

RESEARCH NOTE

Rust Disease on *Erythronium japonicum* Caused by *Uromyces erythronii* in South Korea

Jae Sung Lee¹, Yoo-Kyeong Lee², Bora Kim³, Seong-Jin Lee⁴, Young-Joon Choi^{2,*}, and Hyeon-Dong Shin⁵

¹Department of Agricultural Biology, National Institute of Agricultural Sciences, Rural Development Administration, Wanju 55365, Korea

²Department of Biological Science, Kunsan National University, Gunsan 54150, Korea

³Climate Change and Carbon Research Team, National Institute of Ecology, Seoecheon 33657, Korea

⁴Department of Plant Quarantine, Animal and Plant Quarantine Agency, Gimcheon 39660, Korea

⁵Division of Environmental Science and Ecological Engineering, Korea University, Seoul 02842, Korea

*Corresponding author: yjchoi@kunsan.ac.kr

ABSTRACT

In April 2022 and 2023, severe rust symptoms were observed on *Erythronium japonicum* in Pocheon, Wanju, and Jinan, Korea, with a disease incidence of up to 80%. The symptoms include yellow-to-brown, vein-limited lesions on the leaves, accompanied by orange spermogonia, aecia, and black telia. Morphological characteristics of the rust fungus were consistent with those of *Uromyces erythronii*. Molecular analyses of the internal transcribed spacer and large subunit rDNA regions confirmed this identification, with Korean samples clustering with reference sequences of *U. erythronii*. Pathogenicity tests reproduced typical rust symptoms on inoculated plants, thus fulfilling Koch's postulates. This is the first report of *U. erythronii* causing rust disease on *E. japonicum* in South Korea.

Keywords: Asian fawn lily, Liliaceae, Phylogenetic analysis

OPEN ACCESS

pISSN : 0253-651X
eISSN : 2383-5249

Kor. J. Mycol. 2026 September, 54(3):231–236
<https://doi.org/10.4489/kjm.2026.54.3.2>

Received: June 01, 2026

Revised: July 31, 2026

Accepted: August 18, 2026

© 2026 THE KOREAN SOCIETY OF MYCOLOGY.



This is an Open Access article distributed under the terms of the Creative Commons Attribution Non-Commercial License (<http://creativecommons.org/licenses/by-nc/4.0/>) which permits unrestricted non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Erythronium japonicum Decne., the Asian fawn lily, is a spring-flowering Liliaceae species native to northeastern China, Japan, Korea, and the Russian Far East [1]. This plant is widely cultivated as a popular ornamental plant in Korea owing to its large and attractive flowers. In addition, *E. japonicum* has been traditionally used as a medicinal plant in Korea, and several studies have investigated its phytochemical constituents [2,3].

In April of 2022 and 2023, *E. japonicum* plants at Pocheon (37°45'24"N, 127°09'46"E), Wanju (35°58'24"N, 127°18'12"E), and Jinan (35°45'44"N, 127°24'17"E), Korea, exhibited rust symptoms, with disease incidence reaching up to 80%. Symptoms appeared as yellow to brown, vein-limited spots (Fig. 1A and 1B) on the upper leaf surfaces, with orange-colored spermogonia, aecia (Fig. 1C), and black telia forming mainly on the corresponding lower surfaces (Fig. 1J and 1K) but occasionally on the upper surfaces and petioles. Five representative samples were deposited in the Kunsan National University Herbarium (KSNUH1816, 1817) and Korea University Herbarium (KUS-F32715, F33601, and F33614).

For morphological characterization, the infected leaf tissues were examined using a stereomicroscope (M205C, Leica, Wetzlar, Germany) and a differential interference contrast light microscope (Axio Imager 2, Carl Zeiss, Oberkochen, Germany). The fine surface structures were further investigated using a scanning electron microscope (S-4800 with EDS, Hitachi, Tokyo, Japan). Spermogonia were amphigenous on the leaf blades and petioles, scattered, round, pale yellow, conical-shaped, and present among the aecia (Fig. 1D). Aecia were amphigenous or cauligenous, densely grouped, light yellow to orange, cup-shaped with peridia, and measured 350–520 μm (av. 440 μm) in diameter (Fig. 1E and 1F). Aeciospores were globose to subglobose, polygonal, pale yellow, and measured $20\text{--}26 \times 18\text{--}23$ μm (av. 23.2×20.9 μm) (Fig. 1G and 1H), with a verrucose and hyaline wall (Fig. 1I). No uredinia were observed. Telia were amphigenous, elongated, and measured 390–760 μm (av. 480 μm) in diameter (Fig. 1L). Teliospores were one-celled, ovoid, dark brown, measured $25\text{--}37 \times 20\text{--}25$ μm (av. 30.3×23.0 μm), with a short pedicel (Fig. 1M). The teliospore walls had long ridges that ran lengthwise (Fig. 1N). These morphological characteristics corresponded well with those of *Uromyces erythronii* (DC.) Pass. [4].

To further verify the morphological identification, genomic DNA was extracted from aeciospores and teliospores collected from naturally infected leaves using the MagListo 5M Plant Genomic DNA Extraction Kit (Bioneer, Daejeon, Korea). The internal transcribed spacer (ITS) and large subunit (LSU) rDNA regions were amplified and sequenced using the primers ITS5-u/ITS4rust [5,6] and LRust1R/LRust3 [6], respectively. The PCR products were purified using AccuPrep® PCR/Gel Purification Kit (Bioneer, Daejeon, Korea) and sequenced by Macrogen sequencing service (Macrogen, Seoul, Korea) with the primers used for amplification. The resulting sequences were deposited in GenBank (accession nos. PV545142.1–PV545146.1 for ITS, PV545147.1–PV545151.1 for LSU). The BLASTn results showed that the ITS sequences were identical to three sequences of *U. erythronii* (MH205917.1, MH205916.1, and LC203755.1), and the LSU sequences matched those of *U. erythronii* from *E. japonicum* in Japan (LC203755.1). Phylogenetic trees were constructed by the maximum-likelihood method using MEGA7 [7] with the default settings of the program and the Tamura–Nei model. The robustness of the individual branches was estimated by bootstrapping 1,000 replicates.

Phylogenetic analyses based on both the ITS and LSU sequences consistently placed all Korean samples within the *U. erythronii* clade (Fig. 2A and 2B). In the ITS tree (Fig. 2A), the Korean collections (KSNUH1816, 1817, KUS-F33614, F32715, and F33601) grouped together with authentic *U. erythronii* reference sequences obtained from *E. japonicum* in Japan (LC203755.1) and *E. dens-canis* in Romania (MH205916.1) and Croatia (MH205917.1), forming a highly supported monophyletic clade with a high bootstrap value (BS) of 99%. This clade was clearly separated from other *Uromyces* species, including *U. trifolii-repentis*, *U. viciae-fabae*, *U. beticola*, *U. durus*, *U. gageae*, *U. muscari*, *U. transversalis*, and *U. japonicus*. In the LSU tree (Fig. 2B), all Korean isolates clustered with the Japanese reference sequence of *U. erythronii* (LC203755.1), with strong bootstrap support (BS = 96%). The topology of the LSU tree was congruent with that of the ITS tree, confirming that the Korean specimens were conspecific with *U. erythronii*.

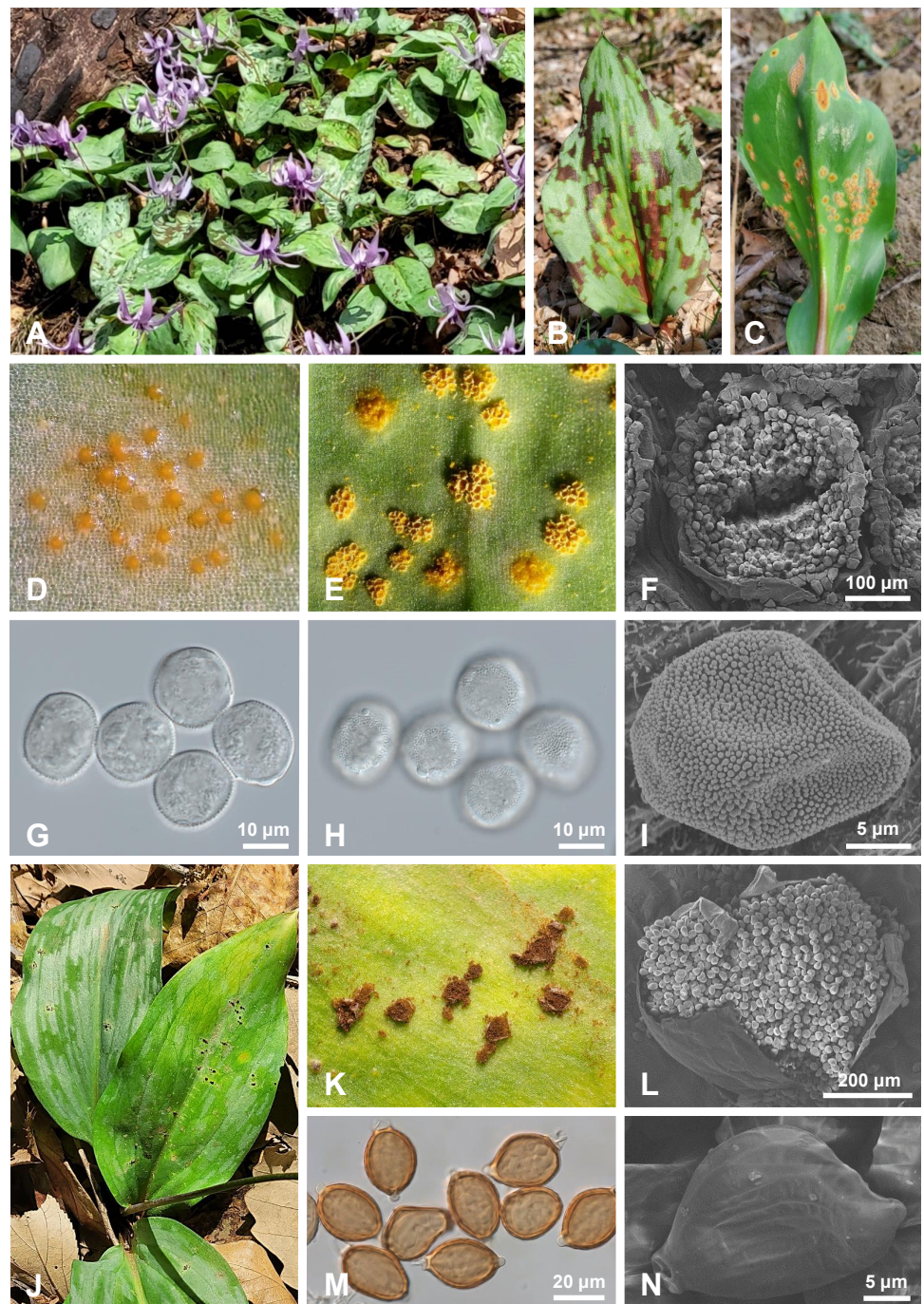


Fig. 1. Rust disease caused by *Uromyces erythronii* on *Erythronium japonicum* in South Korea. A, Rust symptoms on *E. japonicum* in a forest. B, Brown to yellow chlorotic spots on the upper surface of the infected leaf. C, Aecia on the lower leaf surface. D, Spermogonia. E, Aecia. F, Aecium and aeciospores observed using an SEM. G and H, Aeciospores observed using a DIC microscope. I, Verrucose wall ornamentation of an aeciospore under an SEM. J, Telia on the infected leaves. K, Telia. L, Telium and teliospores under an SEM. M, Teliospores under a DIC microscope. N, Wall ornamentation of a teliospore under an SEM. SEM: scanning electron microscope; DIC: differential interference contrast.

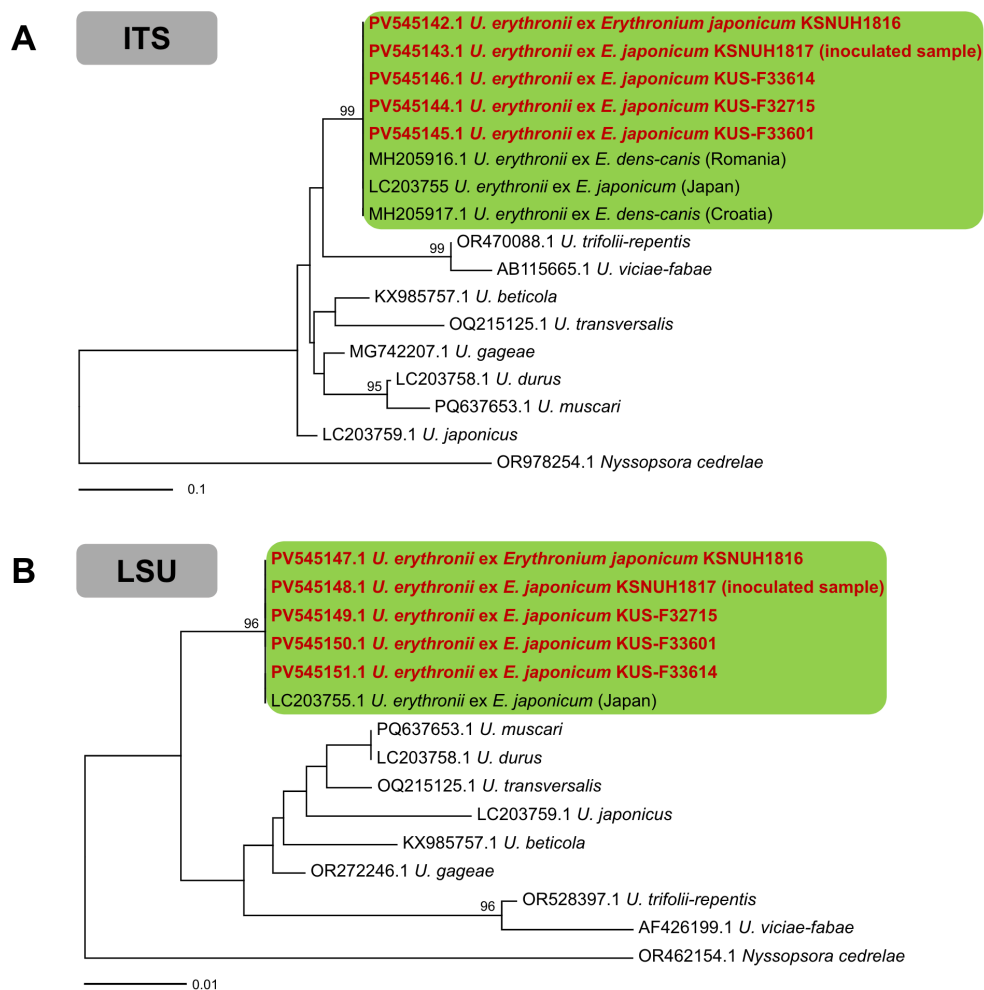


Fig. 2. Maximum-likelihood phylogenetic trees of *Uromyces* species based on ITS (A) and LSU (B) rDNA sequences. Bootstrap support values higher than 60% are shown above the branches. Korean samples are highlighted in bold red. ITS: internal transcribed spacer; LSU: large subunit.

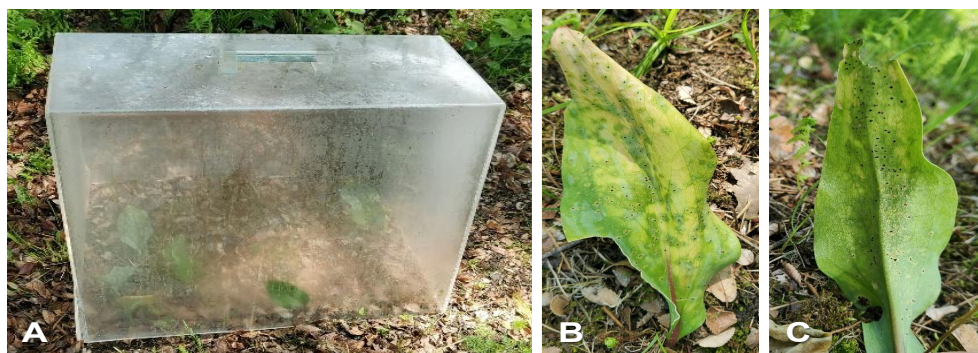


Fig. 3. Pathogenicity test of *Uromyces erythronii* on *Erythronium japonicum*. A, *Erythronium japonicum* plants inoculated with aeciospores and maintained in a plastic chamber. B and C, Telia developed on the upper (B) and lower (C) leaf surfaces two weeks after inoculation.

Pathogenicity was assessed by inoculating three healthy *E. japonicum* plants with aeciospores (1.1×10^6 spores/mL) from naturally infected leaves. Three uninoculated plants served as controls. All plants were maintained in a plastic chamber at 15–20°C with high humidity (Fig. 3A). After two weeks, all inoculated plants developed dark brown telia on their leaves (Fig. 3B and 3C), whereas the control plants remained symptomless. Formation of the telial stage from aeciospore inoculation was consistent with the life cycle of *U. erythronii* previously described by Fukuda and Nakamura [8]. The pathogen on the inoculated plants was confirmed as *U. erythronii* by sequencing, thus fulfilling Koch's postulates.

To our knowledge, this is the first report of rust disease caused by *U. erythronii* on *E. japonicum* in South Korea; however, it has previously been recorded only in Japan and North Korea [9,10]. *Uromyces erythronii* has been reported on *Amana*, *Erythronium*, and *Lilium* species (Liliaceae) in Asia (China and Japan), as well as several European countries (Bulgaria, Croatia, France, Germany, Greece, Hungary, Italy, Romania, Switzerland, Spain, and Ukraine) [11,12]. Considering the high disease incidence and severity observed in Korea, *U. erythronii* may threaten the cultivation and conservation of *E. japonicum*.

CONFLICT OF INTEREST

The authors declare that they have no potential conflict of interest.

ACKNOWLEDGMENTS

This study was supported by grants from the Animal and Plant Quarantine Agency (I-1543086-2025-28-01 & Z-1543086-2025-28-01), Korea.

REFERENCES

1. Mathew B. Plate 411. *Erythronium japonicum*: Liliaceae. Curtis's Bot Mag 2001;18(2):68–73. <https://doi.org/10.1111/1467-8748.00290>
2. Lee MS, Lim SC, Park HJ. Phthalate ester and flavonoids isolated from leaves of *Erythronium japonicum*. Korean J Med Crop Sci 1994;2:67–72.
3. Park YJ, Ku YG, Kang NR, Cho JY, Heo BG. Amino acid contents and various physiological activities of *Erythronium japonicum*. J People Plants Environ 2015;18:345–51. <https://doi.org/10.11628/ksppe.2015.18.5.345>
4. Tykhonenko YY, Sytschak NN, Kagalo AA, Orlov OO. New records of *Uromyces erythronii* (Pucciniales) from Ukraine. Ukr Bot J 2017;74:184–8. <https://doi.org/10.15407/ukrbotj74.02.184>
5. Pfunder M, Schürch S, Roy BA. Sequence variation and geographic distribution of pseudoflower-forming rust fungi (*Uromyces pisi* s. lat.) on *Euphorbia cyparissias*. Mycol Res 2001;105:57–66. <https://doi.org/10.1017/S0953756200003208>
6. Beenken L, Zoller S, Berndt R. Rust fungi on Annonaceae II: The genus *Dasyscypha* Berk. & M.A. Curtis. Mycologia 2012;104:659–81. <https://doi.org/10.3852/11-068>

7. Kumar S, Stecher G, Tamura K. MEGA7: Molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Mol Biol Evol* 2016;33:1870–4. <https://doi.org/10.1093/molbev/msw054>
8. Fukuda T, Nakamura S. Biotic interaction between a rust fungus, *Uromyces erythronii* Pass., and its host plant, *Erythronium japonicum* Decne. (Liliaceae). *Plant Species Biol* 1987;2:75–83. <https://doi.org/10.1111/j.1442-1984.1987.tb00034.x>
9. Hiratsuka N. Uredinales collected in Korea V. *Bot Mag (Tokyo)* 1942;56:53–61. <https://doi.org/10.15281/jplantres1887.56.53>
10. Hiratsuka N, Sato S, Katsuya K, Kakishima M, Hiratsuka Y, Kaneko S, Ono Y, Sato T, Harada Y, Hiratsuka T, et al. The rust flora of Japan. Tsukuba: Tsukuba Shuppankai; 1992.
11. Nagy T, Pfliegler WP, Takács A, Tökölly J, Molnár VA. Distribution, infection rates and DNA barcoding of *Uromyces erythronii* (Pucciniaceae), a parasite of *Erythronium* (Liliaceae) in Europe. *Willdenowia* 2019;49:13–20. <https://doi.org/10.3372/wi.49.49103>
12. Farr DF, Rossman AY. Fungal databases, U.S. National Fungus Collections [Internet]. Beltsville (MD): ARS, USDA; 2025 [cited 2025 Apr 10]. Available from <https://nt.ars-grin.gov/fungaldatabases/>