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# Unveiling host plant associations and cryptic genetic diversity of *Miyalachnus sorini* (Aphididae: Lachninae) on cherry trees in South Korea

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## Abstract

This study presents the first record of *Miyalachnus sorini* Kanturski & Lee, 2024 (Aphididae: Lachninae) in South Korea, thereby extending its known distribution beyond Japan and identifying a new host plant, *Prunus sargentii* (Rosaceae). We describe diagnostic morphological traits across multiple life stages and compare them with those of Japanese populations. Comparative analyses with Japanese populations demonstrated consistent morphological differentiation, notably elevated ratios of the ultimate rostral segment to antennal segments across multiple morphs in the Korean population, indicating potential ecological adaptation. DNA barcoding using the mitochondrial cytochrome c oxidase I gene revealed low intraspecific divergence (average 0.2%) and interspecific divergence (average 10.5%) between *Miyalachnus* sp. and *M. sorini*. Haplotype analysis was performed to investigate the relationship between host plants and cryptic genetic diversity. These findings enhance our understanding of the morphological and genetic diversity of *M. sorini* and underscore the importance of monitoring its spread for informed pest management strategies.

## Introduction

Cherry trees (*Prunus* spp.) play an important ecological, cultural, and economic role in South Korea, serving as ornamental street trees and contributing apiculture and biodiversity (Cho *et al.*, 2021; Lee *et al.*, 2015). Globally, more than 70 aphid species are known to feed on *Prunus*, among which the peach–potato aphid (*Myzus persicae*) is particularly notable for using *Prunus persica* as a primary host before migrating to over 40 secondary host families (Blackman and Eastop, 2025; Holman, 2009). This species is also recognised as a highly efficient vector of numerous plant viruses, including Potato leafroll virus (PLRV) (Pinheiro *et al.*, 2017). Margaritopoulos *et al.* (2000) reported that *M. persicae* populations exhibit host-associated morphological divergence, with tobacco-derived clones possessing longer ultimate rostral segments (URSs) and antennal processus terminalis than those from peach, suggesting genetically based adaptation to different host plants.

The genus *Miyalachnus*, a small East-Asian group within the tribe Miyalachnini (Hemiptera: Aphididae: Lachninae), is associated with *Prunus* species, feeding on young branches often sheltered under soil structures constructed by ants (Kanturski and Lee, 2024; Kanturski *et al.*, 2024). Morphologically, *Miyalachnus* is characterised by the presence of accessory rhinaria in all morphs – one small multiporous placoid sensillum on the processus terminalis of antennomere VI, with others laterally situated on the major rhinarium. Apterous viviparous females exhibit the highest number of tarsal sense pegs and distinct abdominal denticles, while alate viviparous females possess uniformly brown wings (Kanturski *et al.*, 2024). *Miyalachnus sorini*, the type species of this genus, was recently described in Japan, where it is associated with *Prunus* and follows a holocyclic life cycle (Kanturski *et al.*, 2024).

In this study, we report for the first time the occurrence of the tribe Miyalachnini in South Korea through the identification of *Miyalachnus sorini*. The objectives of our study are to (1) describe key diagnostic morphological traits of the fundatrix, apterous viviparous female, alate viviparous female, and ovipara, and compare morphological variation between South Korean and Japanese populations; (2) conduct molecular identification using

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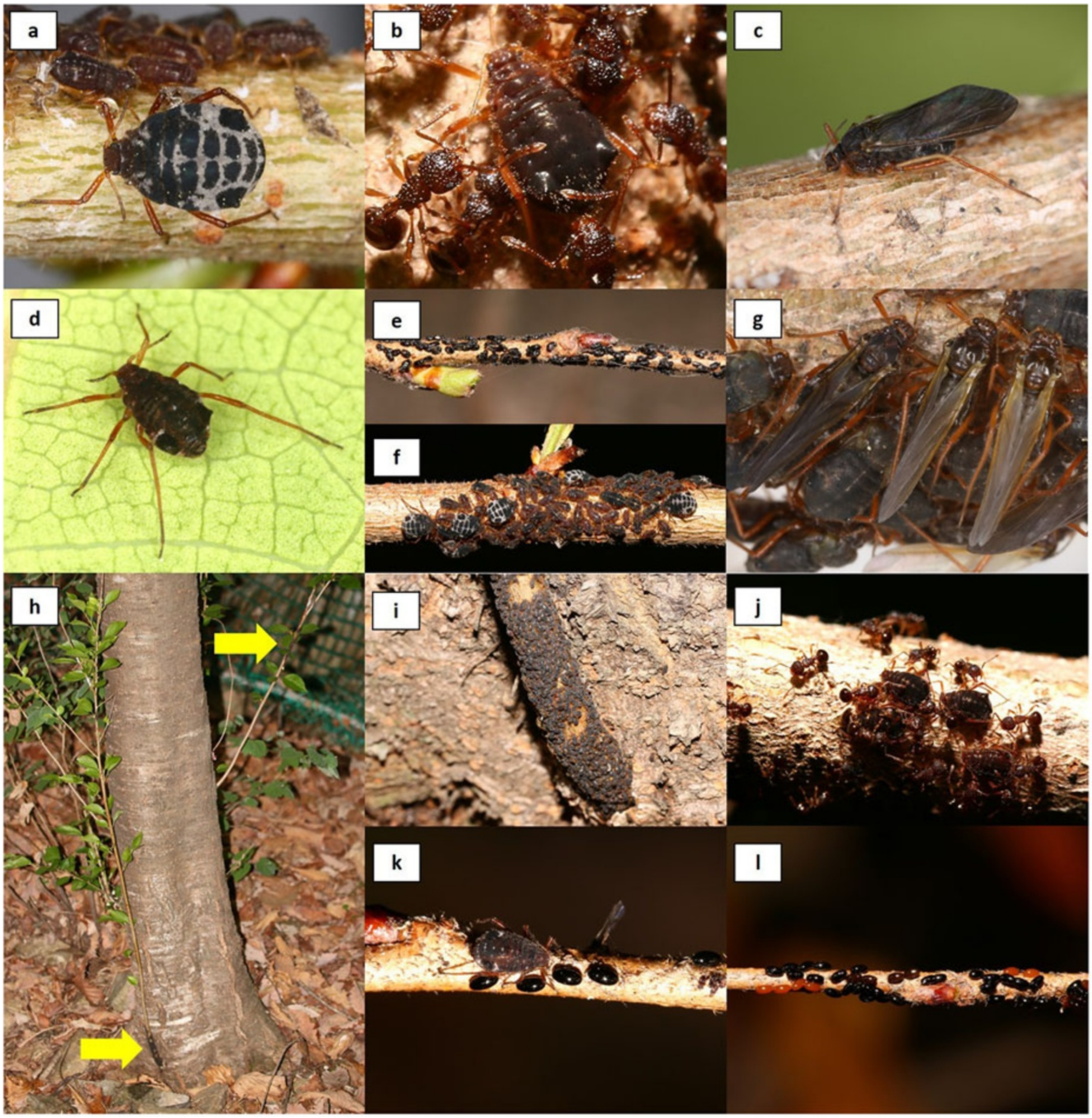

**Figure 1.** *Miyalachnus sorini* in life: (a) fundatrix; (b) apterous viviparous female; (c) alate viviparous female; (d) oviparous female; (e) eggs (spring) on a young branch; (f) colony of fundatrices on the bark of young branch of *Prunus sargentii*; (g) colony of alate viviparous female on the bark of young branch of *P. sargentii*; (h) colonies on the bark of young branches of *P. sargentii*; (i) large colony on the bark of young branch of *P. sargentii* (middle of May); (j) colony of apterous viviparous females on the bark of young branch of *Prunus sargentii*; (k) oviparae laying eggs; (l) reddish brown eggs turn black.

mitochondrial cytochrome c oxidase subunit I (COI) markers, with species-level identification based on phylogenetic analysis using the Neighbour-Joining (NJ) method; (3) explore cryptic genetic diversity and host association patterns through haplotype analysis; and (4) investigate the species' life cycle in South Korea to contribute to a better understanding of its ecological traits.

## Materials and methods

### *Morphological identification*

The aphid samples were preserved in 80% ethanol, and slide glass specimens were mounted in Canada balsam, following the Blackman and Eastop's (2025) method. Measurements and digital images were taken using Leica DMC 5400 (Leica Z16 APO) and Leica DM 4000B (Active Measure version 3.0.3; Mitani Co. Ltd., Japan) cameras. Abbreviations used for descriptions are as follows: ANT, antennae; ANT I, ANT II, ANT III, ANT IV, ANT V, BASE, and PT antennal segments I, II, III, IV, V, base of VI, and processus terminalis of antennomere VI, respectively; BL, body length; MaxW, greatest body width; HW, greatest head width across compound eyes; GP, genital plate; HT I, first segment of hind tarsus; HT Ib, basal length of HT I; HT Id, dorsal length of HT I; HT Iv, ventral length of HT I; HT II, second segment of hind tarsus; SIPH, siphunculi; URS (segment IV + V); FEMORA III, hind femora; TIBIAE III, hind tibiae. All specimens and slide vouchers were deposited in the College for Agriculture

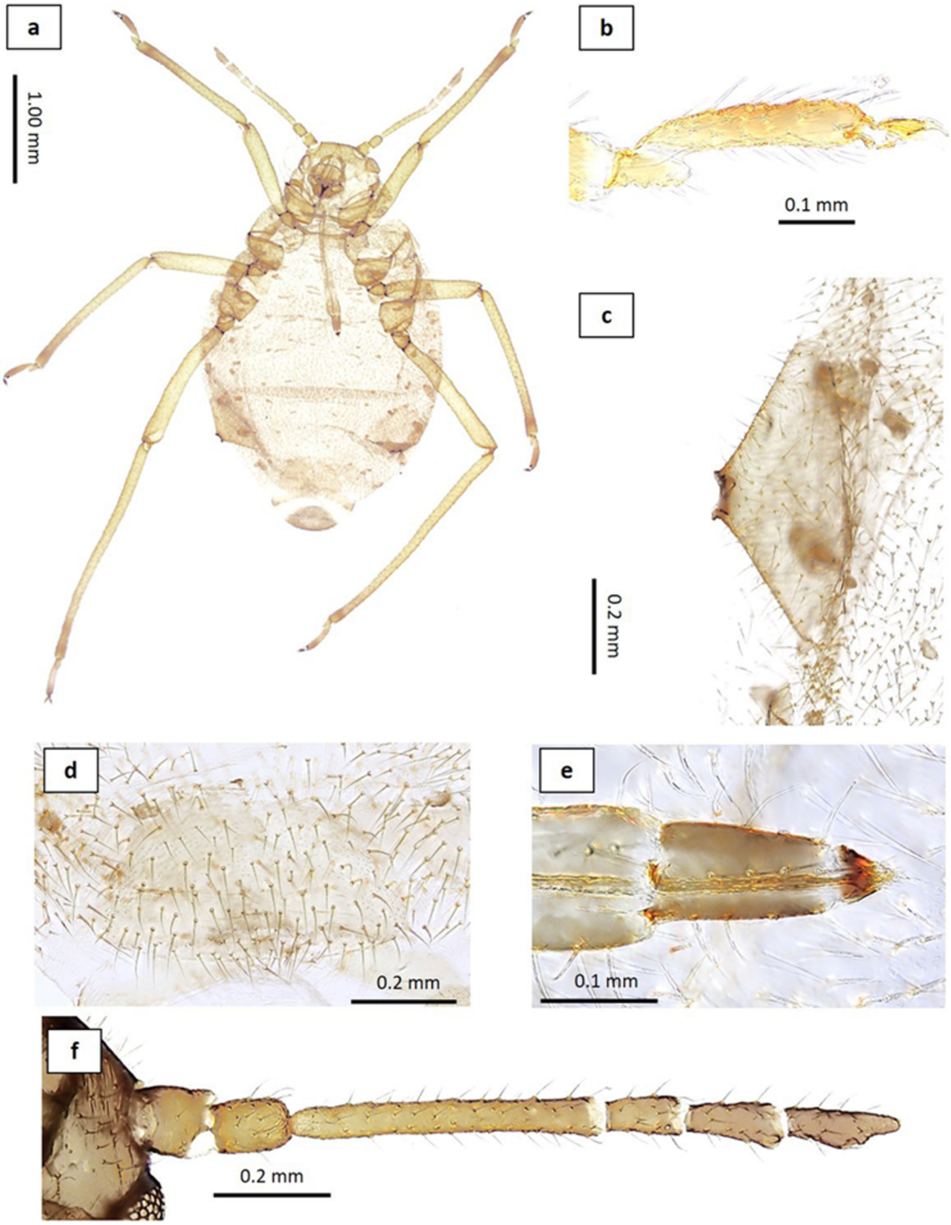

**Figure 2.** *Miyalachnus sorini*, fundatrix: (a) body, (b) HT II, (c) SIPH, (d) GP, (e) URS, (f) ANT.

and Life Sciences, Seoul National University Seoul, South Korea (SNU).

## Molecular protocol

Genomic DNA was extracted from individual samples collected from each colony using the DNeasy Blood & Tissue kit (Qiagen, Dusseldorf, Germany) following modified manufacturer protocols. A 658-bp fragment of the cytochrome oxidase I gene (COI) was amplified using the following primer sets: LepF 5′- ATTCAACCAATCATAAAGATATTGG-3′ and LepR 5′-TAAACTTCTGGATGTCCAAAAAATCA-3′. Polymerase chain reaction (PCR) was performed using AccuPower PCR Premix (Bioneer, Daejeon, Rep. of Korea) in 20 µl reaction volumes. The amplification protocol consisted of an initial denaturation at 94 °C for 3 min; followed by 35 cycles at 94 °C for 30 s, an annealing temperature of 45.2 °C for 30 s, extension at 72 °C for 1 min, and the final extension step at 72 °C for 5 min. PCR products were checked in 1.5% agarose gel, purified, and sequenced at Bionics, Inc. (Seoul, Republic of Korea).

## Molecular data analysis

A total of 10 COI sequences of two *Miyalachnus* species were analysed, including 6 sequences generated in this study and 4 sequences retrieved from GenBank. *Sinolachnus* sp. (GenBank accession number: MT375195) was used as the outgroup. The sequences were deposited in GenBank (accession numbers PV087376 to PV087381) and are detailed in Supplementary Table 1. Raw sequences were assembled and edited using SeqMan Pro v7.1.0 (DNASTAR, Inc., Madison, Wisconsin, USA). Sequence alignment and NJ tree analyses were performed using MEGA 7

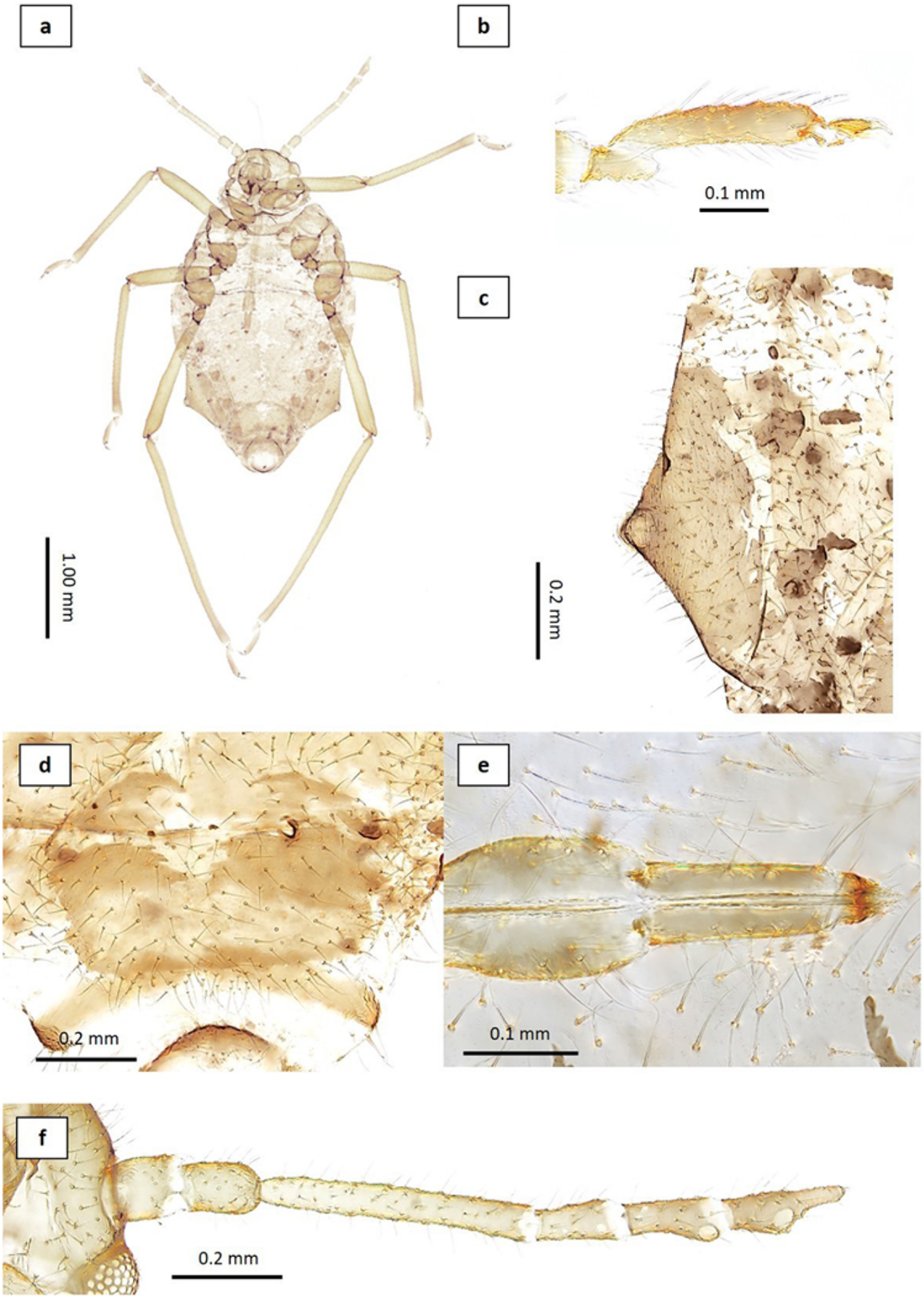

**Figure 3.** *Miyalachnus sorini*, apterous viviparous female: (a) body, (b) HT II, (c) SIPH, (d) GP, (e) URS, (f) ANT.

(Kumar *et al.*, 2016) under the Kimura-2-Parameter (K2P) model. Haplotype data were generated using DnaSP v6.12.03 (Rozas *et al.*, 2017) to identify unique haplotypes. A haplotype network was constructed to infer gene genealogies at the population level using the statistical parsimony approach in TCS v1.2.1 (Clement *et al.*, 2000).

## Results

### Systematic accounts

*Miyalachnus sorini* Kanturski & Lee, 2024.

*Miyalachnus sorini* Kanturski & Lee, 2024: 7, 14.

### Material examined

2, fundatrices, Jangan-gu, Suwon-si, Gyeonggi-do, South Korea, 5.iv.2022, #220405-LMH-1, on *Prunus sargentii* (Rosaceae), leg. M. Lee. (First collection); 5, fundatrices, ditto as first collection, 25.iv.2022, #220425-LMH-1, on *P. sargentii*, leg. M. Lee.; 2, fundatrices, ditto as first collection, 4.v.2022, #220504-LMH-1, on *P. sargentii*, leg. M. Lee.; 1, fundatrix, Jungnang-gu, Seoul, South Korea, 10.iv.2024, #240410-LMH-1, on *P. sargentii*, leg. M. Lee.; 4, apterous viviparous female, ditto as first collection, 3.vi.2022, #220603-LMH-1, on *P. sargentii*, leg. M. Lee.; 7, alate viviparous female, ditto as first collection, 4.v.2022, #220504-LMH-1, on *P. sargentii*, leg. M. Lee.; 4, oviparae, ditto as first

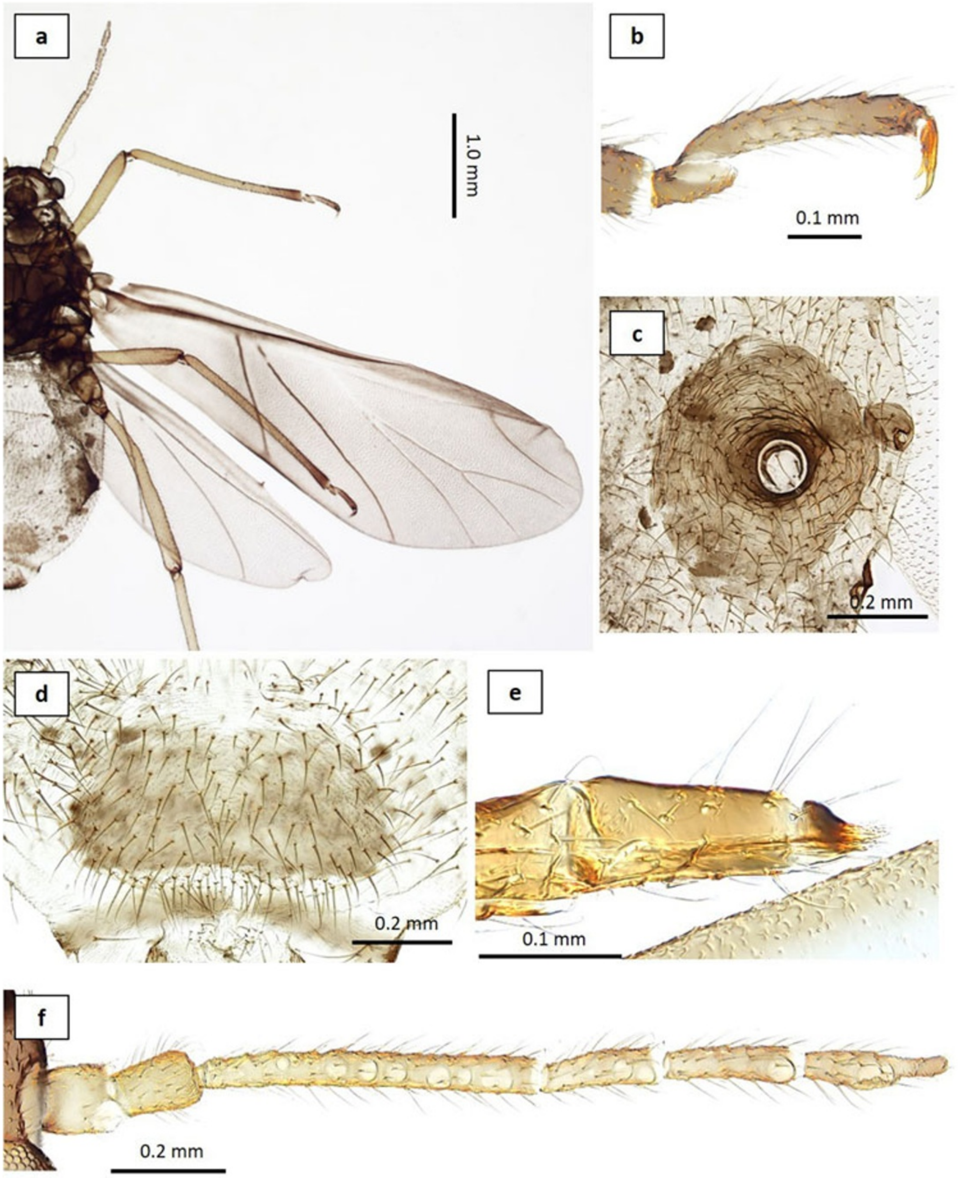

**Figure 4.** *Miyalachnus sorini*, alate viviparous female: (a) body, (b) HT II, (c) SIPH, (d) GP, (e) URS, (f) ANT.

collection, 31.x.2022, #221031-LMH-1, on *P. sargentii*, leg. M. Lee.

## Diagnosis

### *Fundatrix*

ABD II–VI, two small sclerotic plates on ABD VII, and a broken cross-bar on ABD VIII (fig. 2a); HT II 0.53–0.64 × ANT III and 1.31–1.64 × ANT VI. (fig. 2b); SIPH cones large, rounded, 7.30–10.15 × SIPH pore (fig. 2c); GP with 102–123 setae (fig. 2d); URS 0.35–0.41 × ANT III, 0.86–1.08 × ANT VI, and 0.61–0.71 × HT II, with 7–10 accessory setae (fig. 2e); ANT 0.32–0.37 × BL, PT 0.47–0.57 × BASE, ANT III with 0–2, ANT IV with 0–1 secondary rhinaria (fig. 2f).

**Remarks**: The Korean population of *Miyalachnus sorini* exhibits higher ratios of URS/ANT VI and URS/HT II compared to the Japanese population. Specifically, the ratios observed in the Japanese population are URS/ANT VI: 0.76–0.83 and URS/HT II: 0.58, as described by Kanturski and Lee (2024).

### *Apterous viviparous female*

Body strongly sclerotised, abdomen with sclerotised cross-bands (fig. 3a); HT II 0.56–0.66 × ANT III and 1.21–1.44 × ANT VI (fig. 3b); SIPH cones large, rounded, 10.36–12.23 × SIPH pore (fig. 3c); GP in the form of two separate sclerites with 152–174 setae (fig. 2d); URS 0.40–0.46 × ANT III, 0.85–1.05 × ANT VI, and 0.68–0.74 × HT II, with 9–10 accessory setae (fig. 2e); ANT 0.38–0.42 × BL, PT 0.73–0.92 × BASE, ANT III with 0–2, ANT IV with 1–3 secondary rhinaria (fig. 2f).

**Remarks**: The Korean population of *Miyalachnus sorini* exhibits higher ratios of URS/ANT VI and URS/HT II compared to the Japanese population. Specifically, the ratios observed in the

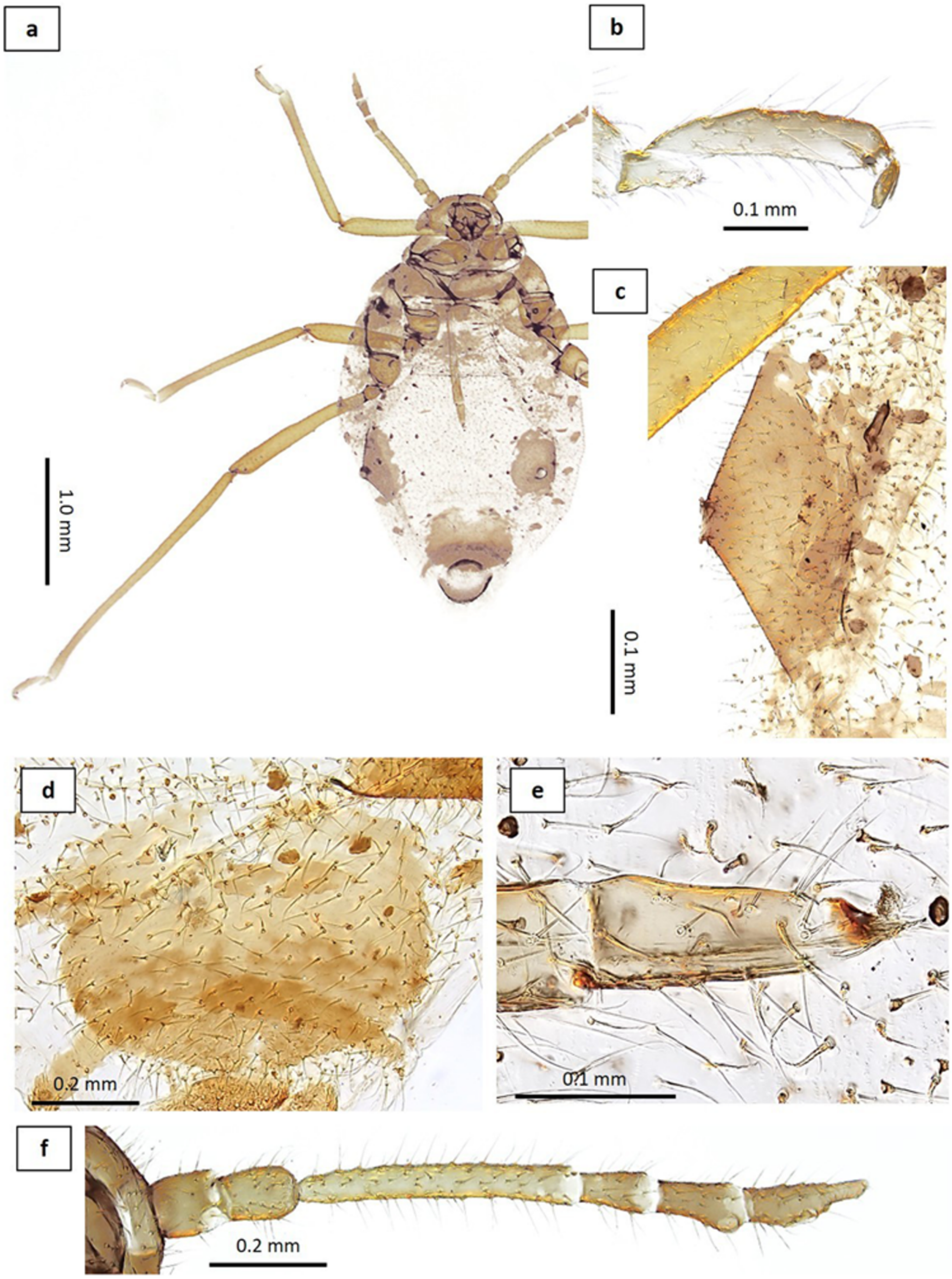

**Figure 5.** *Miyalachnus sorini*, oviparous female: (a) body, (b) HT II, (c) SIPH, (d) GP, (e) URS, (f) ANT.

Japanese population are URS/ANT VI: 0.69–0.78 and URS/HT II: 0.58–0.60, as described by Kanturski and Lee (2024).

### Alate viviparous female

The common node of M1 and M2 under the tip of the pterostigma (fig. 4a); HT II 0.51–0.69 × ANT III and 1.25–1.63 × ANT VI (fig. 4b); SIPH cones large, rounded, 6.26–8.16 × SIPH pore (fig. 4c); GP with 131–155 setae (fig. 4d); URS 0.33–0.39 × ANT III, 0.80–0.95 × ANT VI, and 0.56–0.66 × HT II, with 8–11 accessory setae (fig. 4e); ANT 0.35–0.48 × BL, PT 0.52–0.72 × BASE, ANT III with 8–12, ANT IV with 1–3 secondary rhinaria (fig. 4f).

**Remarks**: The Korean population of *Miyalachnus sorini* exhibits higher ratios of URS/ANT III and URS/ANT VI compared to the Japanese population. Specifically, the ratios observed in the Japanese population are URS/ANT III: 0.31–0.32 and URS/ANT VI: 0.69–0.78, as described by Kanturski and Lee (2024).

### Ovipara

ABDT I–VII with small sclerotic plates and a broken cross-bar on ABD VIII (fig. 5a); HT II 0.59–0.64 × ANT III and 1.23–1.37 × ANT VI (fig. 5b); SIPH cones large, rounded, 8.36–11.30 × SIPH pore (fig. 5c); GP with an indentation on the proximal end, with 185–198 setae (fig. 5d); URS 0.40–0.44 × ANT III, 0.81–0.93 × ANT VI, and 0.65–0.69 × HT

**Table 1.** Genetic divergences within all species included in this study

| **(1) Different taxonomic levels** | | | | |
|---|---|---|---|---|
| Taxonomic level (no. of comparison pairs) | | K2P pairwise distances | | |
| | | Maximum | Minimum | Mean |
| Within species (48) | | 0.4 | 0.0 | 0.2 |
| Between species (30) | | 10.6 | 10.4 | 10.5 |
| **(2) Intraspecific genetic divergence** | | | | |
| Species | Comparison pairs (CP) | Intraspecific genetic divergence | | |
| | | Maximum | Minimum | Mean |
| *Miyalachnus sorini* | 45 | 0.4 | 0.0 | 0.2 |
| *Miyalachnus* sp. | 3 | 0.0 | 0.0 | 0.0 |
| **(3) Interspecific genetic divergence** | | | | |
| **Species** | *Miyalachnus sorini* | | | |
| *Miyalachnus* sp. | CP = 30, 10.5 (10.4–10.6) | | | |

II, with 9–14 accessory setae (fig. 5e); ANT 0.36–0.39 × BL, PT 0.66–0.80 × BASE, ANT IV 0–2, and ANT V 0–1 secondary rhinaria (fig. 5f).

**Remarks**: The Korean population of *Miyalachnus sorini* exhibits higher ratios of URS/ANT VI compared to the Japanese population. Specifically, the ratios observed in the Japanese population are URS/ANT VI: 0.72–0.79, as described by Kanturski and Lee (2024).

## *Genetic divergence*

Genetic divergences (GDs) among all species included in this study are presented in table 1. A total of 48 comparison pairs of two *Miyalachnus* species were calculated within the species. The average intraspecific GD for *Miyalachnus sorini* was 0.2%, with a maximum intraspecific GD of 0.4%. Interspecific GDs were calculated using 30 pairwise comparisons. The minimum interspecific GD was 10.4%, observed between *Miyalachnus sorini* and *Miyalachnus* sp., while the maximum interspecific GD was also 10.6% (average: 10.5%) between the same species pair.

## *NJ tree analysis*

Species identification was conducted using phylogenetic analysis with NJ tree construction, a heuristic approach based on genetic distance. The analysis revealed that *Miyalachnus sorini* and *Miyalachnus* sp. grouped into two distinct clades, designated as clade A and clade B, respectively (fig. 6a). In clade A, South Korean *M. sorini* populations were the first to branch out, followed by the Japanese populations. All diverse populations were formed a single cohesive subclade within clade A, supported by high bootstrap values (BS = 100%).

## *Haplotype analysis*

The TCS network analysis identified five haplotypes from the 14 COI sequences analysed (fig. 6b). Details of haplotype distribution across all individuals are provided in Supplementary Table 2. Among the 13 sequences of *Miyalachnus sorini* and *Miyalachnus* sp., three distinct haplotypes (Hap_1–Hap_4) were detected. Hap_1–Hap_3, representing 10 sequences, were associated with *Miyalachnus sorini*. Hap_1 was observed in populations on *Prunus buergeriana* and *P. serrulata* var lannesiana from Japan. Hap_2 was identified exclusively in populations on *Prunus buergeriana* and *Prunus serrulata* var spontanea from Japan. Hap_3 was observed in populations on *Prunus sargentii* from South Korea. In contrast, Hap_4, representing one sequence, was attributed to *Miyalachnus* sp.

## *Biology*

The life cycle of *Miyalachnus sorini* was investigated through direct observations and analysis of slide-mounted specimens. Fundatrices were first observed in the adult stage on April 5th, producing both apterous and alate nymphs. Colonies were primarily established on young branches. By early May, workers of *Lasius* sp. (Formicidae) were observed attending with the colonies, and by the end of May, some colonies were found within ant-constructed shelters. Adult apterous and alate viviparous females appeared by May 4th. By early June, alate viviparous females had dispersed and were no longer observed. A small number of apterous viviparous females relocated to twigs over 1 m in height, forming colonies until early July. However, no colonies were found on these twigs after mid-July. The sexual generation is presumed to begin from late September to early October. Observations in mid-October revealed that males and oviparae had already mated, and oviparae were beginning to lay eggs on young branches. Eggs were predominantly laid on branches located approximately 1 m above ground level. By mid-November, oviparae were no longer observed.

## *Damage*

In South Korea, *Miyalachnus sorini* was recorded on three *Prunus sargentii* trees across two locations, with two trees in Seoul and one tree in Suwon. This species formed colonies in spring on small branches emerging near the base of the trunk. Each tree had 2–3 such branches, and aphid colonies were observed on all of them (fig. 1h). As late spring approached, the colonies gradually expanded in size, and aphids were also found on thicker branches (with a diameter exceeding 2 cm) located approximately 1 m above

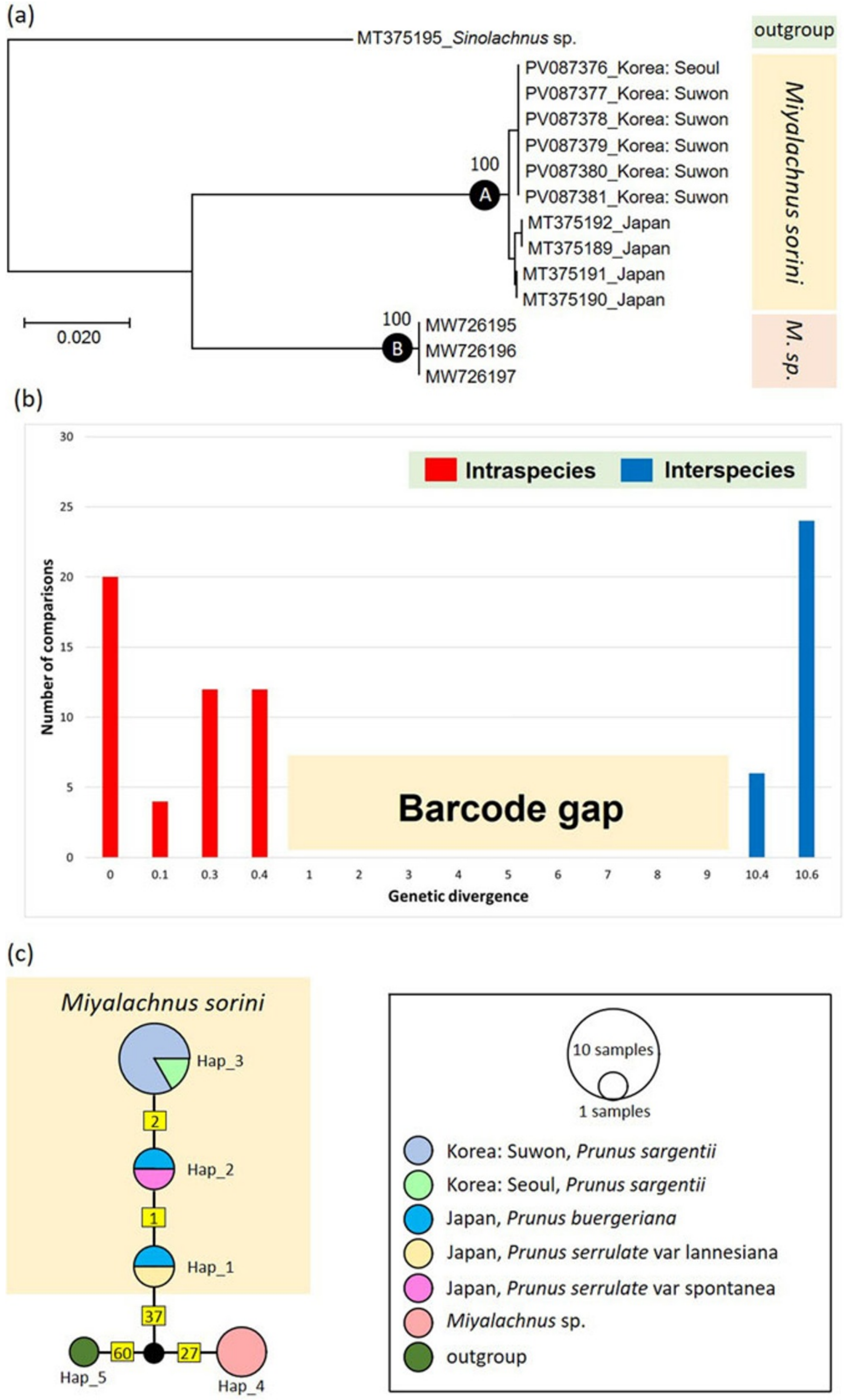

**Figure 6.** Molecular data analysis of *Miyalachnus* species of the 14 COI sequences: (a) Neighbour-joining tree analysis. Species name and distribution information for each individual. (b) Genetic divergence based on the Kimura-2 parameter model for COI sequences according to taxonomic levels. (c) TCS networks of four haplotypes. The pie size is proportional to the haplotype frequency. The number in the box indicates the number of mutations.

the ground. Colony size peaked in early May but declined by mid-July. In October, colonies increased in size again, preparing for winter. In larger colonies, more than 100 individuals, including both adults and nymphs, were observed (fig. 1i). A significant symptom of infestation is the accumulation of black sooty mold on twigs and leaves, caused by the large quantities of honeydew excreted by the aphids.

## Discussion

This study provides the first report of *Miyalachnus sorini* in South Korea, thereby extending its known geographic distribution beyond Japan and establishing a new host association with *Prunus sargentii*. The discovery is significant in that it not only broadens the ecological range of the species but also provides insight into potential host-driven morphological and ecological adaptations. One of the most notable morphological distinctions in the Korean population was the increased ratio of the URS to antennal segment length, compared to Japanese specimens. This trait likely represents a host-specific adaptation to *P. sargentii*, which may differ in phloem accessibility or tissue structure relative to previously recorded hosts (Kanturski *et al.*, 2024).

Morphological characteristics across life stages remained broadly consistent with generic features of *Miyalachnus*, thus validating species-level identification. However, the observed variation – particularly in mouthpart proportions – suggests local adaptation potentially driven by host plant properties such as bark thickness, vascular anatomy, or secondary metabolite profiles. This interpretation is supported by similar host-related morphological divergence in other aphid species, notably *Myzus persicae*, where differences in URS and antennal structure were genetically based and associated with ecological specialisation (Margaritopoulos *et al.*, 2000).

Ecologically, *M. sorini* was observed forming dense colonies on basal branches near the ground, a behaviour that appears to facilitate attendance and protection by mutualistic *Lasius* spp. ants. The construction of ant shelters around colonies and the temporal correlation between colony growth and ant activity strongly suggest a mutualistic relationship, enhancing colony stability and persistence. Similar associations have been well documented in other Lachninae species (Depa *et al.*, 2015, 2017; Lee *et al.*, 2022, 2025; Takada, 2009). The presence of a holocyclic life cycle – including both parthenogenetic and sexual morphs – indicates reproductive plasticity, allowing overwintering and enhancing population resilience in temperate environments such as those found in South Korea.

Molecular analyses confirmed the identity of *M. sorini* and revealed low intraspecific GD (0.2%), consistent with previous barcoding studies in aphids (Foottit *et al.*, 2008). In contrast, the interspecific divergence between *M. sorini* and an unidentified *Miyalachnus* species (10.5%) supports their separation as distinct taxa. TCS network analysis further revealed that the Korean population possesses a unique haplotype (Hap_3), distinct from Japanese populations. This may reflect either recent colonisation events or local host-driven differentiation. The limited genetic variation among Korean samples suggests gene flow among populations or a recent founder event, potentially mediated by the high dispersal capacity of alate morphs and the broad distribution of *P. sargentii* in urban landscapes. While *M. sorini* does not appear to cause significant direct damage through feeding, the production of honeydew supports the development of black sooty mold, which can compromise both the aesthetic value and physiological health of ornamental trees. As *Prunus* species are widely planted in South Korea's urban green spaces, the establishment of *M. sorini* may pose a growing concern, especially under changing climate and land use conditions.

In conclusion, this study highlights the ecological plasticity, host-associated adaptations, and mutualistic interactions that may contribute to the establishment success of *M. sorini* in new environments. Continued monitoring is warranted, especially in urban ecosystems where ornamental *Prunus* species are abundant. Future work should investigate the long-term population dynamics, ant–aphid interactions, and the potential vectoring capacity of *M. sorini* for plant pathogens. These insights will be critical for developing early detection and integrated management strategies to mitigate the potential impact of this emerging aphid species.

**Supplementary material.** The supplementary material for this article can be found at https://doi.org/10.1017/S0007485325100400.

**Author contributions.** ML, MK, and SL designed the study. ML collected all the materials and wrote the manuscript. MK wrote the manuscript. SL supervised the whole process. All four authors revised the manuscript and confirmed the final version.

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**Competing interests.** The authors declare that they have no conflict of interest.

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