



## A new tobamovirus infecting *Hoya* spp.

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During 2019/20, a batch of 6,000 young plants of different *Hoya* spp. (family: *Asclepiadaceae*) was grown in a German nursery. The plants had been originally imported from Thailand and a large proportion developed symptoms consistent with viral infection, e.g. ringspots, necrotic lesions, and irregular chlorosis or chlorotic leaf spots (Fig. 1).

The plants were analysed by electron microscopy and non-enveloped rod-shaped particles were observed, suggesting infection with a tobamovirus (Fig. 2A). Virions showed a cross-reaction with a *Youcai mosaic virus* antiserum (DSMZ, Germany) in immunosorbent electron microscopy (Fig. 2B) but there was no reaction with other tobamovirus antisera. Following mechanical transmission, *Nicotiana benthamiana* and *N. tabacum* developed chlorotic lesions four weeks post inoculation. Total RNA was extracted from infected leaf material and a generic tobamovirus RT-PCR was performed using the Tob-Uni 1 and Tob-Uni 2 primers of Letschert *et al.* (2002). Resulting amplicons of c. 800 bp were Sanger sequenced in both directions (Microsynth SeqLab, Germany). The sequences showed 69.4% nucleotide (nt) identity to *Hoya chlorotic spot virus* (HoCSV; KX434725) (Adkins *et al.*, 2018) indicating the presence of a novel tobamovirus, provisionally named *Hoya tobamovirus* 2 (HoToV2).

Two of the samples (JKI2001336 and JKI2001337) were sequenced using MinION sequencing as described by Gaafar *et al.* (2019). In sample JKI2001336, HoToV2 was detected whilst in sample JKI2001337, HoToV2 and *Tomato spotted wilt virus* were detected in a mixed infection. Pairwise alignment using Clustal Omega (1.2.2) showed that the amino acid (aa) sequences of the movement protein (MP) of the two isolates of HoToV2 share 99.7% aa identity to each other and 52.3% identity to HoCSV. The coat protein sequences of the two isolates are identical and share 67.3% aa identity to HoCSV. Phylogenetic analyses grouped both proteins within the tobamovirus genus close to HoCSV (Fig. 3). Comparison of the nt sequences of HoToV2 isolates with a previous sequence from a hoyo plant infected with a tobamovirus collected in 2014 showed 98.8% and 98.9% nt identities (Richert-Pöggeler *et al.*, 2018), indicating that this virus has been present in hoyo for some time in Germany. The partial sequences of HoToV2 isolates JKI2001336, JKI2001337 and 2014 were deposited in GenBank (Accession Nos. MT750216, MT901191 and MT750217,

respectively).

According to ICTV species demarcation criteria a new species can be considered when the nt sequence identity is <90% based on the whole genome nt sequence (Adams *et al.*, 2017). Based on the current results, we propose HoToV2 as a new species within the genus *Tobamovirus*, family *Virgaviridae*.

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### References

- Adams MJ, Adkins S, Bragard C, Gilmer D, Li D, MacFarlane SA, Wong S-K, Melcher U, Ratti C, Ryu KH, 2017. ICTV Virus taxonomy profile: *Virgaviridae*. *Journal of General Virology* **98**, 1999-2000. <http://dx.doi.org/10.1099/jgv.0.000884>
- Adkins S, D'Elia T, Fillmer K, Pongam P, Baker CA, 2018. Biological and genomic characterization of a novel tobamovirus infecting *Hoya* spp. *Plant Disease* **102**, 2571-2577. <http://dx.doi.org/10.1094/PDIS-04-18-0667-RE>
- Gaafar Y, Lüddecke P, Heidler C, Hartrick J, Sieg-Müller A, Hübner C, Wichura A, Ziebell H, 2019. First report of *Southern tomato virus* in German tomatoes. *New Disease Reports* **40**, 1. <http://dx.doi.org/10.5197/j.2044-0588.2019.040.001>
- Letschert B, Adam G, Lesemann D-E, Willingmann P, Heinze C 2002. Detection and differentiation of serologically cross-reacting tobamoviruses of economical importance by RT-PCR and RT-PCR-RFLP. *Journal of Virological Methods* **106**, 1-10. [http://dx.doi.org/10.1016/S0166-0934\(02\)00135-0](http://dx.doi.org/10.1016/S0166-0934(02)00135-0)
- Richert-Pöggeler KR, Maaß C, Schuhmann S, Schmalowski D, Ponath J, Lockhart, B, 2018. *Tobamovirus* spread and diversity in Anthropocene. *Acta Horticulturae* **1193**, 9-16. <http://dx.doi.org/10.17660/ActaHortic.2018.1193.2>



Figure 1

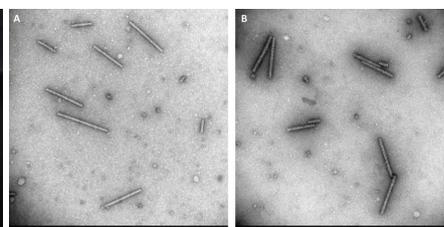


Figure 2

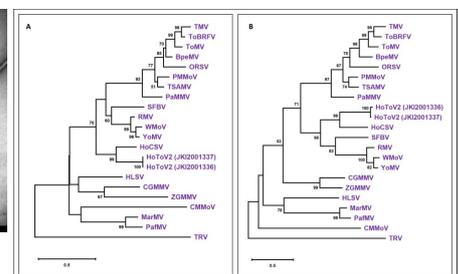


Figure 3

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