1. Introduction

During a recent investigation of lichen-forming and lichenicolous* fungi (*lichenicolous, i.e., growing or inhabiting on lichen thalli [or thalli of lichen-forming fungi]) of Dokdo Islands, two members of the genera Arthonia (Ach.) (Arthoniaceae) and Rufoplaca Arup, Søchting & Frödén (subfamily Caloplacoideae of the Teloschistaceae) were newly found.

Within our study from combined phylogenetic analysis of the Arthoniaceae based on mtSSU and RPB2 sequences, the Arthonia molendoi group was positioned in the monophyletic branch. Several arthonioid species were already known to grow on foliost or fruticost members of the Teloschistaceae, namely Arthonia sytnikii S. Y. Kondr., Arthonia anjutae S. Y. Kondr. et Alstrup and Arthonia descruens var. nana Grube et Hafellner, as well as A. molendoi (Heufl. ex Frauenf.) R. Sant. All of them infect the thallus, and some of them also develop fruiting bodies on the apothecia (hymenia) of their hosts. Selected characters of taxa mentioned above have been recently summarized by Fleischhacker et al. [1], who described a new taxon, Arthonia parietinaria Hafellner et A. Fleischhacker, a member of the A. molendoi group, and compared with Arthonia anjutae, A. sytnikii, as well as Arthonia epiphyscia, and A. molendoi. It was concluded that the status of taxa mentioned at the species level had been confirmed by the taxonomic position of hosts in separate genera of the Teloschistaceae, which recently have been proved by three-gene phylogeny (see [2]). Thus A. parietinaria has hosts of the genus Xanthoria Th. Fr. (as it is correctly stressed by Fleischhacker et al. [1]), while lichenicolous fungi previously recorded on Massjukiella polycarpa (Hoffm.) S.Y. Kondr., Fedorenko, S. Stenroos, Kärnefelt, Elix, Hur & A. Thell and/or Oxneria huculica S.Y. Kondr. are highly likely to belong to different taxa. A. anjutae was confirmed as a species of the genus Teloschistes Norm. (the subfamily Teloschistioideae of the Teloschistaceae), A. as a species of the genus Jackelixia S. Y. Kondr., Fedorenko, S. Stenroos, Kärnefelt & A. Thell, and A. molendoi as a species of the genus Rusavskia S. Y. Kondr. & Kärnefelt (both latter genera, i.e., Jackelixia and Rusavskia) of the subfamily Xanthoriioideae of the Teloschistaceae). The further taxon from the A. molendoi complex, which was confirmed as a species of the genus Orientophila Arup, Søchting & Frödén (subfamily Xanthoriioideae, Teloschistaceae), is segregated in this article.

The genus Rufoplaca Arup, Søchting & Frödén (subfamily Caloplacoideae, Teloschistaceae) was introduced in 2013 for six species and two
additional species have subsequently been described [3–5]. Additionally, to eight species of the genus Rufoplaca, hitherto known from various regions of the Northern Hemisphere, was added one new species found among Dokdo lichens.

The aim of this article was to present legal descriptions of these two taxa of the genera Arthonia and Rufoplaca.

2. Materials and methods

2.1. Taxon sampling

More than 230 lichen specimens were collected in 17 localities of Dokdo Islands, the Republic of Korea in September 2017. The Dokdo specimens, as well as previous collections included in comparative studies and kept in the KoLRI and other herbaria (BP, KW-L, LE, LWG, and VBI), were examined using standard microscopic techniques and hand-sectioned under a dissecting microscope (Nikon SMZ 645; Nikon, Tokyo, Japan). Anatomical descriptions were based on observations of these preparations under a microscope (Nikon Eclipse E200; Nikon, Tokyo, Japan, and Zeiss Scope, A1; Carl Zeiss, Oberkochen, Germany) with digital camera AxioCam ERc 5s. A section of apothecia was prepared with at least two specimens of each newly sequenced species, preferably from different localities, to ensure species determination by avoiding contamination with co-occurring fungi are frequent when using standard DNA isolation protocols on large parts of the lichen thalli. To avoid such contamination, hand-made sections of the hymenium or the thallus were used for direct polymerase chain reaction (PCR) [22]. Any pigmented or crystal-encrusted portions were removed with a razor blade. In addition, the lichen material was sometimes washed with acetone or a 1% KOH solution, and then rinsed with water to remove remnants of pigments.

The material was then added to a tube containing the PCR reaction mixture and amplified directly. Amplification reactions were prepared for a 50 µL final volume containing 5 µL 10× DreamTaq Buffer (Fermentas, Waltham, MA), 1.25 µL of each of the 20 µM primers, 5 µL of 2.5 mg mL⁻¹ bovine serum albumin (Fermentas #B14), 4 µL of each of the 2.5 mM dNTPs (Fermentas), 1.25 U DreamTaq DNA polymerase (Fermentas) and 1 µL of template genomic DNA or tiny fragments of lichen material.

The nuclear ribosomal RNA gene region including the internal transcribed spacers 1 and 2 and the 5.8S subunit (ITS) was amplified using the primers ITS1F [23] and ITS4 [24], the 28S LSU using the primer LR5 [25], and the 12S mtSSU using the primers mtSSU1-mtSSU3R and mtSSU2R [14,20]. Methods of DNA extractions, data on primers, and phylogenetic analysis are provided in our previous article [26].

A fragment of about 1 kb of the RPB2 protein-coding gene was amplified using primers fRPB2-7cF and fRPB2-11aR [27]. The yield of the PCRs was verified by running the products on a 1% agarose gel using ethidium bromide. The amplicons were sequenced by Macrogen® using the amplification primers. Two additional primers, RPB2-2488F and RPB2-2492R [28], were used for sequencing RPB2. See also Park et al. [29] and Kondratyuk et al. [26] for extractions, amplifications, and sequencing procedures.

Sequence fragments were assembled with Sequencher version 4.6 (Gene Codes Corporation, Ann Arbor, MI). Sequences were subjected to MEGABLAST searches to verify their closest relatives and to detect potential contaminations.

2.2. Molecular data

Genomic DNA was isolated from lichen specimens using the CTAB extraction protocol [21]. For some tiny crustose species (e.g., Arthonia or Rufoplaca), contaminations with co-occurring fungi are frequent when using standard DNA isolation protocols on large parts of the lichen thalli. To avoid such contamination, hand-made sections of the hymenium or the thallus were used for direct polymerase chain reaction (PCR) [22]. Any pigmented or crystal-encrusted portions were removed with a razor blade. In addition, the lichen material was sometimes washed with acetone or a 1% KOH solution, and then rinsed with water to remove remnants of pigments.

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Sequence fragments were assembled with Sequencher version 4.6 (Gene Codes Corporation, Ann Arbor, MI). Sequences were subjected to MEGABLAST searches to verify their closest relatives and to detect potential contaminations.

2.3. Phylogenetic analyses

The NucITS, mtSSU, and RPB2 sequences for taxa listed in Table 1 were aligned manually using MacClade version 4.05 (Sunderland, MA) [30].

A conflict was assumed to be significant if two different relationships (one being monophyletic and the other being non-monophyletic) for the same set of taxa were both supported with bootstrap values ≥70% [31].

The mtSSU and RPB2 datasets were concatenated. The combined two-locus dataset consisted of 180 terminals and 1777 unambiguously aligned sites: 856 for the mtSSU and 921 for RPB2. Bayesian inference, maximum likelihood, and parsimony were
<table>
<thead>
<tr>
<th>Species name</th>
<th>Voucher specimen/reference</th>
<th>ITS</th>
<th>12S mt SSU</th>
<th>RPB2</th>
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<td><strong>1. Alyxoria ochrocheila</strong></td>
<td>Ertz et al. [6]</td>
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<td>KF707664</td>
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<td><strong>6. Alyxoria varia</strong></td>
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<td>FJ772243</td>
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<td><strong>10. Arthonia apotheciorum</strong></td>
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<td>KJ850980</td>
<td>KJ851148</td>
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<td><strong>12. Arthonia calcarea</strong></td>
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<td>EU704065</td>
<td>EU704028</td>
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<td><strong>13. Arthonia calcarea</strong></td>
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<td>EU704029</td>
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<td><strong>15. Arthonia calcarea</strong></td>
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<td>KJ850970</td>
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<td><strong>16. Arthonia calcarea</strong></td>
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<td><strong>17. Arthonia dokdoensis</strong></td>
<td>SK L06, South Korea, Dokdo Islands, 07.09.2017 J. J.Woo 171029</td>
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<td><strong>18. Arthonia dokdoensis</strong></td>
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<td><strong>19. Arthonia dokdoensis</strong></td>
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<td><strong>20. Arthonia granitophila</strong></td>
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<td>KJ850981</td>
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<td><strong>21. Arthonia incarnata</strong></td>
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<td>KY983975</td>
<td>KY983983</td>
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<td><strong>22. Arthonia lapidicola</strong></td>
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<td>KJ850989</td>
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<td><strong>23. Arthonia lobariellae</strong></td>
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<td>KJ851127</td>
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<td><strong>25. Arthonia radiata</strong></td>
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<td><strong>27. Arthonia radiata</strong></td>
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<td><strong>28. Arthonia radiata</strong></td>
<td>Ertz et al. [6]</td>
<td>EU704048</td>
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<td><strong>29. Arthonia radiata</strong></td>
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<td>Frisch et al. [7]</td>
<td>KJ850999</td>
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<td><strong>31. Arthonia radiata</strong></td>
<td>Frisch et al. [7]</td>
<td>KJ850997</td>
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<td>KJ850997</td>
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<td><strong>33. Arthonia radiata</strong></td>
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<td>KJ850997</td>
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<td><strong>34. Brigantiaea ferruginea</strong></td>
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<td>KF264623</td>
<td>KF264685</td>
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<td><strong>35. Brigantiaea ferruginea</strong></td>
<td>SK 779; Kondratyuk et al. [12]</td>
<td>KF264622</td>
<td>KF264684</td>
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<td>KJ850991</td>
<td>KJ851124</td>
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<td><strong>37. Caloplaca areolata</strong></td>
<td>Sk 714; Kondratyuk et al. [13]</td>
<td>EU681284</td>
<td>EU680863</td>
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<td><strong>38. Caloplaca cerina</strong></td>
<td>FN 185; Fedorenko et al. [14]</td>
<td>EU681284</td>
<td>EU680863</td>
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<td><strong>39. Caloplaca stillicidiorum</strong></td>
<td>Gaya et al. [15]</td>
<td>KF707646</td>
<td>KF707657</td>
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<td><strong>40. Oxneria huculica</strong></td>
<td>Gaya et al. [16]</td>
<td>JQ301687</td>
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<td><strong>41. Oxneria ulophyllodes</strong></td>
<td>Gaya et al. [16]</td>
<td>JQ301687</td>
<td>JQ301776</td>
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<td><strong>42. Rupfola caemefeltiana</strong></td>
<td>South Korea, Ulleung-do Island, Dodong Port, 11.07.2016 Kondratyuk S. Y. &amp; L. Loko 162024 (KoLRI 040262)</td>
<td>162024</td>
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<td><strong>43. Rupfola caemefeltiana</strong></td>
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<td>162044</td>
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</table>

(continued)
used to estimate the phylogeny of *Arthoniaceae* based on a concatenated sequence matrix of the two loci. For the Bayesian and the maximum likelihood analyses, the best fit model for the two loci, as well as for the codon positions in the RPB2 gene, were calculated by applying the Akaike Information Criterion [32] and the program MrModeltest version 2.2 (Uppsala, Sweden) [33] in conjunction with PAUP* [34]. The prior selection of substitution models supported the GTR + I + C model for both the two individual loci, as well as for each codon position in RPB2. In the Bayesian analysis, the dataset was analyzed in four partitions, mtSSU and by codon positions for RPB2. Posterior probabilities of trees and parameters in the substitution models were approximated with MCMC and Metropolis coupling using the program MrBayes version 3.2.1 (Uppsala, Sweden) [35]. In parsimony analysis, the concatenated dataset was analyzed using the same settings as those used for testing the topological incongruence. The phylogenetic tree of the *Arthoniaceae* obtained from parsimony analysis based on the concatenated mtSSU and RPB2 sequences as the most illustrative one was included in the article (Figure 1).

Three outgroup species *Oxneria ulophyllodes*, *Oxneria Alfredii*, and *O. huculica* were chosen for the *Arthoniaceae* tree, but *Brigantiaea ferruginea* for the *Rufoplaca* phylogenetic tree. These taxa were used as the rooting taxa in all the analyses. In total, the dataset for the multilocus phylogenetic tree included 141 sequences and ca. Hundred specimens representing approximately 70 species, while the final tree presented in this article included 38 specimens representing 23 species.

### 3. Results and discussion

#### 3.1. New taxa

*Arthonia dokdoensis* S. Y. Kondr., L. Lőkös, B. G. Lee, J.-J. Woo et J.-S. Hur, sp. nov. (Figure 2)

MycoBank No.: MB 831133.

This species is similar to *A. parietinaria* but differs in causing much smaller infection spots, and in having smaller ascomata, a lower mean number of ascomata per infection spot, more common conidiomata, and bacilliform conidia.

**Type:** Republic of Korea, Gyeongsangbuk-do, Ulleung-gun, Dokdo-ri, Seodo (= Western) Island, on rocks, growing on thalli of *Orientophila yokjidoensis*, growing together with *Polyozosia aff. dispersa* and *Orientophila dodongensis*. Lat.: 37° 14′ 27″ N, Long.: 131° 51′ 54″ E, Alt.: 100 m a.s.l.

### Table 1. Continued.

<table>
<thead>
<tr>
<th>Species name</th>
<th>Voucher specimen/reference</th>
<th>ITS</th>
<th>12S mt SSU</th>
<th>RPB2</th>
</tr>
</thead>
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<td>54. <em>Rufoplaca scotoplaca</em></td>
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<td>JQ301618</td>
<td>JQ301497</td>
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<td>55. <em>Rufoplaca scotoplaca</em></td>
<td>Arup et al. [3]</td>
<td>KC179457</td>
<td>KC179573</td>
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<td>56. <em>Rufoplaca sp. 43</em></td>
<td>Arup et al. [3]</td>
<td>KC170458</td>
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<td>57. <em>Rufoplaca sp. JV 14429</em></td>
<td>Vondrak et al. [19]</td>
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<td>58. <em>Rufoplaca sp. JV 18681</em></td>
<td>Vondrak et al. (unpubl.)</td>
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<td>59. <em>Rufoplaca sp. D 17245</em></td>
<td>Vondrak et al. (unpubl.)</td>
<td>MG954209</td>
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<td>63. <em>Rufoplaca toktoona</em></td>
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<td>64. <em>Rufoplaca tristiuscula</em></td>
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<td>KC179460</td>
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<td>66. <em>Xanthoria mediterranea</em></td>
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<td>67. <em>Xanthoria monofoliosa</em></td>
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<td>JN984136</td>
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<td>68. <em>Xanthoria parietina</em></td>
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Coll.: Woo, J. J. (171028), 07.09.2017 (KoLRI 045309 sub Polyozosia – holotype); the same locality, growing on thalli of O. yokjidoensis, growing together with Physciella aff. melanchra and Lecanora sp. Coll.: Woo, J. J. (171029), 07.09.2017 (KoLRI 045310 sub O. yokjidoensis – holotype); the same locality, growing on thalli of O. yokjidoensis, growing together with Polyozosia aff. dispersa. Coll.: Woo, J. J. (171030), 08.09.2017 (KoLRI 045311 sub Polyozosia – isotype); the same locality, growing on thalli of O. yokjidoensis, growing together with Polyozosia aff. dispersa, Physciella aff. melanchra, and Diplotomma alboatra. Coll.: Woo, J. J. (171032), 08.09.2017 (KoLRI 045313 sub Polyozosia – isotype); the same locality, growing on thalli of O. yokjidoensis, growing together with Polyozosia aff. dispersa, Physciella aff. melanchra, Buellia ulleungdoensis and Lecanora sp. Coll.: Woo, J. J. (171034), 08.09.2017 (KoLRI 045315 sub Polyozosia – isotype); the same locality, growing on thalli of O. yokjidoensis, growing together with Polyozosia aff. dispersa, Physciella aff. melanchra, Diplotomma canescens, and B. ulleungdoensis. Coll.: Woo, J. J. (171036), 08.09.2017 (KoLRI 045317 sub D. canescens – isotype).

**Morphology:** Lichenicolous fungus forming very indistinct infection spots (from very indistinct to more or less recognizable to 0.5–1 mm across) in the central areolate portion of lobate lichen O. yokjidoensis, where the peripheral zone of host thallii to 1.5–2.5 mm wide with radially orientated lobes usually not damaged; infection spots often include very small, punctiform, scattered, and distant ascomata or conidiomata.

**Figure 1.** Position of the newly described *Arthonia dokdoensis* in the phylogenetic tree of the Arthoniaceae obtained from parsimony analysis based on concatenated mtSSU and RPB2 sequences.
Ascomata (0.08–0.1–0.13–0.14) mm wide, single, round and more or less regular, scattered and distant, and rather inconspicuous, or aggregated in very irregular shape aggregations with 5–10 apothecia together in spots to 0.4–0.6 mm diam./across, often covering one side/portion of the host thalline areole, and better seen. In section, epihymenium olivaceous brown to blackish brown, 4.6–8 mm thick; hymenium 32–40 μm high, in the middle and lower portions more or less hyaline; interascal hyphae branched and anastomosing ca. 2 mm wide; subhymenium (48–56–64–80) μm thick, hyaline or light brown; asci clavate, 8-spored; ascospores hyaline (0–1-septate; lower cell slightly attenuated, 9.6–12.8 × 4–4.8 μm (42 measurements).

Conidiomata very often observed below ascomata and probably especially numerous at first stages of infection development; conidia bacilliform, 3–4 × 0.8 μm.

Ascomatal gel I + red; KI + blue; asci with KI + blue ring-structure.

Ecology: The species grows in the crustose central portion of thalli of lobate lichens O. yokjidoensis and O. dodongensis growing on siliceous rock.

Etymology: It is named after the type locality, namely Dokdo Islands, Republic of Korea, Eastern Asia.

Distribution: It is so far known only from the type collection in Dokdo Islands, Republic of Korea, Eastern Asia, where it is rather abundant.

Taxonomic notes: The lichenicolous fungus A. dokdoensis usually damages the central portion to 0.5–1 mm across, while it hosts thalli to 7–8 mm across with peripheral zone to 1.5–2.5 mm wide with radially orientated lobes, which are usually not damaged by lichenicolous fungi.

Very small ascomata (ca. 80–120 μm in diam. at first) are rather scattered and distant, and are very
barely noticeable. Lichenicolous fungus is usually better distinguished when aggregated ascomata form irregular, often confluent aggregations to 0.4–0.5 mm wide. At this stage, ascomata of lichenicolous fungus often entirely cover the areoles of the central portion of host thalli. The A. dokdoensis infection on thalli of O. yokjidoensis can be most easy to be recognized at the latest stage.

Sometimes numerous brown hyphae with rounded cells to 4–4.8 μm wide are also observed in host thalli damaged by A. dokdoensis. On the other hand, they probably belong to another lichenicolous fungus.

Additional specimens examined: Republic of Korea, Gyeongsangbuk-do, Ulleung-gun, Dokdo-ri, Seodo (= Western) Island, on rock, growing on thalli of O. yokjidoensis growing together with Buellia halonia, and Lecanora sp. Lat.: 37° 14′ 29.04″ N, Long.: 131° 51′ 51.4″ E, Alt.: 20–25 m a.s.l. Coll.: Park, J. S. (170860), 07.09.2017 (KoLRI 045141 sub B. halonia); Dongdo Island, on rock, growing on thalli of O. yokjidoensis growing together with O. dodongensis, Polyozosia aff. Dispersa, and Physciella aff. melanchra. Lat.: 37° 14′ 21.61″ N, Long.131° 52′ 5.71″ E, Alt.: 12 m a.s.l. Coll.: Oh, S. O. (171086), 08.09.2017 (KoLRI 045367 sub Polyozosia aff. dispersa); Seodo Island, near the top level of the trail, on rock, growing on thalli of O. yokjidoensis growing together with Myriolecis aff. dispersa, B. ulleungdoensis and Physciella aff. melanchra. Lat.: 37° 14′ 30.02″ N, Long.: 131° 51′ 50.44″ E, Alt.: 25 m a.s.l. Coll.: Lee, B. G. (170928), 07.09.2017 (KoLRI 045209 sub O. yokjidoensis); Seodo Island, on rocks, growing on thalli of O. yokjidoensis growing together with Rufoplasa toktoana. Lat.: 37° 14′ 27″ N, Long.: 131° 51′ 54″ E, Alt.: 100 m a.s.l. Coll.: Woo, J. J. (171044), 07.09.2017 (KoLRI 045325 sub R. toktoana).

R. toktoana S. Y. Kondr., L. Lőkös et J.-S. Hur, sp. nov. (Figure 3)

MycoBank No.: MB 825110.

Similar to Rufoplasa kaerfelftiana but different in having well distinct and much larger thallus, thinner and K—cortical layer of thallus, larger and biatorine-like apothecia, lower hymenium and narrower paraphysis tips and shorter and narrower ascospores, and mainly hardly visible and narrower ascospore septum.

Type: Republic of Korea, Gyeongsangbuk-do, Ulleung-gun, Dokdo-ri, Seodo Island, on rocks, growing together with O. yokjidoensis damaged by A. dokdoensis, Lecanora sp. and Physciella sp. Lat.: 37° 14′ 27″ N, Long.: 131° 51′ 54″ E, Alt.: 100 m a.s.l. Coll. Woo, J. J. (171044), 07.09.2017 (KoLRI 045325 – holotype of R. toktoana); the same locality, growing together with O. yokjidoensis, Coll: Woo, J. J. (171045), 07.09.2017 (KoLRI 045326 – isotype of R. toktoana).

Morphology: Thallus rather thick, areolate to continuous, whitish gray, or grayish-white; apothecia seem to be biatorine, orange, or somewhat reddish-orange. Thalline areoles (0.5–1.5–2.5 mm across. Thallus in section to (64–)80–160–(280) μm thick, cortical layer 8–11.2–(12.8) [–24] μm thick, very thin, paraplectenchymatous, cell lumina rounded to 4.8 μm in diam.; algal zone filling in the whole thallus below cortical layer to 80(–96) μm thick; algal cells trebouxoid, 16–19.2(–22.4) μm in diam.

Apothecia to 0.9–1 mm in diam. and 0.2–0.27 mm thick in section, seem to be biatorine, while lecanorine or zeorine in section; 1–3(–5) per areole; in section thalline exciple to 80–96(–112) μm thick, cortical layer not distinct or very thin, to 8–16 μm thick, better seen on underside, paraplectenchymatous; true exciple (56–)80–96(–112) [–144] μm wide in the uppermost lateral portion, more or less scleroplectenchymatous, hyphal lumina to 1.6 μm, and to 16–32(–48) μm thick in lower lateral and to 16 μm thick in the basal portion, more or less Blastenia-type in the latter two portions or scleroplectenchymatous; hymenium 64–72 μm high, epihymenium 8–11.2 μm thick, dark brown; paraphysis tips more or less brownish, richly branched to 2.4–4 μm in diam. in K brownish color disappearing; subhymenium (48–)80–96 μm thick, hyaline, without oil; asci 8-spored, but usually only simple ascospore seen (in K too); ascospores narrowly ellipsoid, mainly simple observed, sometimes becoming slightly darker or slightly brownish (9.6–)11.2–12.8(–14.4) × 3–4.8 μm in water (45 measurements) and 11.8–13.4(–14.4) × 3.6–3.9(–4.5) μm in K (37 measurements); septum very rarely observed, usually seen only at sides of equatorial portions in water to (0.5–)1–2.4 μm wide in water and better seen in K (0.5–)1.5–2(–2.5) μm thick. Conidiomata and conidia not observed.

Chemistry: Epiphyllumenium K + crimson-purple, while brownish color disappearing. Cortical layer of thalline exciple K+ purple only in the uppermost lateral portion. Cortical layer of thallus K−.

Ecology: It grows on siliceous rock in the supralitoral zone.

Etymology: It is named after the type locality, namely Dokdo Islands (in Korean Tokto Islands), Republic of Korea, Eastern Asia.

Distribution: The species is so far known from the type collection Dokdo Islands, as well as Ulleung-do Island, both the Republic of Korea, Eastern Asia, where it was rather abundant in some places.

Taxonomic notes: R. toktoana is similar to R. kaerfelftiana S. Y. Kondr., L. Lőkös et J. S. Hur, recently described from Ulleung-do Island, South Korea (Eastern Asia), but differs in having well distinct
and much larger thallus and larger thalline areoles or often forming almost continuous thallus (thalline areoles (0.5–)1.5–2.5 mm vs. (0.2–)0.4–0.8 mm across, usually very indistinct, distant, and scattered), in having thinner and K–/C0 cortical layer of thallus (8–11(–13) μm vs. 30–40(–50) μm thick, K– purple), in having larger and biatorine-like apothecia (vs. seem to be lecanorine), in having lower hymenium (65–70 μm vs. 70–90 μm high) and narrower paraphysis tips (2.4–4 μm vs. to 5(–6) μm in diam.), and in having shorter and narrower ascospores ((9.5–)11–13(–14.5)×3–4.8 μm vs. (10–)12–15(–16) × 7–8 μm) and mainly hardly visible and narrower ascospore septum ((0.5–)1–2.4 μm vs. (4–)5–6(–7) μm wide) [4].

Additional specimens examined: Republic of Korea, Gyeongsangbuk-do, Ulleung-gun, Dokdo-ri, Seodo Island, on rocks, growing together with Caloplaca dodongensis. Lat.: 37° 14’ 26.66” N, Long.: 131° 51’ 51.50” E, Alt.: 20 m a.s.l. Coll.: Lee, B. G. (170909), 07.09.2017 (KoLRI 045190 sub R. toktoana); the same locality, growing together with B. ulleungdoensis, Coll.: Lee, B. G. (170910, 170911), 07.09.2017 (KoLRI 045191, KoLRI 045192 sub R. toktoana); Republic of Korea, Gyeongsangbuk-do, Ulleung-gun, Ulleung-eup, Dodong-ri, Dodong Port, on siliceous rocks. Lat.: 37° 28’ 59.9” N, Long.: 130° 54’ 40.7” E, Alt.: 20 m a.s.l. Coll.: Kondratyuk, S. Y., Lökös, L. (162040), 11.07.2016 (KoLRI 040278).

3.2. Discussion

A. dokdoensis is similar to the recently described A. parietinaria in having ascomata distributed over the surface of the host thallus, including apothecial...
Margins and hymenia, but differs in causing much smaller infection spots (to 0.5 mm across, often rather indistinct, vs. to 3–5 mm diam.), in having smaller ascomata (80–120(–140) μm vs. up to 0.25 mm in diam.), in having lower mean number of ascomata per infection spot (to 5–10 vs. (10–)120–30(–50)), in having more common conidiomata being often aggregated, while ascomata rarely observed (vs. ascomata well developed while conidiomata usually indistinct), and in having bacilliform conidia (vs. ellipsoid; unfortunately measurements on conidia not provided in the original description) [1]

(Table 2).

A. dokdoensis is similar to A. molendoi but differs in causing much smaller infection spots (to 0.5 mm in diam. often rather indistinct vs. to 3–5 mm diam. across), in having higher mean number of ascomata per infection spot (5–10 vs. 1–5(–10) in A. molendoi), in having smaller ascomata (80–120(–140) μm vs. 0.1–0.24 mm in diam.), in having lower hymenium (32–40 vs. 45–50 μm high) and thicker subhymenium (64–80 μm vs. 50–60 μm thick), in having shorter and narrower ascospores (9.6–12.8 × 4–4.8 μm vs. 11–14 × 5–6.5 μm), as well as being hyaline ascospores (not being slightly pigmented with age), and in having bacilliform conidia (pycnidia of A. molendoi still not observed after Grube [36]), as well as in the lack of a gelatinous epispore [36].

Unfortunately, a relatively recent full description of A. molendoi published only in Grube [36] is still incomplete. Fleischhacker et al. [1] also provided some data on the diagnostic characters of A. molendoi. Unfortunately, data on some measurements of ascomata, subhymenium, and shape or morphology of conidia are still missing.

Thus far, all species of the A. molendoi aggregation have been recorded from the members of the subfamily Xanthorioideae of the Teloschistaceae (see [2]), i.e., genera Rusavskia (type host of A. molendoi s. str.), Xanthoria (type host of A. parietinaria), Orientophila (type host of A. dokdoensis) and Calogaya. On the other hand, material of A. molendoi previously recorded from members of the genus Calogaya is in urgent need of revision and may belong to another taxon.

The data confirm the conclusion of Grube [36] in that careful studies of the A. molendoi complex are still needed in the future to determine if specimens on different lineages in Caloplaca and Xanthoria belong to the same species.

Arthonia destruens differs from taxa of the A. molendoi complex are still needed in the future to determine if specimens on different lineages in Caloplaca and Xanthoria belong to the same species.

Arthonia destruens differs from taxa of the A. molendoi complex are still needed in the future to determine if specimens on different lineages in Caloplaca and Xanthoria belong to the same species.

Fleischhacker et al. [1] segregated Ar. parietinaria growing on the members of the Xanthoria s. str. from the A. molendoi complex, which was believed to be foliose lichens of the genera Xanthoria and Rusavskia, as well as crustose lichens of the genus Calogaya (the former Caloplaca saxicola group). After segregation of A. parietinaria from the complex mentioned, A. molendoi is confirmed to Rusavskia elegans (type host) and to other species of the genus Rusavskia, as well as of the genus Calogaya.

The suggestion about the worldwide distribution of A. parietinaria and Holarctic is somewhat doubtful given that the host lichen species Xanthoria parietina itself is confirmed only from a few collections outside Europe and the Mediterranean region. Most records of Xanthoria parietina from outside Europe belong to other taxa (Kondratyuk, in prep.) and even to various genera of the Teloschistaceae in

### Table 2. Comparison of morphological/anatomical characters of Arthonia dokdoensis, A. parietinaria and A. molendoi.

<table>
<thead>
<tr>
<th>Characters</th>
<th>Arthonia dokdoensis</th>
<th>Arthonia parietinaria</th>
<th>Arthonia molendoi</th>
</tr>
</thead>
<tbody>
<tr>
<td>Infection spots</td>
<td>to 0.5 mm across, often rather indistinct</td>
<td>to 3–5 mm in diam.</td>
<td>to 3–5 mm in across</td>
</tr>
<tr>
<td>Mean number of ascomata per infection spot</td>
<td>to 5–10</td>
<td>(10–)20–30(–50)</td>
<td>1–5(–10)</td>
</tr>
<tr>
<td>Ascomata (in diam.)</td>
<td>(80–120(–140) μm)</td>
<td>up to 0.25 mm</td>
<td>0.1–0.24 mm</td>
</tr>
<tr>
<td>Hymenium (μm high)</td>
<td>32–40</td>
<td>30–45</td>
<td>45–50</td>
</tr>
<tr>
<td>Subhymenium (μm thick)</td>
<td>64–80</td>
<td>[data not provided in the original description][1]</td>
<td>30–60 μm</td>
</tr>
<tr>
<td>Ascospores (μm)</td>
<td>9.6–12.8 × 4–4.8, hyaline</td>
<td>(9–)10–12(–13.5) × (3–)4–5(–6), hyaline with thin hyaline epispore (getting condensed and brownish with age)[1]</td>
<td>11–14 × 5–6.5, slightly pigmented with age</td>
</tr>
<tr>
<td>A gelatinous epispore</td>
<td>absent</td>
<td>usually indistinct while ascomata well developed</td>
<td>present pycnidia of Arthonia molendoi still not observed after Grube [30]</td>
</tr>
<tr>
<td>Conidiomata</td>
<td>being often aggregated, more common while ascomata rarely observed</td>
<td>ellipsoid; unfortunately measurements on conidia not provided in the original description][1]</td>
<td>pycnidia of Arthonia molendoi still not observed after Grube [30]</td>
</tr>
<tr>
<td>Conidia</td>
<td>bacilliform</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Hosts</td>
<td>Orientophila ssp.</td>
<td>Xanthoria parietina</td>
<td>Rusavskia ssp.</td>
</tr>
</tbody>
</table>
current stage (see [2]). Fleischacker et al. [1] hesi-
tated to use modern generic groups of the
Teloschistaceae, but the generic groups Jackelixia, Rusavskia, Massjukiella, and Oxneria, recently
received further confirmation [2,37].

Unfortunately, the diagnostic character of the A. molendoi complex, such as fast vine red reaction of
hymenium (in contrast to I + blue then red in case
of Arthonia destruens or Arthonia incarnata), was
not discussed in the description of A. parietina-
rria [1].

Initially, close relations of the Korean material of
A. dokdoensis to Arthonia patellaria (ITS phylo-
genomes of the members of the Arthoniaceae. On
the other hand, only very limited data exists on the ITS
nrDNA sequences of the family Arthoniaceae, while
phylology of this family and the entire Arthoniales
is built mainly on nrLSU, mtSSU, and RPB2 sequen-
ces. An attempt was made to obtain the three
sequences mentioned above. On the other hand,
only the mtSSU and RPB2 sequences for the new
taxon could be obtained.

A separate mtSSU and RPB2 analysis (not
shown) revealed that A. molendoi is positioned in a
separate branch from the Arthonia s. str. branch.
The same results were obtained in the combined
phylogenetic analysis based on concatenated mtSSU
and RPB2 sequences (Figure 1).

It was firstly found in this study that the A. molendoi
group is positioned within the Bryostigma
clad of the combined phylogenetic tree of the
Arthoniaceae based on concatenated mtSSU and
RPB2 sequences. The Bryostigma clade includes the
genus Bryostigma Poelt et Döbbeler with type spe-
cies Bryostigma muscigenum (Th. Fr.) Frisch et G.
Thor, as well as members of the A. molendoi group
[38]. We agree with previous authors [9] that there
is probably more than one generic group within the
Bryostigma clade. Positions of seven of ten taxa of
the Bryostigma clade are confirmed by combined
mtSSU and RPB2 sequences (Figure 1), as well as by
nrLSU phylogeny [1].

A. dokdoensis, together with the following two
species, i.e., Arthonia phaeophysicae and A. parieti-
naria, for which molecular data were provided, are
the members of the A. molendoi complex. Unfortunately, only data on nrLSU sequences of A. parietina-
rria were recorded and illustrated in phylo-
genetic tree by Fleischacker et al. [1] from this spe-
cies of the A. molendoi complex. These data could
not be obtained from GenBank within this study. A. epiphytica, the position of which should be con-
firmed by molecular data in the future, is highly
likely to be a member of the Bryostigma molendoi
complex. These taxa, which are characterized by
lichenicolous habit, as well as numerous ascomata
forming very characteristic aggregations in host thal-
lus, may be segregated in the future in a separate
genus. On the other hand, only insufficient data
exist on differences of lichenicolous taxa and lichen-
forming fungi of the Bryostigma s. l. clade, as well
as epiphytophilous Bryostigma muscigenum (Th. Fr.)
Frisch et G. Thor itself (i.e., the genus Bryostigma
s. str.).

These results provide further evidence for the still
incomplete understanding of the character evolution
in Arthonia s. l. and the relevance of morphological
characters used for the delimitation of genera and
species groups in Arthoniaceae, as was previously
shown, e.g., by the studies of Frisch and Thor [39],
Frisch et al. [40,41], and Aptroot et al. [42]. Given
the combination of morphological characters pre-
sented above, in addition to the isolated position on
the phylogenetic tree in Figure 1, A. incarnata
appears to be a rather common species in old-
growth forests in Japan (collected only once in
Korea) [9], and cannot be connected easily with any
of the generic names currently accepted in the syn-
onymy of Arthonia [43]. At the current state of
knowledge and with a proper revision of Arthonia s.
still pending, this species should be in Arthonia
for the time being instead of describing it for
another poorly monotypic genus.

R. toktoana is also similar to the recently
described Rufoplacea ulleungensis S. Y. Kondr.,
L. Lökös et J. S. Hur, from Ulleung-do Island, South
Korea (Eastern Asia), but differs in having much
better developed and often almost continuous thal-
lus (vs. rather indistinct and consisting of distant
and scattered areoles), in having larger apothecia (to
0.9–1 mm vs. (0.2–)0.3–0.8 mm diam.), in having
shorter and narrower ascospor( es (9.5–
11–13(–14.5)×3–4.5 µm vs. 14–16(–18) × 4–5.5(–6)
(µm), while ascospore septum (0.5–)1–2.4 µm vs.
1.5–2(–2.5) µm wide) is similar [5] (Table 3).

R. toktoana is similar to “Caloplaca” fraudans
(Th. Fr.) H. Olivier growing on sea coastal rock,
rarely on wood or bones, in Arctic regions of the
Holarctic, but differs in having well distinct, thick
thallus, in having concave or plane light reddish
orange apothecia (vs. convex, dark orange, or rusty
red), in having rather thin own margin and con-
colorous with apothecium disc (vs. to 0.1–0.2 mm
wide slightly shiny and lighter of disc, bright orange,
or yellow), in having thinner subhymenium (vs.
60–100(–130) µm thick), in having lower hymenium
(65–70 µm vs. 85–100 µm high), in having shorter
and narrower ascospor es (9.6–)
11–13
(–14.5)×3–4.8 µm vs. (10–)12–14(–15)×4–6 µm),
and in having slightly narrower (or mainly
undeveloped) ascospore septum (0.5–1.5–2.4 μm vs. 2.5–4.5 μm wide) [44].

*R. toktoana* is similar and can be keyed to *Caloplaca erythrocarpa* (Pers.) Zwackh growing on limestones, sandstones enriched by calcium in Europe, the Caucasus, Asia (Syria, Israel, Jordania, and Egypt), and North Africa, but differs in having larger apothecia (0.9–1 mm vs. 0.2–0.5–0.8 mm in diam.), in having biatorine, but lecanorine or zeorine in section apothecia (vs. zeorine), in having superficial (vs. seem to be immersed) apothecia; in having irregular and larger thalline areoles (0.5–1–1.5 mm vs. 0.2–0.5–(1–1) mm across), in having 1 apothecium per areole (vs. (1–2)–3 apothecia per areoles in the center of thallus); in having dull orange or dull reddish orange disc (vs. dark red, dark rusty red, to dark rusty brown), in having weakly developed, seen at sides or on underside thalline margin (vs. own margin lighter of disc, red-orange, thin, and permanent), in having narrower and shorter ascospores (9.6–11–13(–14.5) × 3–4.8 μm vs. 12–16(–18) × (5–)7–9(–10) μm, and in having narrower ascospore septum (0.5–1–2.4 μm vs. 3–5 μm wide [40].

Twenty-five sequences are available for members of the genus *Rufoplaca* in GenBank. The main portion of data was provided by Arup et al. [3], while a few specimens were added by J. Vondraková et al. [17–19]. On the other hand, after ITS phylogeny, the Eastern Asian material, i.e., *R. toktoana* and *R. kaernefeltii*, for which molecular data are for the first time provided in this article, form a separate branch within the genus *Rufoplaca* (Figure 4). Both Eastern Asian taxa have the highest level of

| Table 3. Comparison of morphological/anatomical characters of *Rufoplaca toktoana*, *Rufoplaca kaernefeltiana*, and *Rufoplaca ulleungdoensis*. |
|---|---|---|
| Characters | *Rufoplaca toktoana* | *Rufoplaca kaernefeltiana* | *Rufoplaca ulleungdoensis* |
| Thallus | well distinct and large | usually very indistinct | rather indistinct and consisting of distant and scattered areoles | 0.3–0.7(–1.3), distant and separate to aggregated in small groups |
| Thalline areoles mm across | (0.5–)1.5–2.5, well distinct or often forming almost continuous thallus | (0.2–)0.4–0.8, usually very indistinct, distant and scattered | 7–9 and K– | 0.2–0.3–0.8 mm, often in groups, biatorine |
| Cortical layer of thallus (μm thick) | 8–11(–13) and K– to 0.9–1 mm, biatorine-like | 30–40(–50), K+ purple | 3–5(–6) |
| Apothecia | Hymenium (μm high) | 65–70 | 70–90 |
| Paraphyses tips (μm in diam.) | 2.4–4 | to 5(–6) | 4(–) |
| Ascospores (μm) | (9.5–)11–13(–14.5) × 3–4.5 | (10–)12–15(–16) × 7–8 | 14–16(–18) × 4–5.5(–6) |
| Ascospore septum (μm wide) | (0.3–)1–2.4, mainly hardly visible | | 1.5–2(–2.5) |

Figure 4. Phylogenetic tree of the genus *Rufoplaca* based on ITS nrDNA showing position of the new species *R. toktoana* and the recently described *Rufoplaca kaernefeltiana*. |

FN1 185 *Caloplaca cerina* | 162024 *Rufoplaca kaernefeltiana* |
SK 714 *Caloplaca arenolata* | 162044 *Rufoplaca kaernefeltiana* |
162040 *Rufoplaca toktoana* | 162044 *Rufoplaca kaernefeltiana* |
SK L03 *Rufoplaca toktoana* | SK L07 *Rufoplaca toktoana* |
SK L08 *Rufoplaca toktoana* | 120253 *Xanthoria coomae* |
Rufoplaca sp. 269867 | | |
Rufoplaca aff arenaria KF007908 | | |
Rufoplaca oxfordens KCI179456 | | |
Rufoplaca subpallida KCI179459 | | |
Rufoplaca tristiscula KCI179460 | | |
Rufoplaca arenaria KT934385 | | |
Rufoplaca sp. MG954203 | | |
Rufoplaca arenaria KCI179455 | | |
Rufoplaca sp. MG954209 | | |
Rufoplaca sp. 43 KCI179458 | | |
Rufoplaca scotoplace KCI179457 | | |
Rufoplaca scotoplace QJ031618 | | |
FNN 177 *Xanthoria parietina* | | |
120253 *Xanthoria coomae* | | |
Xanthoria mediterranea | | |
SK 3191 *Xanthoria monofoliola* | | |
SK 780 *Brigantiaea ferruginea* | | |
SK 779 *Brigantiaea ferruginea* | | |
bootstrap support. Therefore, the material of both taxa mentioned is rather homogenous from the molecular point of view.

4. Conclusion

The species diversity of the Bryostigma s. lat. clade includes 13 species based on a combined phylogenetic analysis of the Arthoniaceae based on mtSSU and RPB2 gene sequences. Data on ITS nrDNA sequences are provided herein for the first time for A. dokdoensis, R. kaernefeltiana, and R. toktoana.

Acknowledgments

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Disclosure statement

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