



## NEW DISEASE REPORT

# First report of *Exobasidium gracile* causing galls on *Camellia sasanqua* in Switzerland and in Europe

C. Compagnoni<sup>1</sup> | L. Beenken<sup>2</sup> | J. Orbach<sup>2</sup> | D. Frey<sup>1,2</sup> <sup>1</sup>Museo cantonale di storia naturale, Lugano, Switzerland<sup>2</sup>Swiss Federal Research Institute WSL, Birmensdorf, Switzerland

## Correspondence

D. Frey, Museo cantonale di storia naturale, Viale Carlo Cattaneo 4, 6900 Lugano, Switzerland. Email: [david.frey@ti.ch](mailto:david.frey@ti.ch)

## KEYWORDS

emerging diseases, fungal pathogens, neomycete, Theaceae

In May 2024, symptoms consistent with those caused by an *Exobasidium* species were observed on *Camellia sasanqua* in a private garden in the Maggia Valley, southern Switzerland (46.25°N, 8.7°E). Affected leaves became swollen, deformed, and spongy, with a light green hue and red tones, in contrast to the original dark green appearance and the leathery, coriaceous texture (Figure. 1). The galls formed due to the intercellular growth of the fungus within the leaf epidermis, causing the leaf thickness to more than double. These symptoms and the host plant *C. sasanqua* are in agreement with previous reports of *Exobasidium*

*gracile* in Asia (Shirai, 1896; Akai, 1939; Mims *et al.*, 2007; Lee *et al.*, 2015). The total rainfall in May was 305.9 mm, which is higher than the mean of 189.6 mm calculated between 1991 and 2020; the temperature ranged from 10.6 – 18.7°C in May, where a temperature deviation of -1.3°C from the 1991–2020 mean was observed (Locarno Monti; Federal Office of Meteorology and Climatology, 2022). A month later, the leaves showed signs of rot at fungal proliferation sites (Figure. 2). As the season progressed, the cool, humid conditions favourable to *Exobasidium* declined (Chen *et al.*, 2023).



**FIGURE 1** Leaves of *Camellia sasanqua* infected by *Exobasidium gracile* show galls in May 2024.

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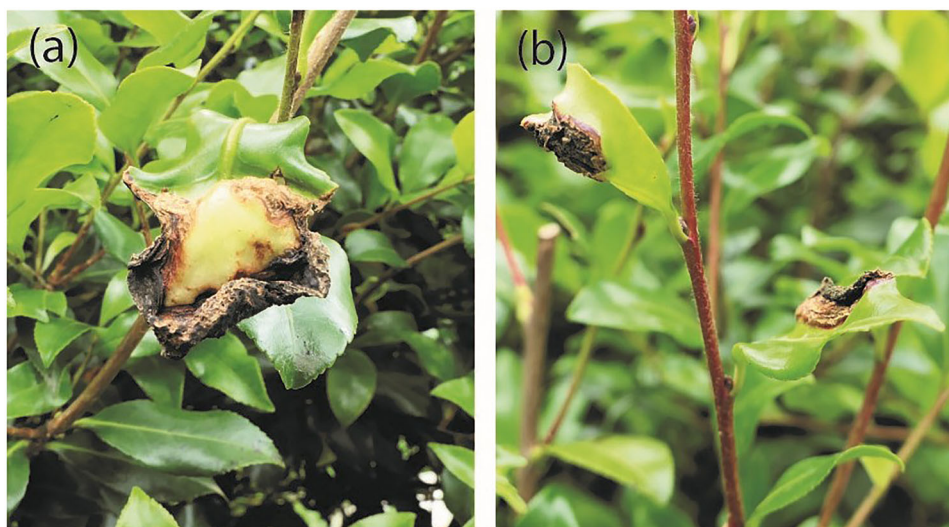


**FIGURE 2** Leaves of *Camellia sasanqua* infected by *Exobasidium gracile* showing signs of rot in June 2024.

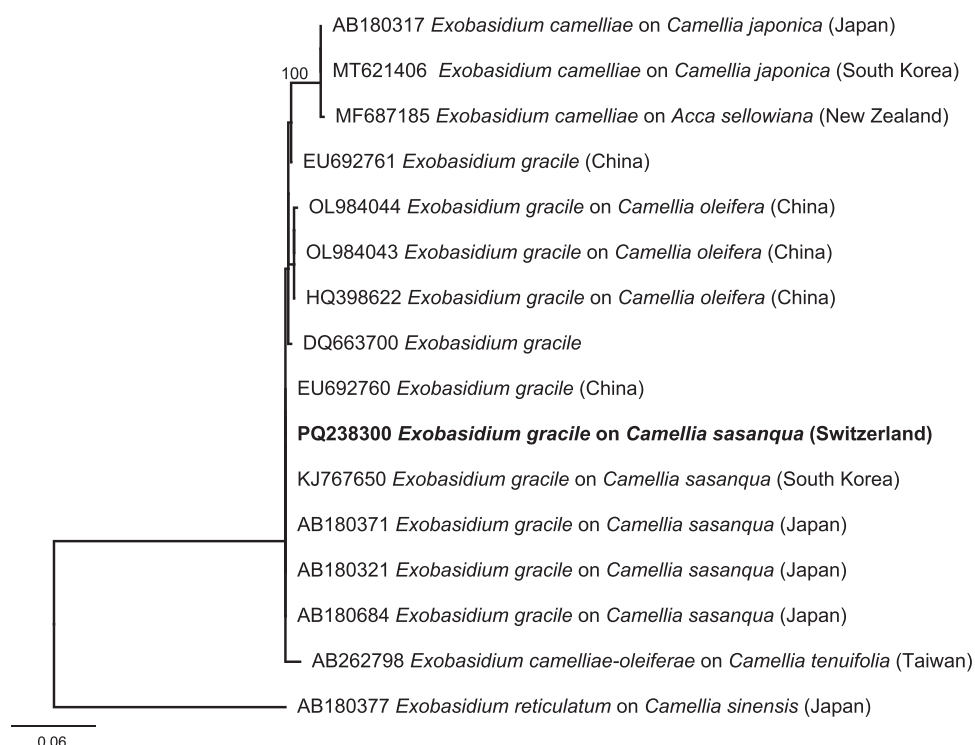


**FIGURE 3** Maximum likelihood analysis of *Exobasidium* spp. on *Camellia* based on ITS1-5.8S-ITS2 sequences performed by RAXML v. 8.2.11 as implemented in Geneious Prime 2021.1.1 (<https://www.geneious.com>). Bootstrap values > 80 (1,000 replications) are indicated at nodes. GenBank accession number, host tree and country of origin are given where available. The Swiss sample is printed in bold.

Since no spores were found for morphological identification, cultivation or infection tests, DNA was directly extracted from a 4 mm<sup>2</sup> piece of infected leaf (isolation PHP24\_0812) for molecular analysis. The ITS region of rDNA was amplified and sequenced using the standard ITSF1/ITS4 primers for fungi. A BLAST search with the obtained ITS sequence (GenBank Accession No. PQ238300) showed more than 99%

identity with sequences of *E. gracile* deposited in GenBank (EU692760, EU692761), only 98% identity with the sequence of *E. camelliae-oleiferae* and 97% identity with those of *E. camelliae*. In a phylogenetic analysis, the Swiss sample clustered with all other *E. gracile* sequences in a single clade (Figure. 3). A voucher specimen is deposited at the Museo cantonale di storia naturale, Lugano (LUG 20000).



The very close match of the barcode sequence, in combination with the typical symptoms on *C. sasanqua*, lead to the conclusion that the fungus belongs to *E. gracile* (even if the microscopic features of the fungus could not be checked). This is the first report of this fungus in Switzerland and Europe. There is a potential risk to ornamental plantations of the host plant.

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## ORCID

L. Beenken <https://orcid.org/0000-0001-8663-7616>

D. Frey <https://orcid.org/0000-0002-4603-0438>

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