



First report of *Viola white distortion associated virus* in *Viola tricolor* in the United Kingdom

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In February 2014 a sample of *Viola tricolor* ssp. *tricolor* was submitted to Fera from outdoor bedding plants grown in Yorkshire, UK. The sample was sent in following the appearance of symptoms including bleaching and distortion (Fig. 1). The sample was tested by ELISA for *Cucumber mosaic virus* (CMV) and with generic antisera for the presence of potyviruses. The sample was negative in each case. In October 2014 a further *Viola* sample was submitted from a grower in Wiltshire, UK, with up to 10% of the stock affected by similar symptoms. Again, the results of ELISA testing for CMV and potyviruses were negative. Samples were screened using an Illumina MiSeq as described by Adams *et al.* (2014). The tripartite genome (GenBank Accession Nos. RNA1-KX196166, RNA2-KX196165, RNA3-KX196164) of a putative sub-group 4 ilarvirus was recovered from the samples having 96% similarity to *Viola white distortion associated virus* (VWDaV) (GU168941; Fig. 2). To confirm the presence of the virus in the samples a real-time PCR assay was designed (F: 5'-AAGGGAAGAAAGCGAAGACTGTT-3', R: 5'-TCACAGAGTGATCAACCAATCGT-3', probe: 5' Fam-TAGAGATGCCAAACCCGTAACATAAAACG-BHQ1 3') from consensus sequences from this study and the sequences described by Cuiffo *et al.* (2014). In each case the samples were positive for the presence of VWDaV.

Cuiffo *et al.* (2014) associated the presence of VWDaV with symptoms consistent with pansy mottle syndrome, a disorder recognised since the 1960's. To investigate this link, during the summer of 2015, samples were collected from nurseries across England (West Sussex, Hertfordshire and

East Yorkshire) which had pansy plants exhibiting bleaching and/or distortion. Samples of asymptomatic pansies from the same cultivars were also submitted as a 'healthy control'. Between 63.5-73.3% of the 300 pansies tested from affected cultivars were positive for VWDaV with no clear correlation to observable symptom or geographic origin. This report supports the conclusions from Cuiffo *et al.* (2014) that the virus is probably disseminated widely in germplasm of *Viola* spp.

Acknowledgements

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References

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Figure 1

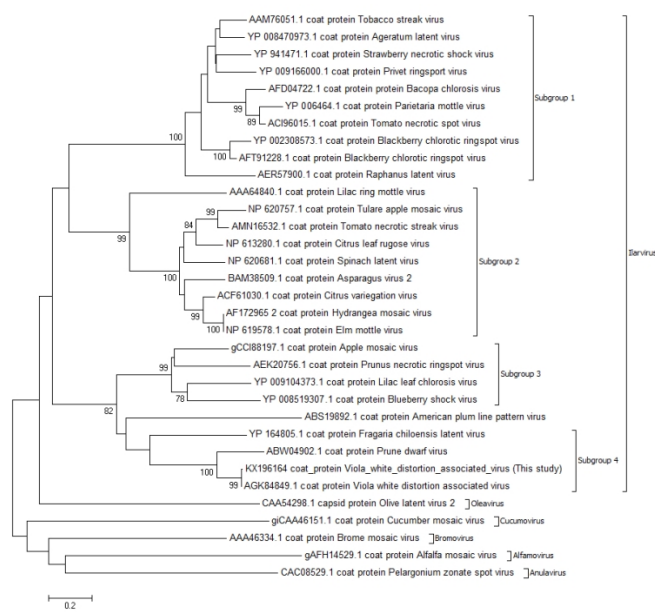


Figure 2

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