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Review of Japanese Pine Bast Scale, *Matsucoccus matsumurae* (Kuwana) (Coccomorpha: Matsucoccidae), Occurring on Japanese Black Pine (*Pinus thunbergii* Parl.) and Japanese Red Pine (*P. densiflora* Siebold & Zucc.) from Korea

Jinyeong Choi [1,2], Deokjea Cha [3], Dong-Soo Kim [3] and Seunghwan Lee [1,2,*]

1 Insect Biosystematics Laboratory, Department of Agricultural Biotechnology, Seoul National University, Seoul 151-921, Korea
2 Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul 151-921, Korea
3 Forest Biomaterials Research Center, National Institute of Forest Science, Jinju 52817, Korea
* Correspondence: seung@snu.ac.kr; Tel.: +82-2880-4703; Fax: +82-2873-2319

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Abstract: *Matsucoccus matsumurae* (Kuwana, 1905), commonly known as Japanese pine bast scale, is a destructive pest on pine trees in North America, East Asia, and Northern Europe. The spread of damage to black pine trees, *Pinus thunbergii* Parl., due to *M. matsumurae* has been reported throughout Southern and some Eastern and Western coastal regions in Korea, under the name *M. thunbergianae*, which was described by Miller and Park (1987). Recently, *M. thunbergianae* was synonymized with *M. matsumurae* by Booth and Gullan (2006), based on molecular sequences and morphological data. However, *M. thunbergianae* is still considered a valid species in Korea. Since supporting data for the synonyms are unavailable in any DNA database (e.g., GenBank and BOLD), we performed morphological and molecular comparisons to review the results of Booth and Gullan (2006) using samples of *M. matsumurae* collected from Japan and topotype materials of *M. thunbergianae* from Korea. Our study supports the opinion of Booth and Gullan (2006), as the morphological features of the adult female and male of *M. thunbergianae* are identical to those of *M. matsumurae*, and DNA sequences (18S and 28S) of *M. thunbergianae* show identical or very low genetic distances with those of *M. matsumurae*. Additionally, regional sampling of Korea produced the first documented occurrence of *M. matsumurae* in Jeju.

Keywords: *Matsucoccus thunbergianae*; black pine bast scale; taxonomy; synonym

1. Introduction

The genus *Matsucoccus* Cockerell [1], belonging to the archaeococcoid family Matsucoccidae, comprises about 38 species worldwide [2]. Except for six fossil species described from Baltic amber, all 32 extant species exclusively occur on *Pinus* spp. in the Holarctic and Neotropical regions [2]. Among them, some species are the most destructive pests on pine trees; for example, *Matsucoccus acalyptus* Herbert on pinyon pine (*Pinus edulis* Engelm.) and single-leaf pinyon (*P. monophylla* Torr. and Frém.); *M. bisetosus* Morrison and *M. vexillorum* Morrison on ponderosa pine (*P. ponderosa* P. and C. Lawson); and *M. matsumurae* (Kuwana) on Chinese pines (*P. tabuliformis* Carrière and *Pinus massoniana* D. Don.), Japanese black pine (*P. thunbergii* Parl.), and red pine (*P. resinosa* Sol. ex Aiton) [3–7].

Females and males of *Matsucoccus* species have sexually dimorphic life cycles after the second-instar nymphs, which are known as "cysts" in the feeding and overwintering stages (Figure 1). The females

are neotenic, including three stages (occasionally four in *M. vexillorum* Morrison), whereas the males have five stages, including a prepupa and pupa, and grow functioning wings as adults (for the life cycle details of *Matsucoccus*, see Foldi [5]).

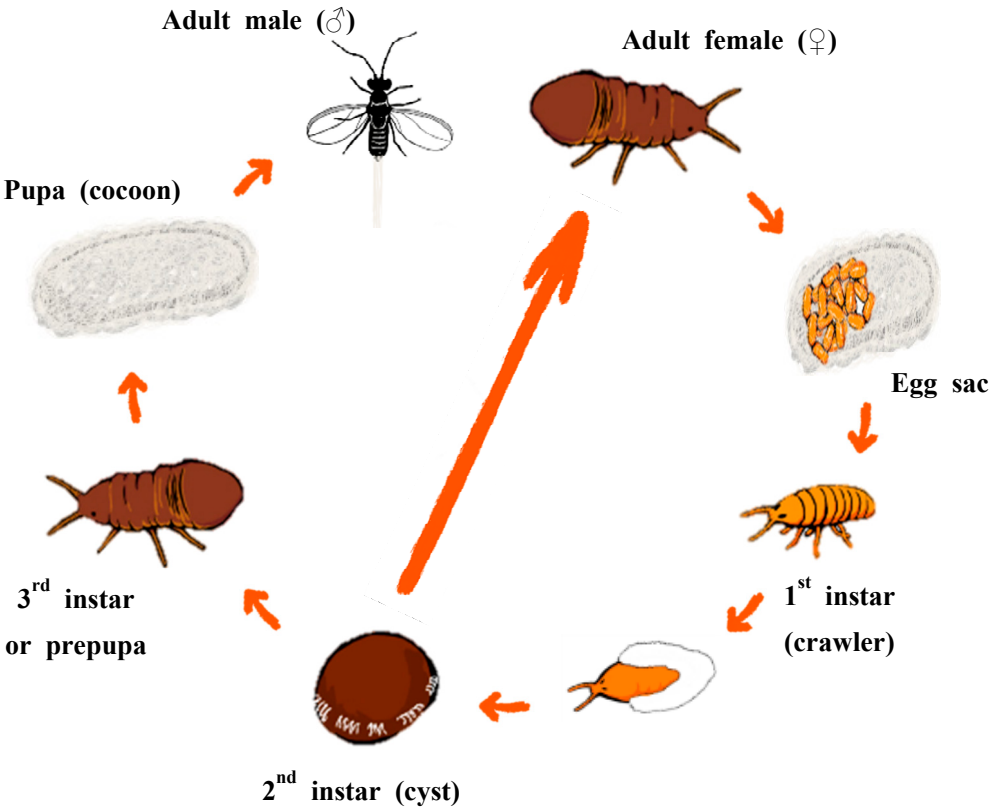

Figure 1. General life cycle of *Matsucoccus* species.

The Japanese pine bast scale, *Matsucoccus matsumurae*, was described by Kuwana [8] as a new species on Japanese black pine (*Pinus thunbergii* Parl.) in Tokyo, Japan, and was mainly found in China, Japan, and Korea. In China, more than 70,000 km^2 of pine forest damage by *M. matsumurae* had been reported each year between the 1970s–1980s despite attempts at chemical control [7,9].

In Korea, there had been no reports of significant damage by *Matsucoccus matsumurae* after the species was first found by Kanda [10], until a heavy infestation was detected on about 12,000 ha of Japanese black pine in the Southwestern coastal area of Korea [11]. This damage was found to be caused by a new species, *M. thunbergianae* Miller & Park [11], which was distinguished based on differences in morphological characteristics and in the number of generations from the congeners, *M. matsumurae* and *M. resinosae* Bean & Godwin. However, several studies implied that *M. matsumurae*, *M. resinosae*, and *M. thunbergianae* could be the same species. For example, the three species showed strong cross-attractiveness to sex pheromones [12,13], the main component of which was identical for the three species [14,15]. Finally, *M. thunbergianae* and *M. resinosae* were synonymized with *M. matsumurae* by Booth and Gullan [16], mainly based on their similarities in morphology and molecular sequences of 18S and 28S rDNA. However, *M. thunbergianae* is still considered a valid species in Korea [6,17–19] despite suggestions that the two species are synonymous, and an evaluation between *M. thunbergianae* collected from Korea and *M. matsumurae* was not possible due to the absence of DNA data from any available database.

In this study, we collected true *Matsucoccus matsumurae* from Fukuoka, Japan, and topotype materials of *M. thunbergianae* from Goheung, Korea, on the Japanese black pine to compare their morphologies and molecular sequences. To examine the spread of *M. matsumurae*, regional sampling

was performed in Korea. Based on those data, we provide morphological and molecular characteristics of *M. matsumurae* and its current distribution in Korea.

2. Materials and Methods

2.1. Sample Collection

Eight populations of *Matsucoccus* sp. from Japan and Korea were sampled for morphological and molecular analyses (Figure 2; Table 1). To sample *M. matsumurae*, a population of *Matsucoccus* sp. (assumed to be *M. matsumurae*) on *Pinus thunbergii* was collected from Fukuoka in Japan. To sample *M. thunbergianae*, a population of *Matsucoccus* sp. (assumed to be topotype materials of *M. thunbergianae*) on *P. thunbergii* was collected from Goheung in Korea. For regional sampling in Korea, six populations of *Matsucoccus* sp. on *P. densiflora* or *P. thunbergii* were collected from Buan, Jeju, Pohang, Sacheon, Seoul, and Taean in Korea. Each population was preserved in 95% ethanol and stored at −20 °C for molecular analysis and morphological identification.

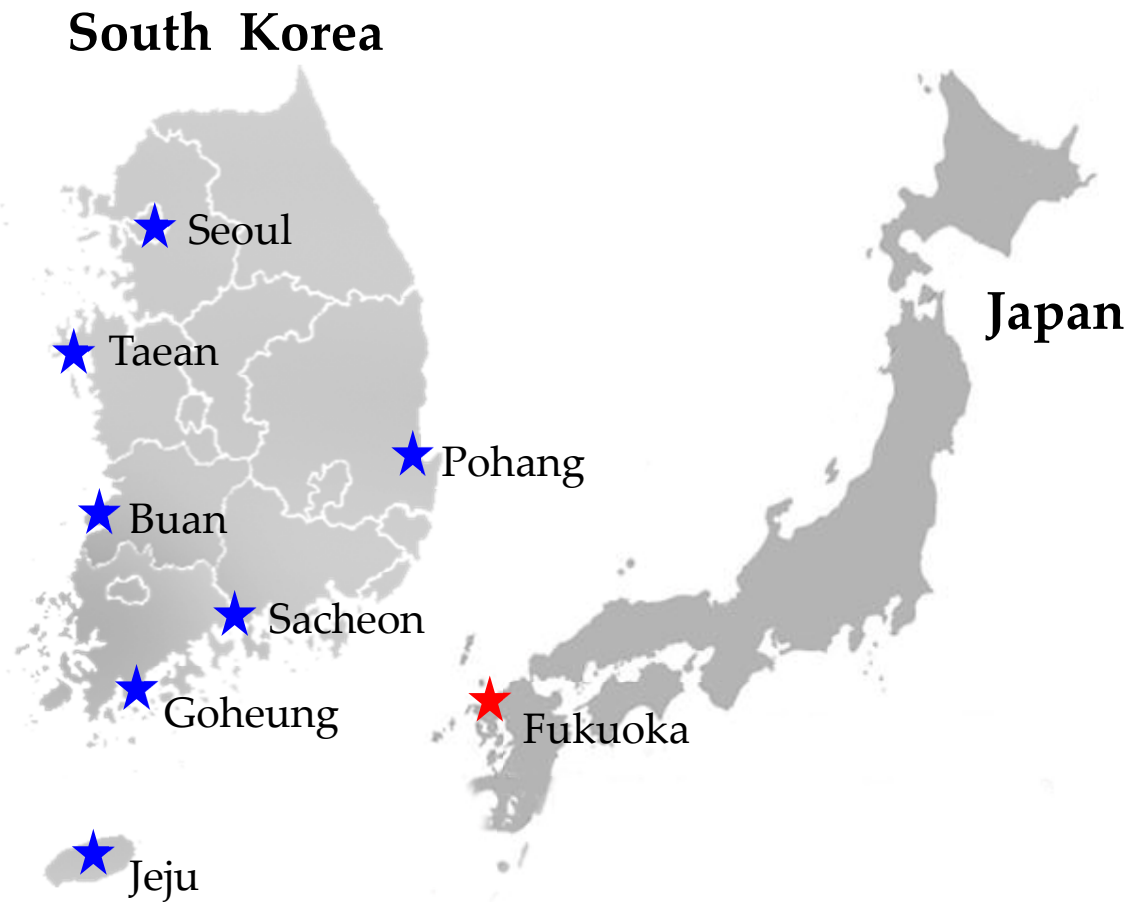

Figure 2. Sampling localities of *Matsucoccus* sp. in Korea and Japan.

Table 1. Collection data of samples used in this study (GPS coordinates; WGS84 coordinate system).

Species	Sex	Host	Locality	GPS		Date	Collector	GenBank Accession No.	
				North	East			18S	28S
Matsucoccus sp.	Female	*Pinus thunbergii*	Goheung, South Korea	34.631599	127.380838	Jan., 2017	D. Cha	-	-
Matsucoccus sp.	Male	*Pinus thunbergii*	Goheung, South Korea	34.631599	127.380838	Jan., 2017	D. Cha	MH574839	MH574783
Matsucoccus sp.	Male	*Pinus thunbergii*	Buan, South Korea	35.596690	126.486645	Jan., 2017	D. Cha	MH574841	MH574785
Matsucoccus sp.	Male	*Pinus thunbergii*	Jeju, South Korea	33.530302	126.718108	Jan., 2017	D. Cha	MH574845	MH574789
Matsucoccus sp.	Male	*Pinus thunbergii*	Pohang, South Korea	36.055884	129.576762	Jan., 2017	D. Cha	MH574843	MH574787
Matsucoccus sp.	Male	*Pinus thunbergii*	Sacheon, South Korea	34.948513	128.050597	Jan., 2017	D. Cha	MH574840	MH574784
Matsucoccus sp.	Male	*Pinus densiflora*	Seoul, South Korea	37.598240	127.024651	Jan., 2017	D. Cha	MH574844	MH574788
Matsucoccus sp.	Male	*Pinus thunbergii*	Taean, South Korea	36.781692	126.132603	Jan., 2017	D. Cha	MH574842	MH574786
Matsucoccus sp.	Female	*Pinus thunbergii*	Fukuoka, Japan	33.580591	130.278336	Jan., 2017	D. Cha	-	-
Matsucoccus sp.	Male	*Pinus thunbergii*	Fukuoka, Japan	33.580591	130.278336	Jan., 2017	D. Cha	MH574846	MH574790

2.2. Morphological Identification

For morphological comparison, the adult females and males of *Matsucoccus* sp. from Fukuoka and Goheung were mounted on glass microscope slides using the methods of Danzig and Gavrilov-Zimin [20]. Morphological descriptions of *Matsucoccus* spp. in Foldi [5] and Morrison [21] were used to identify the adult females and males of slide-mounted specimens. Photomicrographs of the specimens were produced with a digital camera (Infinity3, Lumenera Corporation, Ottawa, Canada) mounted on a compound light microscope (DM 4000B, Leica Microsystems, Wetzlar, Germany). The slide specimens were deposited in either (i) the Insect Biosystematics Laboratory, Seoul National University, Korea (SNU), or (ii) Southern Forest Resources Research Center, National Institute of Forest Science (NIFS).

2.3. Molecular Analyses

Genomic DNA isolation was performed with the DNeasy Blood and Tissue kit (Qiagen, Inc., Dusseldorf, Germany) following the manufacturer's protocols. For molecular comparison, we selected two nuclear ribosomal RNA genes (partial 18S and D2–D3 region of 28S). These two loci were amplified from the total DNA of the adult males of *Matsucoccus* sp. from Fukuoka and Goheung as well as other regions (Buan, Jeju, Pohang, Sacheon, Seoul and Taean). We designed primers based upon Margarodidae spp. 18S and 28S sequences from GenBank. Primer sequences used for the polymerase chain reaction (PCR) are given in Table 2. PCR was conducted with AccuPower PCR PreMix (Bioneer, Daejeon, Korea) in 20 ml including 0.4 μM of each primer, 20 μM dNTPs, 20 μM MgCl2, and 0.05 μg DNA template. The PCRs for 18S and 28S were performed under the following conditions: An initial denaturation step at 95 °C for 3 min, followed by 35 cycles at 95 °C for 30 s, 60 °C for 30 s, and 72 °C for 1 min and a final extraction step at 72 °C for 1 min. PCR products were visualized in 1.5% agarose gel electrophoresis. All amplified samples were purified using the QIAquick PCR purification kit (Qiagen, Inc., Dusseldorf, Germany) and sequenced using an automated sequencer (ABI Prism 3730 XL DNA Analyzer) at Macrogen Inc. (Seoul, Korea). Both strands of each sample were assembled and edited with SeqMan Pro ver. 7.1.0 (DNASTAR, Inc., Madison, WI, USA). The alignment was carried out using MEGAX [22], including sequences of *Matsucoccus macrocicatrices* Richards (used as reference, KF053072 for 18S; KF040573 for 28S) and *Icerya purchasi* Maskell (used as outgroup, AY426078 for 18S; KT199077 for 28S) downloaded from GenBank. The uncertain regions of sequences were removed, and 361 base pairs from *18S* and 462 base pairs from *28S* were used for the analyses. All sequences used in this study were deposited into GenBank under the accession number (from MH574783 to MH574790 for 28S; from MH574839 to MH574846 for 18S; Table 1). Genetic distances were measured in MEGAX using a neighbor-joining tree with the Kimura two-parameter model [23].

Table 2. Primers used in this study.

Gene Regions	Direction	Primer Name	Sequences (5′–3′)	Annealing Temperature
18S	Forward	Matsu_18S_F	CATGTCTAAGTGCAAGCCGG	60 °C
	Reverse	Matsu_18S_R	CCTCATAAGAGTCCCGTATCG	60 °C
28S	Forward	Matsu_28S_F	AAACCACAGCCAAGGGAACG	60 °C
	Reverse	Matsu_28S_R	TTTTCTGACACCTCTCGCTG	60 °C

3. Results

3.1. Morphological Comparison

The morphological characteristics of adult females and males of *Matsucoccus thunbergianae* from Korea are identical to those of *M. matsumurae* from Japan.

3.1.1. Adult Females

Based on the morphological information of *Matsucoccus* spp. in Foldi [5] (Figure 3), adult females of *Matsucoccus* sp. from Fukuoka, Japan, were identified as *M. matsumurae*. In addition, adult females of *Matsucoccus* sp. from Goheung, Korea, are morphologically similar to those of Fukuoka in eight morphological characteristics (Figure 4): (i) Nine-segmented antenna, with bases placed close together, and the scape and pedicel distinctly longer and wider than the associated flagellar segment (Figures 3A and 4B); (ii) two pairs of thoracic spiracles, each with numerous tracheae (Figures 3I and 4E,G); (iii) seven pairs of abdominal spiracles with a structure similar to that of thoracic spiracles (Figures 3G and 4E,F); (iv) femur, tibia, and tarsus, each with a reticulated surface (Figure 3H); (v) a pair of ventral setae present on each abdominal segment III–VII (Figures 3F2 and 4I); (vi) multilocular disc-pores each with 9–13 loculi and about 40–85 pores around the vulva (Figures 3E and 4D); (vii) cicatrices present in transverse rows across abdominal segments III–VII, numbering 180–280 (Figures 3D and 4H); (viii) bilocular tubular ducts in transverse rows on the head, thorax, and abdomen (Figures 3C and 4C).

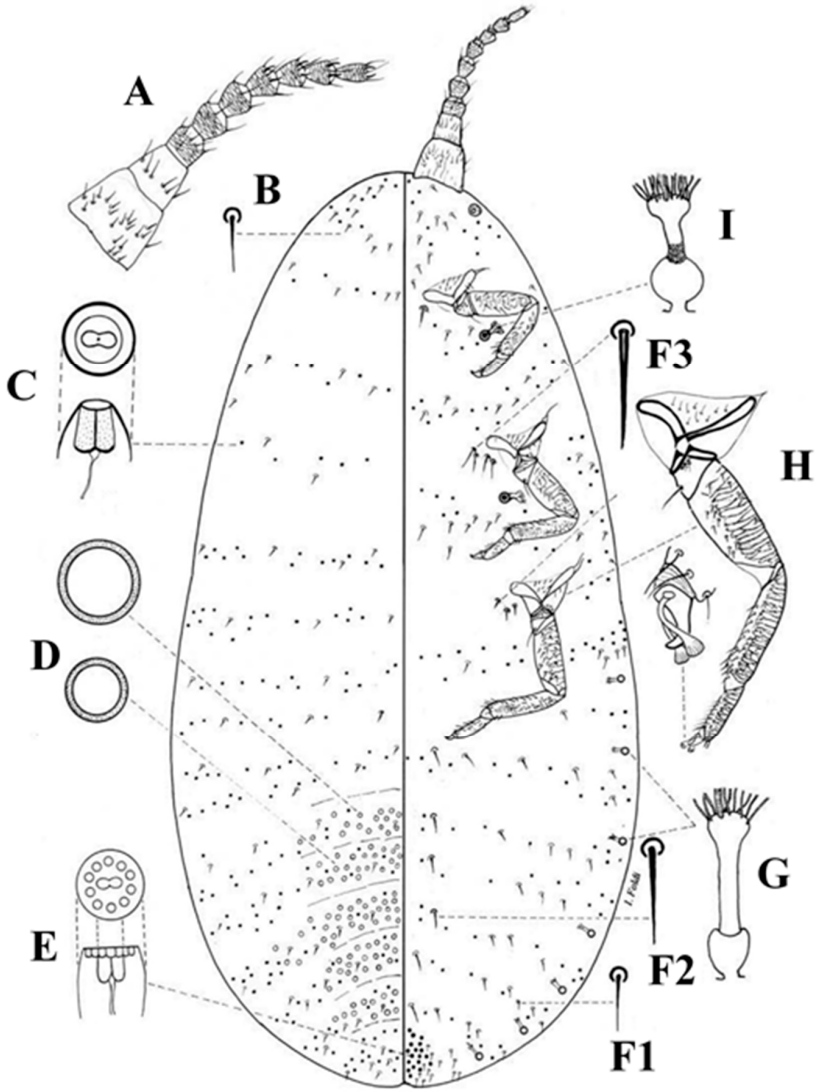

Figure 3. *Matsucoccus matsumurae* (Kuwana, 1905), adult female, from Foldi [5]. **A**, antenna; **B**, dorsal seta; **C**, bilocular tubular duct; **D**, cicatrices; **E**, multilocular disc-pore; **F1–3**, ventral setae; **G**, abdominal spiracle; **H**, leg; **I**, thoracic spiracle. This figure was reproduced with permission of I. Foldi.

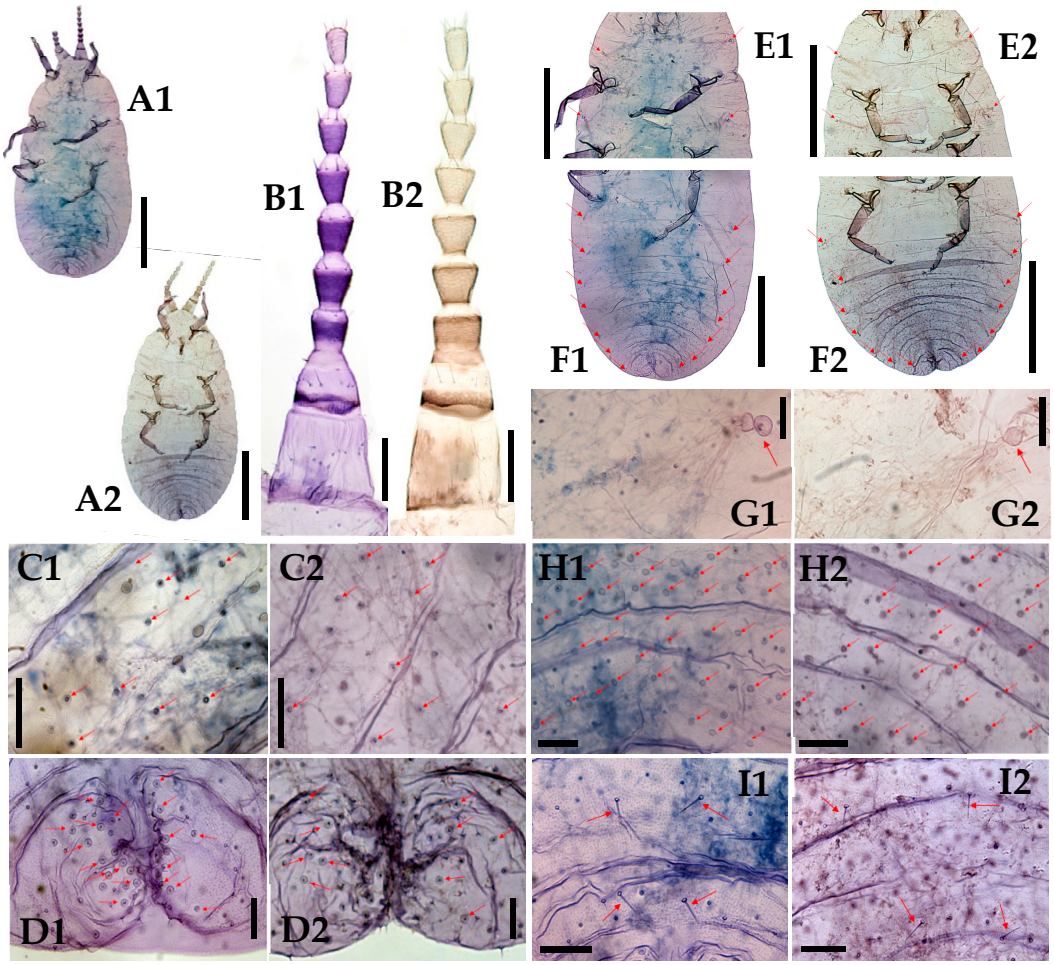

Figure 4. Morphological comparison of the adult females from Goheung (first) and Fukuoka (second). **A**, bodies; **B**, antennae; **C**, bilocular tubular ducts; **D**, multilocular disc-pores; **E**, thoracic spiracles; **F**, abdominal spiracles; **G**, spiracles with numerous tracheae; **H**, cicatrices; **I**, ventral setae on abdomen. Scale lines for A, E, F = 1 mm; B = 100 μm; C, D, G, H, I = 50 μm.

3.1.2. Adult Males

Based on the morphological information of *Matsucoccus* spp. in Morrison [21] (Figure 5), adult males of *Matsucoccus* sp. from Fukuoka were identified as *M. matsumurae*. In addition, adult males of *Matsucoccus* sp. from Goheung were morphologically similar to those of Fukuoka, based on seven morphological characteristics (Figure 6): (i) Ten-segmented antenna, each with short and stout scape and pedicel, but slender and cylindrical in each flagellar segment (Figures 5F and 6F); (ii) a head wider than it is long (transversely elongated), with antennal bases placed close together and large compound eyes (Figures 5C and 6B); (iii) slender legs with reticulated tarsus and stout claws without denticles (Figures 5D and 6G); (iv) wings with a reticulated costal complex that continues to the apex and two main veins extending from the wing base to its apex in the medial area with its under margin directed sharply downward on the basal area (Figure 5I–J and Figure 6C–D); (v) halteres are broadest at the apex, each with about six long and slender setae (Figures 5G and 6H); (vi) abdomen with elongated multilocular tubular pores, clustered in a transversely ovoid area near the apex of the abdomen (Figures 5A and 6I); (vii) the penis sheath is broad at the base and tapers to a rounded tip, while the aedeagus is slender, strongly curved, and protrudes beyond the apex of the penis sheath (Figures 5A and 6E).

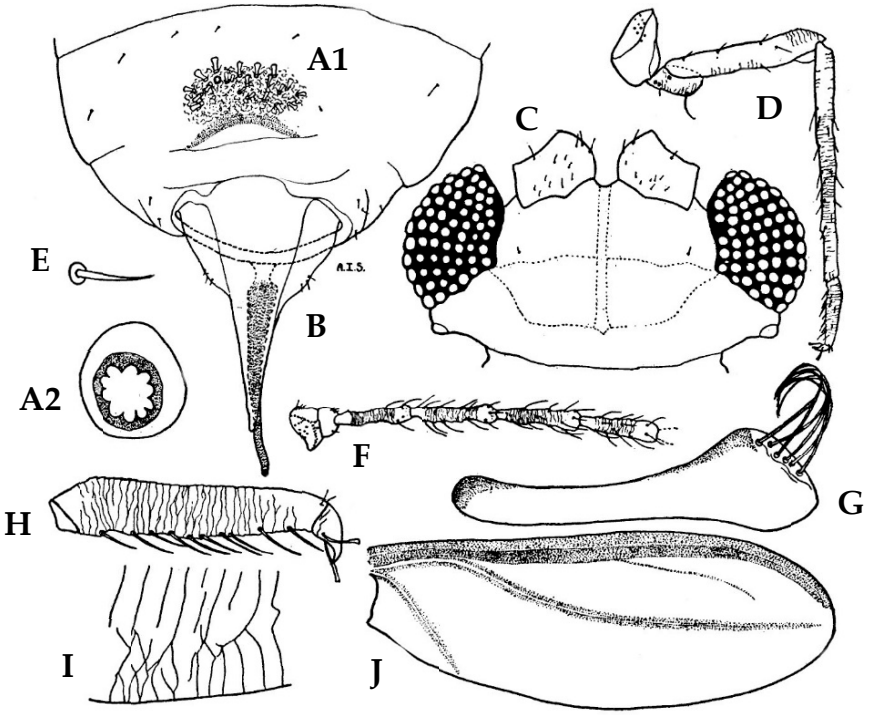

Figure 5. *Matsucoccus matsumurae* (Kuwana, 1905), adult male, from Morison [21]. **A1–2**, multilocular tubular pores near apex of abdomen; **B**, genitalia (aedeagus and penis sheath); **C**, head; **D**, leg; **E**, ventral abdominal seta; **F**, antenna; **G**, halter; **H**, tarsus and claw; **I**, wing venation; **J**, wing.

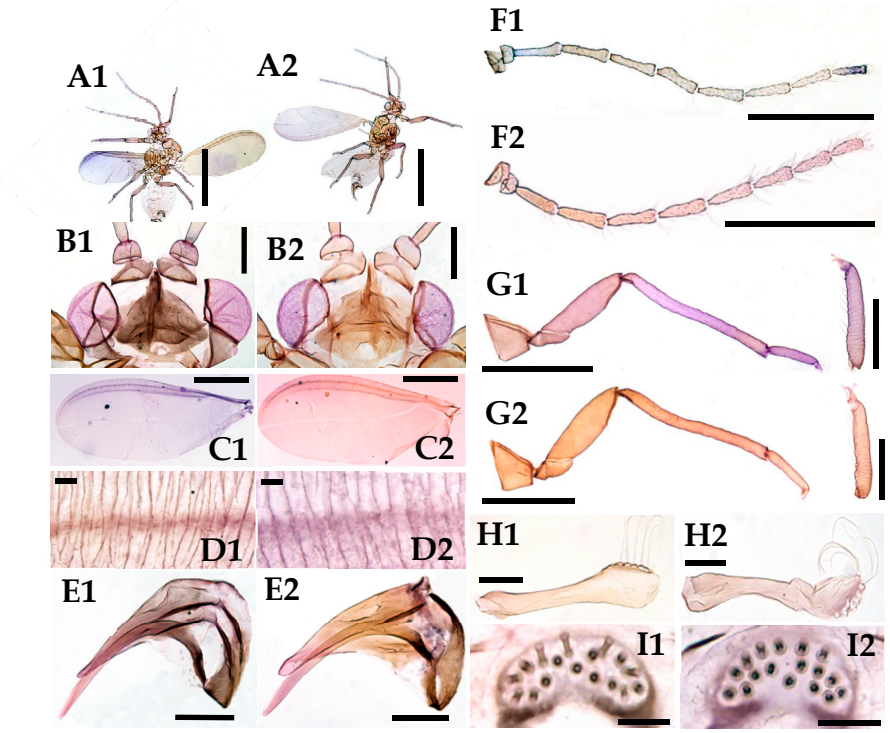

Figure 6. Morphological comparison of the adult males from Goheung (first) and Fukuoka (second). **A**, bodies; **B**, heads; **C**, wings; **D**, reticulated costal complexes; **E**, genitalia (aedeagus and penis sheath); **F**, antennae; **G**, legs, and tarsi and claws; **H**, halteres; **I**, multilocular tubular pores. Scale lines for A = 1 mm; B, E, G (bar beside tarsus and claw) = 100 μm; C = 0.5 mm; D = 10 μm; F = 500 μm; G (bar under entire leg) = 300 μm.

3.2. Molecular Comparison

The DNA sequences (18S rDNA and 28S rDNA) of *Matsucoccus* sp. from Korea showed identical or very small genetic distances compared to those of *M. matsumurae* from Japan. Each neighbor-joining tree and genetic distances of 18S and 28S sequences among the samples are presented in Figure 7 and Tables 3 and 4, respectively.

The 18S sequences of *Matsucoccus* sp. from seven populations in Korea (Buan, Goheung, Jeju, Pohang, Sacheon, Seoul, and Taean) were almost identical to those of *M. matsumurae* from a population in Japan (Fukuoka). The genetic distances ranged from 0% to 0.6% among these samples (Figure 7A; Table 3).

The 28S sequences of *Matsucoccus* sp. from seven populations in Korea (Buan, Goheung, Jeju, Pohang, Sacheon, Seoul, and Taean) were identical to those of *M. matsumurae* from a population in Japan (Fukuoka). No genetic distances were observed among these samples (Figure 7B; Table 4).

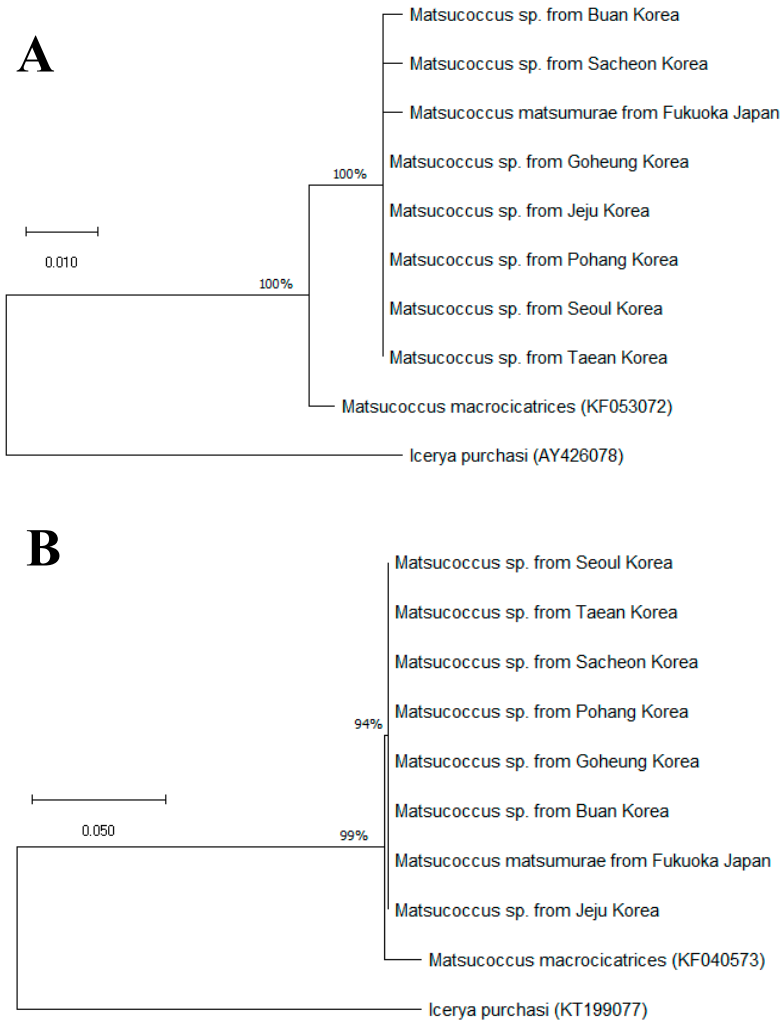

Figure 7. Neighbor-joining (NJ) tree analyses (using Kimura 2-parameter model) of seven regional populations of *Matsucoccus* sp. from Korea and *M. matsumurae* from Japan. **A**. 18S; **B**. 28S.

Table 3. Genetic distances (%) of 18S sequences estimated by Neighbor-joining with Kimura-2 parameter model.

No.		1	2	3	4	5	6	7	8	9	10
1	*Matsucoccus matsumurae* from Fukuoka, Japan										
2	*Matsucoccus* sp. from Buan, Korea	0.6									
3	*Matsucoccus* sp. from Goheung, Korea	0.3	0.3								
4	*Matsucoccus* sp. from Jeju, Korea	0.3	0.3	0.0							
5	*Matsucoccus* sp. from Pohang, Korea	0.3	0.3	0.0	0.0						
6	*Matsucoccus* sp. from Sacheon, Korea	0.6	0.6	0.3	0.3	0.3					
7	*Matsucoccus* sp. from Seoul, Korea	0.3	0.3	0.0	0.0	0.0	0.3				
8	*Matsucoccus* sp. from Taean, Korea	0.3	0.3	0.0	0.0	0.0	0.3	0.0			
9	*Matsucoccus macrocicatrices* (KF053072)	1.7	1.7	1.4	1.4	1.4	1.7	1.4	1.4		
10	*Icerya purchasi* (AY426078)	11.2	11.2	10.8	10.8	10.8	11.2	10.8	10.8	10.2	

Table 4. Genetic distances (%) of 28S sequences estimated by Neighbor-Joining with Kimura-2 parameter model.

No.		1	2	3	4	5	6	7	8	9	10
1	*Matsucoccus matsumurae* from Fukuoka, Japan										
2	*Matsucoccus* sp. from Buan, Korea	0.0									
3	*Matsucoccus* sp. from Goheung, Korea	0.0	0.0								
4	*Matsucoccus* sp. from Jeju, Korea	0.0	0.0	0.0							
5	*Matsucoccus* sp. from Pohang, Korea	0.0	0.0	0.0	0.0						
6	*Matsucoccus* sp. from Sacheon, Korea	0.0	0.0	0.0	0.0	0.0					
7	*Matsucoccus* sp. from Seoul, Korea	0.0	0.0	0.0	0.0	0.0	0.0				
8	*Matsucoccus* sp. from Taean, Korea	0.0	0.0	0.0	0.0	0.0	0.0	0.0			
9	*Matsucoccus macrocicatrices* (KF040573)	1.5	1.5	1.5	1.6	1.5	1.5	1.5	1.5		
10	*Icerya purchasi* (KT199077)	28.7	28.7	28.7	30.4	28.7	28.7	28.7	28.7	29.3	

4. Discussion

The original description of *Matsucoccus thunbergianae* has weak evidence to support it as a new species [11]. This new species was proposed based on the quantitative morphological features (especially in the adult males) and the number of generations per year, which might be considered as autapomorphic features that differentiated it from its congeners, such as *M. matsumurae* and *M. resinosae*. However, the characteristics of *M. thunbergianae* vary considerably according to environmental conditions (e.g., altitude, host plant, locality, and seasons), and all of the quantitative morphological traits have significant overlap among the three species. These points agree well with the opinions of Foldi [5] and Booth and Gullan [16], and are supported by the empirical tests of Boratynsky [24], Rieux [25], Ben-Dov [26], McClure et al. [27], and Miller and Park [11]. In this context, *M. thunbergianae* had been assigned an uncertain taxonomic status before it was synonymized with *M. matsumurae* [16]. As demonstrated by Booth & Gullan [16], the molecular and morphological features of the *Matsucoccus* species occurring on *Pinus thunbergii* and *P. densiflora* in Korea, which have been considered to be *M. thunbergianae*, are identical to those of *M. matsumurae* in this study.

The taxonomic validities of some species in the genus *Matsucoccus* have been controversial. Other congeners of *M. matsumurae*, such as *M. boratynskii* Bodenheimer & Neumark, *M. dahuriensis* Hu & Hu, *M. gallicolus* Morrison, *M. liaoningensis* Tang, *M. pini* (Green), and *M. yunnanensis* Ferris, have very similar morphology and differ in only a few characteristics [5,16]. Although we tentatively identified *Matsucoccus* species from Korea as *M. matsumurae*, further molecular and morphological studies with type specimens of those problematic species are needed, as the case research of Booth & Gullan [16] and this study both suggest that *M. matsumurae*, *M. thunbergianae*, and *M. resinosae* should be considered the same species.

The accurate identification of pest species is essential to establish an effective strategy of pest management. In this study supporting the results of Booth & Gullan [16], the *Matsucoccus* species occurring on *Pinus thunbergii* and *P. densiflora* in Korea should be recognized as *M. matsumurae* instead of *M. thunbergianae*. Until now, the control measures for species recognized as *M. thunbergianae* have been restrictively suggested in Korea; for example, chemical insecticides, such as fenitrothion 50EC and buprofezin 40SC [6], pheromone sticky traps [18], and yellow sticky traps [19]. On the other hand, biological control measures for *M. matsumurae*, such as entomopathogenic fungi, *Lecanicillium fungicola* strain HEB02, *L. lecanii* strain V3.4504 and V3.4505, *Fusarium incarnatum-equiseti* strain HEB01 [7,28], and natural enemies belonging to about 32 species [7], were proposed from China. In addition to this, studies were published on morphological changes in the antenna [29], and the wax glands and wax secretion [30] that might apply to the pest management of this species. Although Korean populations of *M. matsumurae* should be compared with the lineages from China using molecular tools, the results of this research will be useful to control the pests occurring on *P. thunbergii* in Korea.

In this study, *Matsucoccus matsumurae* occurring on *Pinus thunbergii* is reported for the first time from Jeju, Korea. We also observed the recent occurrence of *M. matsumurae on P. densiflora* from Seoul, although this area was recorded as one of the distributions of the species in Korea [31]. According to the results of Lim et al. [17], the occurrence of species under the name of *M. thunbergianae* was confirmed in all Southern coastal regions and some parts of Eastern and Western coastal regions, but it was not discovered in Chungcheongbuk-do, Daejeon, Jeju, or Seoul. In China, *M. matsumurae* also mainly damaged *P. densiflora*, which is widely distributed in Korea, along with *P. thunbergii*. Therefore, monitoring of this pest should be performed to investigate its exact occurrence and damage to *Pinus* species in the extensive regions that have previously been overlooked, especially in the Central and Northern inlands of Korea as well as Jeju.

The origin of Korean populations of *Matsucoccus matsumurae* is unclear, namely whether it is an indigenous species or an invasive species. Although there is no detailed information about the origin of host plants, *Pinus densiflora* and *P. thunbergii*, in the Korean Peninsula, both species are recognized as native *Pinus* species in Korea [32–34]. *P. thunbergii*, the main host plant of *M. matsumurae*, occurs mainly along Southern coastal areas of Korea [34]. According to Kim & Zsuffa [35], a number of

P. thunbergii (ca. 308,624 trees) had been planted for reforestation (ca. 105,863 ha) of South Korea in the period between 1953 and 1990. Based on this evidence, the current outbreak of *M. matsumurae* could not be explained only with "introduction and sudden spread of invasive populations." Moreover, the reproductive adult females of most scale insects, including *M. matsumurae*, have a sedentary lifestyle and very low dispersal ability (they are wingless) except for long-distance migration on the air currents as well as human-mediated transport [35,36]. To understand the possible circumstances concerning the outbreak of *M. matsumurae* in Korea, population genetic analyses using microsatellite markers or double digest restriction-site associated DNA sequencing (ddRAD-seq) are needed for various regional samples from China, Japan, and the USA, as well as Korea.

5. Conclusions

Based on the morphological and molecular evidence, our research corroborates the results of Booth & Gullan (2006) who synonymized *Matsucoccus thunbergianae* with *M. matsumurae*. These results imply the potential use of entomopathogenic fungi and natural enemies that were proposed from China to establish effective pest management in Korea. In addition, the occurrence of *M. matsumurae* is newly reported from Jeju, Korea in this study.

Author Contributions: J.C. and S.L. identified the pest based on morphological and molecular analyses and wrote the first draft of this paper; D.C. and D.-S.K. collected the materials used in this study and carried out the molecular experiments.

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