

NEW DISEASE REPORT OPEN ACCESS

First Report of Ornithogalum Virus 3 Infecting *Eucomis* spp. in Japan

Yasuhiro Tomitaka¹ | Momoko Matsuyama¹ | Taketoshi Ueno² | Hironobu Yanagisawa³

¹National Agriculture and Food Research Organization, Institute for Plant Protection, Tsukuba, Ibaraki, Japan | ²National Agriculture and Food Research Organization, Institute of Fruit Tree and Tea Science, Higashi-Hiroshima, Hiroshima, Japan | ³National Agriculture and Food Research Organization, Central Region Agricultural Research Center, Tsukuba, Tsukuba, Ibaraki, Japan

Correspondence: Yasuhiro Tomitaka (tomitaka.yasuhiro839@naro.go.jp)

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Mosaic symptoms were noted on pineapple lily, *Eucomis* sp. (family Hyacinthaceae), in at least 10 out of 20 plants cultivated in a field in Chiba Prefecture, Japan in 2015 (Figure 1). Flexuous, filamentous, viral-like particles, approximately 800 nm long, were observed using transmission electron microscopy in the sap of diseased leaves (Figure 2), suggesting that the plants were infected with a virus in the family *Potyviridae*. To confirm, total RNA was extracted from diseased leaves using the RNeasy Plant Mini kit (Qiagen, Germany) and RT-PCR was conducted using potyvirus universal primer sets according to Zheng et al. (2010). Amplicons of the expected size, approximately 350 bp, were observed by electrophoresis. These amplicons were cloned into the Zero Blunt TOPO cloning vector (Invitrogen, USA) and nucleotide sequences of nine clones, independently constructed, were determined (GenBank Accession Nos. LC060458–LC060466). Nucleotide sequence identities among the clones were 98.3%–100% and BLASTn analyses showed that their sequence was 97.1%–97.4% identical with Ornithogalum virus 3 (OV3) (KY769717) (Mostert et al. 2021). The virus was not detected from asymptomatic healthy plants.

To exclude the infection with other virus species, high-throughput sequencing using the Ion PGM system (ThermoFisher Scientific, USA) was conducted using dsRNA isolated from one diseased plant of *Eucomis* sp. which had been previously tested, according to the method of Yanagisawa et al. (2016). Four contigs, 587, 933, 1478, and 2345 nts, were obtained from the analysis and the BLASTn analyses revealed that all of the contigs shared 98.5%–99.3% nucleotide identity with OV3 (KY769717). The complete nucleotide sequence of the polyprotein

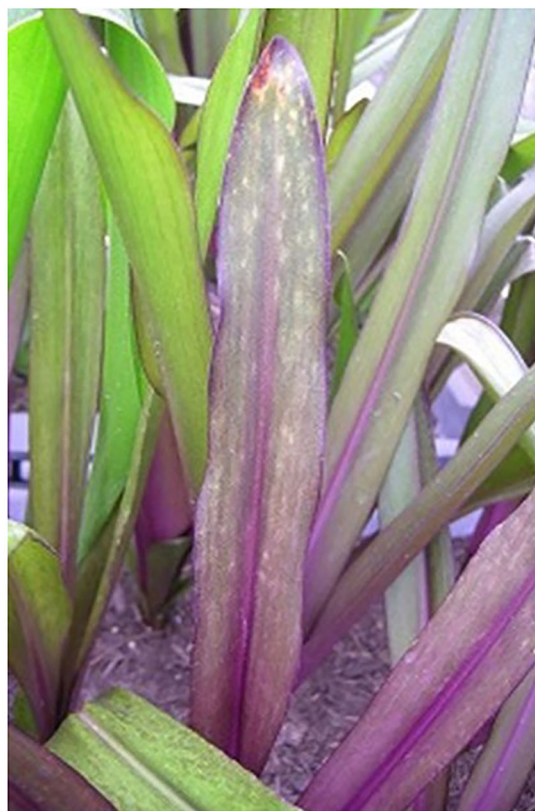


FIGURE 1 | Symptom observed on the leaves of *Eucomis* sp. in the field in Japan.

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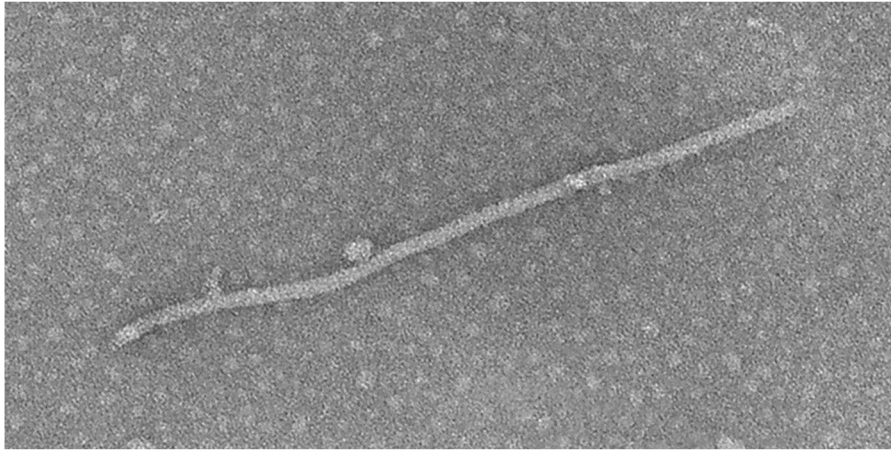


FIGURE 2 | Virus-like particle observed in the sap of the leaves of diseased *Eucomis*.

of OV3 was determined by Sanger sequencing using specific primers for OV3 genome (LC866604).

To investigate whether OV3 is the causal agent of the mosaic symptom observed in *Eucomis*, *Chenopodium quinoa*, and *Nicotiana benthamiana* were inoculated with sap prepared from the leaves of a diseased plant. However, no symptoms were observed and the virus was not detected in the inoculated plant by RT-PCR. In conclusion, the results show that the virus infecting the diseased *Eucomis* sp. is OV3. To the best of our knowledge, this is the first report of the detection of OV3 in *Eucomis*.

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