500th generation was sampled. The first 50% of trees were discarded as burn-in and a 50% majority rule consensus tree was calculated.

Maximum likelihood was performed with the RAxML-HPC Black Box v. 8.2.10 implemented in the CIPRES Science Gateway (Miller et al. 2010) using rapid bootstrapping and full ML analysis under the GTR+GAMMA approximation allowing for a proportion of invariable sites. The analysis was stopped automatically after 102 bootstrap replicates using the bootstopping option implemented in RAxML (Pattengale et al. 2009).

Results

Phylogeny

We generated 13 new sequences for Galbinothrix caesiopruinosa: 7 mtSSU and 6 nLSU (Table 1). Sequencing of RPB2 failed for all samples using the general primers RPB2-7cF and RPB2-11aR (Liu et al. 1999). Galbinothrix is recovered as sister to the remaining Chrysotrichaceae, separated from the other genera within the family – Chrysotrix and Melarthonis – and Arthonia mediella by long branches.

Only five (mtSSU) and four (nLSU) variable nucleotide positions have been identified for the analyzed specimens of G. caesiopruinosa. Two specimens from Japan [13/Jp247 and 13/Jp253 (Type!)] from Chichibu-Tama-Kai National Park, Nagano] differ in three of these nucleotide positions (mtSSU) from the other samples, but generally the collections from Japan and Korea are not separated in our analyses.

Taxonomy

Galbinothrix Frisch, G. Thor, K. H. Moon & Y. Ohmura, gen. nov.

MycoBank MB 828448.

Diagnosis: The monotypic genus Galbinothrix is characterized within Chrysotrichaceae by its thin and discontinuous to fissured-aroeolate thallus lacking pulvinic acid derivatives; dark brown, adnate, thinly to densely bluish grey pruinose ascomata with well-developed reddish brown pigmented proper exciple and epithecium; and usnic and isousnic acids as secondary lichen compounds. Galbinothrix is superficially similar to Chrysotrix caesia, but differs from this species and from all other Chrysotrichaceae by its larger oblong ascosporae (27–36 × 5–7 μm), with distinct epispore, and the narrowly clavate to almost tubular ascii (75–115 × 19–26 μm).

Generic type: Galbinothrix caesiopruinosa Frisch, G. Thor, K. H. Moon & Y. Ohmura

Galbinothrix caesiopruinosa Frisch, G. Thor, K. H. Moon & Y. Ohmura, sp. nov. (Figs 1A–E)

MycoBank MB 828449.

Diagnosis: The only species of Galbinothrix with the same diagnostic characters as the genus.

Type: Japan, Shinano Prov., Nagano Pref., Minamisaki-gun, kumagawa River, 35°57′05.3″E, on smooth bark of Alnus sp. in riverine forest, elev. 1414 m, 28 May 2013, Frisch 13/Jp253 & Ohmura (TNS – holotype; KB, UPS and hb Frisch – isotypes).

Description. Thallus rather variable, pale to dark greyish green to yellowish olive, thin and discontinuous to fissured-aroeolate, matte, consisting of discrete to confluent patches ca 0.1–0.3 mm diam., up to 0.15 mm thick, with uneven to shallowly warty to distinctly bullate to almost subgranular surface, partly endophloeodal; prothallus not observed. Photobiont layer 40–80 μm thick; photobiont chlorococcoid, the cells 5–19 × 4–17 μm; hyphae 2.0–3.0 μm wide, adpersed with pale granular crystals. Calcium oxalate crystals not observed. Ascomata with
constricted base adnate, emarginate in surface view, weakly convex, rounded to slightly angular, 0.2–0.35 mm diam., up to 0.12 mm tall, covered by thin to dense coarse bluish grey pruina, dark brown beneath. Proper exciple 7–20 µm wide, reddish brown, conglutinated, of compacted paraphysoidal hyphae, inspersed with pale granular crystals 1–3 µm wide, some hyaline leafy crystals 2–10 µm in size attached to the outer edge (not dissolving in sulphuric acid, dissolving in KOH). Epithecium reddish brown, 15–18 µm tall, conglutinated, of compacted tips of the paraphysoids (crystals as in the proper exciple). Hymenium hyaline to pale reddish brown,
60–70 µm tall, the asci closely spaced. Hypothecium hyaline to pale reddish brown, 25–80 µm tall, of 1.5–2.0 µm wide, branched and anastomosed, short-celled [3–5–7] µm hymata to subparaplectenchymatic. Paraphysoids densely branched and anastomosed, with lumina ca 1 µm wide, in parallel strands in between the asci; tips 1.5–2.5 µm wide, extending horizontally above the asci, with reddish brown pigments along the outer walls and in the gelatinous matrix. Ascii narrowly clavate to almost tubular, 27–36 × 5–7 µm, with reddish brown perispore, and (4–5) narrowly clavate to almost tubular large oblong ascospores, 27–36 × 5–7 µm, with distinct, ca 0.5 µm wide epispore (total wall-thickness ca 1 µm); ascospore septation starting with the median septum, with the two secondary septa appearing simultaneously. Pycnidia not observed.

Chemistry. Thallus containing usnic (major) and isousnic (minor to trace) acids (16/Kr367, 526, 585, 586, 614 tested), C–, KC–, K–, Pd–, UV–; thallus patchily I+ pale vinose/ KI+ pale blue. Ascomatal gel I+ vinose/ KI+ blue. Asci with KI+ blue ring in tholus. Brown pigments in the epiparasite turning olive-green in K.

Etymology. The generic name is formed from the Latin galbinus (= greenish yellow) and the suffix thrix to indicate the color of the thallus and the relationship with Chrysotrichia in Chrysotrichaceae. The epithet caesiopruinosus indicates the bluish grey pruinose ascomata.

Ecology and distribution. Most collections of G. caesiopruinosus were made from thin-stemmed deciduous trees with smooth bark, including species of Acer, Alnus and Fraxinus. It was collected once from smooth-barked Abies and once from fissured bark of Salix. The species appears to be most common in rather shady and humid riverine forests, but was likewise collected in humid ravines and river valleys from exposed, planted trees along roadsides and in parking lots (Acer spp. including A. mono). Galbinothrix caesiopruinosus is known from Hokkaido and central Honshu in Japan as well as from the eastern mountain range of the Korean peninsula. It appears to be a rather common and widespread species in suitable habitats in Eastern Asia.

Specimens examined. JAPAN. Hokkaido. Abashiri Prov., Monbetsu-gun, Engaru-cho, Ikutahara-Kiyosato, 43°51’06.3″N, 143°29’18.7″E, on bark of Salix sp. in riverine forest, 290 m, 29 May 2012, Frisch 12/Jp150 & Ohmura (TNS, hb Frisch); ibid., on bark of Alnus sp., Frisch 12/Jp151 (hb Frisch); Honshu, Shimotsuke Prov., Tochigi Pref., Nikko City, 20 km WNW of Nikko, Yumoto village, at entrance to house with exhibition of Nikko National Park, 36°48.290′N, 139°25.384′E, open mixed coniferous/deciduous forest, on bark of Acer mono, 1500 m, 28 Sept. 2017, Thor 35459 (UPS); Kozuke Prov., Gunma Pref., Kunitsu-mura, 4.2 km ESE of Kunitsu, Arakawa River, 36°43.311′N, 139°21.821′E, deciduous forest, on Alnus sp., 1780 m, 4 Oct. 2016, Thor 35834 (UPS); Shinano Prov., Nagano Pref., Minamisaku-gun, Kawanami-mura, Chichibu-Tama-Kai National Park, along Chikumagawa River, 35°57’.10.4″N, 138°42’36.7″E, on smooth bark of thin-stemmed tree along road, 1453 m, 28 May 2013, Frisch 13/Jp247 & Ohmura (TNS, hb Frisch); Kai Prov., Yamanashi Pref., Yamanashi-shi, Miura-cho, Kichijoji, 35°49.22.8″N, 138°38.48.3″E, on Acer sp., 1530 m, 5 July 2012, Frisch 12/Jp282 & Ohmura (TNS). KOREA. Gangwon-do, Pyeongchang-gun, Yongpyeong-myeon, Nodong-ri, Mt. Gyeong, Nodong Valley trail, 37°42.282′N, 128°29.098′E, on young deciduous tree in forest, 820 m, 2 Oct. 2016, Frisch 16/Kr521, Kashiwadani, Moon & Printzen (hb Frisch); ibid., on young Acer sp., Frisch 16/Kr520, Kashiwadani, Moon & Printzen (hb Frisch); ibid., 37°42.316′N, 128°29.149′E, on thin-stemmed deciduous tree in forest, 820 m, Frisch 16/Kr526, Kashiwadani, Moon & Printzen (KB, hb Frisch); ibid., on thin-stemmed Fraxinus sp., Frisch 16/Kr527, Kashiwadani, Moon & Printzen (KB, hb Frisch); ibid., Jinbu-myeon, Odae-san-ro, Mt. Odae, Sangwon Temple, 37°47.096′N, 128°33.491′E, on deciduous tree, 950 m, 3 Oct. 2016, Frisch 16/Kr564, Kashiwadani, Moon & Printzen (hb Frisch); ibid., along Odae Stream, 37°44.335′N, 128°35.164′E, on young Acer sp. in parking area, 680 m, 4 Oct. 2016, Frisch 16/Kr585, 586, Kashiwadani, Moon & Printzen (KB, hb Frisch); Inje-gun, Buk-myeon, Yongdari-ri, Mt. Seorak, en route from Baekdam-sa Temple to Youngsi-am Temple, along Baekdam Valley, 38°09.567′N, 128°22.462′E, on thin-stemmed Quercus sp. in light forest near stream, 475 m, 14 June 2016, Frisch 16/Kr367 & Moon (hb Frisch); ibid., 38°10.029′N, 128°22.732′E, on deciduous tree in forest, 490 m, 6 Oct. 2016, Frisch 16/Kr614, Kashiwadani, Moon & Printzen (KB, hb Frisch); ibid., 38°09.471′N, 128°22.405′E, on Acer sp. in forest, 520 m, Frisch 16/Kr616, Kashiwadani, Moon & Printzen (hb Frisch); ibid., where the road crosses the river ca 1.5 km NW of Baekdam Temple, 38°09.85–10.25′N, 128°22.50′E, open mixed coniferous/deciduous forest, on deciduous tree, 450–550 m, 21 Oct. 2006, Thor 20692 (UPS).

Discussion. The new genus and species is well accommodated in Chrysotrichaceae on account of its morphological characters, including: (1) the adnate rounded ascomata with an epithecium of horizontally extending tips of the paraphysoids, (2) branched and netted paraphysoids, (3) asci related to the Arthonia-type (see below), (4) hyaline, predominantly 3-septate ascospores, and (5) the chlorococcane photobionts. In the molecular phylogeny in Figure 2, Galbinothrix caesiopruinosus is shown to be genetically distant from the other genera currently accepted in Chrysotrichaceae, including Chrysotrichia and Melarthonia, as well as from Arthonia mediaeli, based on mtSSU and nLSU sequence data. The latter species is kept here in Arthonia as it will be treated with related taxa in a forthcoming publication.

Galbinothrix caesiopruinosus is readily distinguished from other Chrysotrichaceae by the combination of the following characters: (1) crustose rimose to areolate thallus lacking pulvinic acid derivatives, (2) reddish brown well-defined proper exciple and epithecium, (3) large oblong ascospores, 27–36 × 5–7 µm, with distinct perispore, and (4) narrowly clavate to almost tubular asci of 75–115 × 19–26 µm. Despite their elongated shape and rather large size, the asci of Galbinothrix are best classified as a variant of the Arthonia-type as
defined by Grube (1998). *Chrysothrix caesia* is the only species in the family that shows superficial similarity with *Galbinothrix* in lacking pulvinic acid derivatives, the brownish, white pruinose ascomata, and reddish brown pigment in the proper exciple, epithecium, and hypothecium. In addition to the leprose thallus containing zeorin along with usnic acid, this species and all other *Chrysotrichaceae* differ from *Galbinothrix* by their much smaller, thin-walled ascospores lacking a distinct epispore (in the range of 9–23 × 2.5–6 µm; outer wall and septa ≤ 0.5 µm), and clavate to broadly clavate asci measuring 20–45 × 8–15 µm (own measurements; Laundon 1981; Kalb 2001; Jagadeesh Ram et al. 2006; Elix & Kantvilas 2007).

*Melarthonis* differs additionally by the greenish, minutely granular thallus, the strongly convex black ascomata with ± anticlinal excipular hyphae having tips up to 2 µm wide and pigmented dark brown, and narrowly obvoid to spindle-shaped ascospores, 10.0–14.0 × 2.5–4.0 µm. *Arthonia mediella* differs by having black, strongly convex ascomata; small, narrowly obvoid to spindle-shaped ascospores (10.0–17.0 × 3.0–5.0 µm); and capitative tips of the interascal filaments with distinct dark brown caps.

*Galbinothrix caesiopruinosa* is a uniform species except for its thallus, which varies from pale to dark greyish green in shady localities, while thalli from more exposed sites are distinctly yellowish olive. Some specimens have a rather inconspicuous thallus consisting of low, dispersed, areola-like warts, while in others the thallus forms a continuous, distinctly fissured-areolate crust. The areolae can be more or less flat and thin, or distinctly bullate to almost coarsely subgranular.

**Acknowledgements**

This study was funded in Japan by a Grant-in-Aid relating to a JSPS Postdoctoral Fellowship for Foreign Researchers (no. 23–01706) to A. Frisch, and JSPS KAKENHI (no. 24300314) for Y. Ohmura, and in Korea by the National Institute of Biological Resources, Korea (grants NIBR 201401039, 201501105, 201601105 to Kwang Hee Moon), all of which are gratefully acknowledged. Permission to collect lichens in Nikko National Park in 2017 was most kindly granted to G. Thor by the Nikko National Park management office, Ministry of Environment (no. 1706215, 380, 381). The Nikko District Forest Office of the Nihon Paper Company in Gunma Prefecture most kindly gave permission to collect lichens on Mt. Oku-Shirane (Mt. Nikko-Shirane). A. Frisch and K. H. Moon thank Dr. Jeong Eun Han for assistance in the field.

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