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Identification of a potential pathway of the exotic black weevil (Coleoptera: Curculionidae) in South Korea

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Abstract. The black weevil, *Aclees taiwanensis* Kôno (Coleoptera: Curculionidae), is one of the primary pests of fig trees in southeastern Asia and southern Europe. Thought to be of subtropical and tropical Asian origin, including China, the weevil was first found in southern areas of South Korea in July 2020. Subsequently, it was found in the following five cities: Haenam, Hampyeong, Jindo, Sinan, and Tongyeong (RDA 2020). Attempts to trace a possible pathway for the exotic black weevil suggested that this species probably followed pathways of illegal importation of infested plants from Taiwan and was unintentionally introduced into South Korea based on analysis of a Pest Information System (PIS) database, a phylogenetic analysis of mitochondrial cytochrome c oxidase subunit I gene (COI) sequences data, and interviews with fig growers. In addition, this exotic weevil could expand to other regions of South Korea since proper control methods for this weevil pest have not yet been developed and some fig trees are cultivated using eco-friendly farming practices. Therefore, constant monitoring will be required for the invasive alien weevil species which seriously damages the trunk of fig trees.

Key words. *Aclees taiwanensis* Kôno, invasive species, trace, illegal importation, plant pest

ZooBank registration. urn:lsid:zoobank.org:pub:9D72525F-608D-4028-A24D-9F3F866257F9

Introduction

Globalization has brought about a marked increase in international trade and travel and along with climate warming, an ever-increasing possibility of the spread and establishment of alien invasive species from tropical to temperate areas, and their repercussions (Perrings et al. 2005; Diagne et al. 2020). These biological invasions have a massive impact and cause huge economic losses worldwide. When it comes to the costs caused by invasive insects, it has been estimated at a minimum of US \$76.0 billion per year globally (Diagne et al. 2020). The South Korean weather is also becoming warmer and numerous imported subtropical and tropical plants into the country are being grown in greenhouses or open-fields. These reasons may be the cause of why South Korea has many exotic plant insect pests (Park 2010; PIS 2021). Quarantine of pests found on imported plant material is one of the nation's critical missions that safeguards natural and agricultural environments from the introduction of exotic injurious pests. One of the major focuses of the Animal and Plant Quarantine Agency (APQA) is to conduct the national surveillance program for pests of economic importance such as fruit flies, scale insects and weevils, and to detect and identify exotic pests early enough to prevent their establishment in the country and potential spread to other areas of the country. Knowledge of possible pathways associated with intercepted pests can be used to design science-based regulations to prevent future establishment of exotic pests (Park 2010; Halbert et al. 2020).

Many weevils (Coleoptera: Curculionoidea) are considered pests because of their ability to damage and kill crops in South Korea. Approximately 605 species of weevils have been recorded from South Korea (Lee 2019);

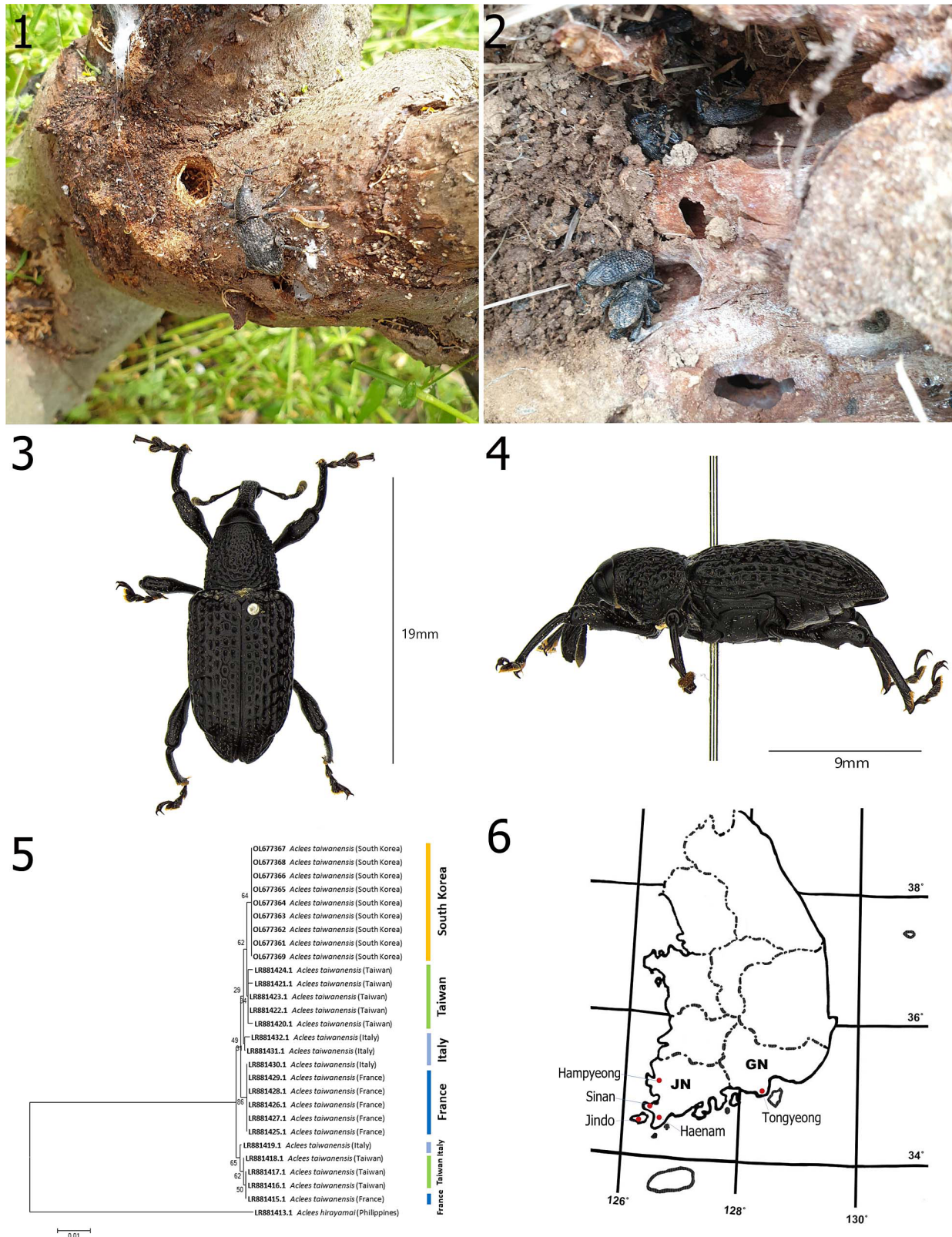
currently, the weevils in South Korea are comprised of 12 families, with most of them (72.4%) placed in the family Curculionidae. Some of these such as *Lissorhoptrus oryzophilus* Kuschel (Eriirhinidae), *Listroderes costirostris* Schoenherr and *Hypera postica* (Gyllenhal) (Curculionidae) were introduced to South Korea over the last half century or so (Park 2010). The black weevil, *Aclees taiwanensis* Kôno (Curculionidae), which is thought to be of subtropical and tropical Asian origin, including China, has recently been detected in South Korea (Hong et al. 2020). The black weevil is a pest of fig trees, *Ficus carica* L. (Moraceae) (Ciampolini et al. 2005). The black weevil has also been introduced to Italy and France where it is associated with severe damage to fig trees (Hong et al. 2020). The larvae of *A. taiwanensis* damage the fig trees, digging alimentation galleries in the trunk and surface roots compromising the phloem flux and causing plant death (Farina et al. 2021). Damage caused by the adults are of minor consequence and concern unripe fruits, leaves and buds of young plants (Hong et al. 2020; Farina et al. 2021). The black weevil was first discovered on *F. carica* in the southern area (Haenam) of South Korea in July 2020 and is considered to have been already established locally in the exterior environment (Hong et al. 2020; RDA 2020). The only observed host plant in South Korea is *F. carica* (Fig. 1–2). So far, *A. taiwanensis* in South Korea appears to be restricted to the southern region of the country where fig trees are grown—Haenam, Hamae, Jeonpyeong, Jindo, Sinan of Jeollanamdo (JN) and Tongyeong of Gyeongsangnamdo (GN) (RDA 2020). The original source of the population of this exotic black weevil which was discovered in the southern areas of South Korea in 2020 is unknown. Here we provide its potential pathway based on a Pest Information System (PIS) database, a phylogenetic analysis of mitochondrial cytochrome c oxidase subunit I gene (COI) sequences data, and interviews with fig growers where the black weevil was detected.

Materials and Methods

To understand the importance of the international trade of host plants associated with the black weevil as a pathway, data on imported plant materials and interception records were collected from the Pest Information System (PIS) database developed by the Animal Plant Quarantine Agency (2021). A total of 3098 consignments of *Ficus benjamina* L., *F. carica* L. and *F. elastica* Roxb. (Moraceae), known host plants of *A. taiwanensis*, were recorded from neighboring countries, China (3082) and Taiwan (16) over the past 11 years (2010–2020).

In 2021, we collected adult specimens for molecular analysis in Haenam and Sinan (JN) where the black weevil has occurred (Fig. 3–4). First, they were identified morphologically to species using keys and diagnoses in available literature (Hong et al. 2020; Merregalli et al. 2020). Photographs were taken using a Leica M165C microscope with a Dhyana 400DC-Tucsen camera. Then, *A. taiwanensis* specimens were DNA extracted using the NucleoSpin® DNA Insect Kit. PCRs were conducted using the standard COI barcoding primers LepF1/LepR1 (Hebert et al. 2004). PCR thermocycling was done under the following conditions: 5 min at 94°C; 35 cycles of 30 sec at 94°C, 30 sec at 54°C, 45 sec at 72°C; 1 min at 72°C; held at 4°C. Amplified PCR products were sequenced at Macrogen. Newly generated sequences (GenBank accessions: OL677361–OL677369) were aligned using MEGA6 (Tamura et al. 2013). The barcode sequences generated in the present study were compared with sequences submitted by other researchers in GenBank and BOLD databases using BLASTn (Altschul et al. 1990; Ratnasingham and Hebert 2007).

The COI gene sequences of black weevils from three countries and different sites were previously amplified and uploaded into GenBank. We downloaded the 18 COI gene sequences from GenBank (LB881415–LB881432) for inferring a phylogenetic tree. The phylogenetic tree was constructed using the neighbor-joining (NJ) phylogenetic approach in MEGA6, using the COI sequence from *Aclees hirayamai* Kôno (LR881413) serving as an outer group (Saitou and Nei 1987; Tamura et al. 2013) (Fig. 5). The optimal tree with the sum of branch length = 0.148 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches (Felsenstein 1985). The tree is drawn to scale, with branch lengths in the same units as those of the pairwise genetic distances used to infer the phylogenetic tree. The pairwise genetic distances were computed using the p-distance method (Nei and Kumar 2000), and are in the units of the number of base differences per site. The analysis involved 28 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair. There were a total of 657 positions in the final dataset.



Figures 1–6. Black weevil (*Aclees taiwanensis* Kôno), NJ tree and regional map of South Korea. 1–2) Adult weevil on a fig tree. 3) Adult, dorsal view (JN: 1042 Aphae-ro, Aphae-eup, Sinan-gun, 14-vii-2021). 4) Adult, lateral view (same data). 5) A phylogenetic tree for all black weevil COI genes. 6) Distribution map of black weevil in South Korea.

Results and Discussion

The first detection of *A. taiwanensis* in South Korea was from Haenam (JN) located in the southern region of the country where populations of the weevil were noted in July 2020 on fig (*F. carica*) farms. It was additionally found in five cities, Haenam, Hampyeong, Jindo, Sinan (JN) and Tongyeong (GN) based on an occurrence survey conducted by RDA in 2020 (Fig. 6).

There are many different types of pathways through which this *Aclees* weevil of subtropical and tropical Asian origin, may move from one place to another such as in the case of plants infested with larvae brought in by travelers from overseas, moving infested plants globally by aircraft or mail. According to the PIS database (2021), the black weevil was not intercepted at South Korean ports of entry on its imported host plants between 2010 and 2020. This weevil is not a regulated pest in South Korea, however, shipments of plants or parts of plants that can serve as a host for *Aclees taiwanensis* have been regulated strictly. Although strict inspections and regulations were put in place in the 2010s, illegal importation of young seedlings of its host plants from China, Taiwan, Indonesia and Myanmar were found in hand luggage and international mail (16 cases from 2010 to 2020) and were destroyed accordingly (PIS 2021). These interceptions indicate that the weevil was probably unintentionally introduced into South Korea by the illegal importation of infested young trees and subsequently spread to other areas of the country. In addition, a neighbor-joining (NJ) phylogenetic tree using the COI sequences was constructed for geographic populations of black weevils including South Korea to infer the probable origin of invasive alien species. Evidently, all populations of South Korea were clustered into a single group. The tree suggested that all black weevils found in South Korea showed a higher genetic affinity with Taiwanese black weevils (Fig. 5). These results indicate movement of *Ficus* plants could be a pathway of introduction for the black weevil. This pathway is the likely source of South Korea's established population of *A. taiwanensis*. Also, such information could be useful in import inspecting of its host plants.

According to interviews of growers and extension specialists engaged in the surveillance of plant pests where the black weevil has occurred, the damage by this weevil has been observed for at least two to three years. The black weevil appears to have been introduced into South Korea at least three years ago and successfully established due to the suitable climatic conditions, available host plants and high adaptability to a new habitat. In addition, this exotic weevil could result in an expansion into other regions of South Korea since proper control methods for this weevil pest are not yet developed and some fig trees are cultivated using eco-friendly farming practices. Therefore, constant monitoring will be required for this invasive alien weevil species that seriously damages the trunks of fig trees to enable the timely application of management practices to minimize potential losses of *Ficus* plants and to prevent the spread to other areas of the country.

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Literature Cited

- Altschul SE, Gish W, Miller W, Myers EW, Lipman DJ. 1990. Basic local alignment search tool. *Journal of Molecular Biology* 215: 403–410.
- Ciampolini M, Regalin R, Perrin H. 2005. *Aclees cribratus*, nuovo per l'Italia, nocivo al fico allevato in vivaio. *L'Informatore Agrario* 47: 69–71.
- Diagne C, Leroy B, Gozlan RE, Vaissière AC, Assailly C, Nuninger L, Roiz D, Jourdain F, Jarić I, Courchamp F. 2020. InvaCost, a public database of the economic costs of biological invasions worldwide. *Scientific Data* 7: 277.

- Farina P, Mazza G, Benvenuti C, Cutino I, Giannotti P, Conti B, Bedini S, Gargani E. 2021.** Biological notes and distribution in southern Europe of *Aclees taiwanensis* Kôno, 1933 (Coleoptera: Curculionidae): A new pest of the fig tree. *Insecta Mundi* 12(1): 5.
- Felsenstein J. 1985.** Confidence limits on phylogenies: An approach using the bootstrap. *Evolution* 39: 783–791.
- Halbert SE, Moore MR, Bartlett CR, Allen JS. 2020.** Identification of planthoppers (Hemiptera: Delphacidae) intercepted on aquarium plants in Florida and elucidation of a potential pathway for exotic aquatic and semiaquatic pests. *Insecta Mundi* 0775: 1–6.
- Hebert PDN, Penton EH, Burns JM, Janzen DH, Hallwachs W. 2004.** Ten species in one: DNA barcoding reveals cryptic species in the neotropical skipper butterfly *Astrapes fulgerator*. *Proceedings of the National Academy of Sciences USA* 101: 14812–14817.
- Hong KJ, Park DK, Lee SM. 2020.** First report of the exotic fig weevil, *Aclees taiwanensis* Kôno (Coleoptera: Curculionidae) in Korea. *Korean Journal of Applied Entomology* 59(4): 277–280.
- Lee SH. 2019.** National species list of Korea, III. Insects (Hexapoda). Designzip; Seoul. 988 p.
- Meregalli M, Boriani M, Bollino M, Hsu CF. 2020.** Review of the species of *Aclees* described by Kôno (Coleoptera: Curculionidae: Molytinae). *Zootaxa* 4768: 146–150.
- Nei M, Kumar S. 2000.** Molecular evolution and phylogenetics. Oxford University Press; New York. 348 p.
- Park JS. 2010.** Compendium of exotic plant pests and weeds. National Plant Quarantine Service; Anyang, South Korea. 292 p.
- Perrings C, Dehnen-Schmutz K, Touza J, Williamson M. 2005.** How to manage biological invasions under globalization. *Trends in Ecology and Evolution* 20(5): 212–215.
- PIS (Pest Information System). 2021.** Pest Information System (internal database Plant Quarantine Technology Center/APQA, South Korea). Available at <https://10.110.128.100> (Last accessed December 2021.)
- Ratnasingham S, Hebert PDN. 2007.** BOLD: the Barcode of Life Data System (<http://www.barcodinglife.org>). *Molecular Ecology Notes* 7: 355–364.
- RDA (Rural Development Administration). 2020.** Report on occurrence survey of the black weevil in southern regions of South Korea. RDA/Extension Service Bureau Disaster Management Division; South Korea. 8 p.
- Saitou N, Nei M. 1987.** The neighbor-joining method: A new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution* 4: 406–425.
- Tamura K, Stecher G, Peterson D, Filipowski A, Kumar S. 2013.** MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. *Molecular Biology and Evolution* 30: 2725–2729.

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