

Genome sequences of Beet curly top Iran virus, Oat dwarf virus, Turnip curly top virus, and wheat dwarf virus identified in leafhoppers

Kamali, Mehdi; Heydarnejad, Jahangir; Pouramini, Najmeh; Masumi, Hossain; Farkas, Kata; Kraberger, Simona; Varsani, Arvind

Genome Announcements

DOI:

10.1128/genomeA.01674-16

Published: 23/02/2017

Publisher's PDF, also known as Version of record

Cyswllt i'r cyhoeddiad / Link to publication

Dyfyniad o'r fersiwn a gyhoeddwyd / Citation for published version (APA): Kamali, M., Heydarnejad, J., Pouramini, N., Masumi, H., Farkas, K., Kraberger, S., & Varsani, A. (2017). Genome sequences of Beet curly top Iran virus, Oat dwarf virus, Turnip curly top virus, and wheat dwarf virus identified in leafhoppers. *Genome Announcements*, *5*(8), [e01674-16]. https://doi.org/10.1128/genomeA.01674-16

Hawliau Cyffredinol / General rights

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
 - You may not further distribute the material or use it for any profit-making activity or commercial gain
 You may freely distribute the URL identifying the publication in the public portal?

Take down policyIf you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.







Genome Sequences of Beet curly top Iran virus, Oat dwarf virus, Turnip curly top virus, and Wheat dwarf virus Identified in Leafhoppers

Mehdi Kamali,^a Jahangir Heydarnejad,^a Najmeh Pouramini,^a Hossain Masumi,^a Kata Farkas,^b Simona Kraberger,^{b,d} Arvind Varsani^{b,c,e}

Department of Plant Protection, College of Agriculture, Shahid Bahonar University of Kerman, Kerman, Irana; School of Biological Sciences, University of Canterbury, Christchurch, New Zealandb; Department of Clinical Laboratory Sciences, University of Cape Town, Cape Town, South Africac; Department of Microbiology, Immunology and Pathology, Colorado State University, Fort Collins, Colorado, USAd; The Biodesign Center for Fundamental and Applied Microbiomics, Center for Evolution and Medicine, School of Life Sciences, Arizona State University, Tempe, Arizona, USAe

ABSTRACT Implementation of a vector-enabled metagenomics approach resulted in the identification of various geminiviruses. We identified the genome sequences of *Beet curly top Iran virus, Turnip curly top viruses, Oat dwarf viruses*, the first from Iran, and *Wheat dwarf virus* from leafhoppers feeding on beet, parsley, pumpkin, and turnip plants.

ew molecular-based methods have facilitated the rapid identification of various plant and animal viruses, especially small single-stranded DNA viruses. Furthermore, vector-enabled metagenomic (VEM) approaches using these methods have proven very useful for the identification of plant virus circulation in various agricultural regions (1-4). Here, we used a VEM approach to identify geminiviruses (5) circulating in farms in Zafar-Abad, Iran, in 2013 by sampling of plant leafhoppers from different genera feeding on beet (Beta vulgaris; n = 1), parsley (Petroselinum crispum; n = 1), pumpkin (Cucurbita pepo; n = 1), and turnip (Brassica rapa; n = 3) plants. The insects were homogenized in SM buffer and processed as described by Dayaram et al. (6-9). The viral DNA was enriched for circular molecules using rolling-circle amplification, and this was sequenced on an Illumina sequencing platform at Novogene (Hong Kong). The paired-end reads were de novo assembled using ABySS 1.9 (10), and viral sequences were identified using BLASTx against a local viral protein sequence database. Contigs with BLASTx hits to geminivirus sequences (5, 11) were identified. Abutting primers were designed and used for PCR amplification to recover full viral genomes. These were cloned and sequenced at Macrogen, Inc. (South Korea). Two Oat dwarf virus (ODV) genomes that were recovered from leafhoppers feeding on beet and turnip share 99.8% identity and 97% with the only other ODV identified infecting oat (Avena sativa) in Germany. To date, ODV has not been reported in Iran, and therefore, these genome sequences (accession numbers KX533458 to KX533459) represent the first genome sequences of ODV from Iran. Six Wheat dwarf virus (WDV) genomes recovered from leafhoppers feeding on beet (n = 2), turnip (n = 2), pumpkin (n = 1), and parsley (n = 1)1) display 13.6% diversity (accession numbers KX533460 to KX533465); however, compared with genomes of WDV in public databases, they are most closely related to recently identified sequences from Iran, sharing >97% genome-wide identity. The Beet curly top Iran virus (BCTIV; accession number KX533466) and Turnip curly top virus (TCTV; accession numbers KX533467 to KX533468) sequences share 94% and 99% identity with previously described isolates, respectively. The BCTIV and TCTV genomes were

Received 13 December 2016 **Accepted** 16 December 2016 **Published** 23 February 2017

Citation Kamali M, Heydarnejad J, Pouramini N, Masumi H, Farkas K, Kraberger S, Varsani A. 2017. Genome sequences of *Beet curly top Iran virus*, *Oat dwarf virus*, *Turnip curly top virus*, and *Wheat dwarf virus* identified in leafhoppers. Genome Announc 5:e01674-16. https://doi.org/10.1128/genomeA.01674-16.

Copyright © 2017 Kamali et al. This is an openaccess article distributed under the terms of the Creative Commons Attribution 4.0

Address correspondence to Jahangir Heydarnejad, jheydarnejad@yahoo.com, or Arvind Varsani, arvind.varsani@asu.edu. Kamali et al.

recovered from leafhoppers feeding on turnip, and the two TCTV genomes share 90% identity.

Leafhoppers transmitted several destructive viral and prokaryotic diseases, such as curly top of sugar beet and turnip crops (12) and citrus stubborn (13) in Iran. We analyzed the beet, parsley, pumpkin, and turnip plants being fed on by leafhoppers in this study and did not detect ODV or WDV infection. This is perhaps not surprising, as vectors play a crucial role in viral transmission and movement, and *Psammotettix alienus* has been shown to transmit ODV (14) and WDV (15). It is therefore probable that these leafhoppers acquired ODV and WDV when feeding on infected grasses prior to being sampled.

VEM has proven a useful tool not only in this case where we identified and recovered the genomes of ODVs and WDVs circulating in Fars province of Iran but also in identifying the first mastrevirus in the Caribbean (2), novel begomovirus species (3), and known and novel plant-infecting viruses in an unlikely vector, mosquitoes (16).

Accession number(s). The complete genome sequences for the four viruses have been deposited in GenBank under accession numbers KX533466 (BCTIV), KX533458 to KX533459 (ODV), KX533467 to KX533468 (TCTV), and KX533460 to KX533465 (WDV).

ACKNOWLEDGMENTS

This study was supported by a grant (SBU1393-370319) from Shahid Bahonar University of Kerman, Kerman, Iran. A.V. is supported by the National Research Foundation of South Africa.

REFERENCES

- Rosario K, Marr C, Varsani A, Kraberger S, Stainton D, Moriones E, Polston JE, Breitbart M. 2016. Begomovirus-associated satellite DNA diversity captured through vector-enabled metagenomic (VEM) surveys using whiteflies (Aleyrodidae). Viruses 8:e36. https://doi.org/10.3390/ v8020036.
- Rosario K, Padilla-Rodriguez M, Kraberger S, Stainton D, Martin DP, Breitbart M, Varsani A. 2013. Discovery of a novel mastrevirus and alphasatellite-like circular DNA in dragonflies (Epiprocta) from Puerto Rico. Virus Res 171: 231–237. https://doi.org/10.1016/j.virusres.2012.10.017.
- Rosario K, Seah YM, Marr C, Varsani A, Kraberger S, Stainton D, Moriones E, Polston JE, Duffy S, Breitbart M. 2015. Vector-enabled metagenomic (VEM) surveys using whiteflies (Aleyrodidae) reveal novel *Begomovirus* species in the new and old worlds. Viruses 7:5553–5570. https://doi.org/ 10.3390/v7102895.
- Ng TF, Duffy S, Polston JE, Bixby E, Vallad GE, Breitbart M. 2011. Exploring the diversity of plant DNA viruses and their satellites using vectorenabled metagenomics on whiteflies. PLoS One 6:e19050. https:// doi.org/10.1371/journal.pone.0019050.
- Varsani A, Navas-Castillo J, Moriones E, Hernández-Zepeda C, Idris A, Brown JK, Murilo Zerbini F, Martin DP. 2014. Establishment of three new genera in the family *Geminiviridae: Becurtovirus, Eragrovirus* and *Turncur-tovirus*. Arch Virol 159:2193–2203. https://doi.org/10.1007/s00705-014-2050-2.
- Dayaram A, Galatowitsch M, Harding JS, Argüello-Astorga GR, Varsani A. 2014. Novel circular DNA viruses identified in *Procordulia grayi* and Xanthocnemis zealandica larvae using metagenomic approaches. Infect Genet Evol 22:134–141. https://doi.org/10.1016/j.meegid.2014.01.013.
- Dayaram A, Galatowitsch ML, Argüello-Astorga GR, van Bysterveldt K, Kraberger S, Stainton D, Harding JS, Roumagnac P, Martin DP, Lefeuvre P, Varsani A. 2016. Diverse circular replication-associated protein encoding viruses circulating in invertebrates within a lake ecosystem. Infect Genet Evol 39:304–316. https://doi.org/10.1016/j.meegid.2016.02.011.
- 8. Dayaram A, Potter KA, Moline AB, Rosenstein DD, Marinov M, Thomas JE, Breitbart M, Rosario K, Argüello-Astorga GR, Varsani A. 2013. High global

- diversity of cycloviruses amongst dragonflies. J Gen Virol 94:1827–1840. https://doi.org/10.1099/vir.0.052654-0.
- Dayaram A, Potter KA, Pailes R, Marinov M, Rosenstein DD, Varsani A. 2015. Identification of diverse circular single-stranded DNA viruses in adult dragonflies and damselflies (Insecta: Odonata) of Arizona and Oklahoma, USA. Infect Genet Evol 30:278–287. https://doi.org/10.1016/ j.meegid.2014.12.037.
- Simpson JT, Wong K, Jackman SD, Schein JE, Jones SJ, Birol I. 2009. ABySS: a parallel assembler for short read sequence data. Genome Res 19:1117–1123. https://doi.org/10.1101/gr.089532.108.
- Muhire B, Martin DP, Brown JK, Navas-Castillo J, Moriones E, Zerbini FM, Rivera-Bustamante R, Malathi VG, Briddon RW, Varsani A. 2013. A genome-wide pairwise-identity-based proposal for the classification of viruses in the genus *Mastrevirus* (family *Geminiviridae*). Arch Virol 158: 1411–1424. https://doi.org/10.1007/s00705-012-1601-7.
- Hosseini Abhari E, Heydarnejad J, Massumi H, Hosseini Pour A, Izadpanah K. 2016. Natural hosts, vector and molecular detection of *Beet curly* top virus (BCTV) in southeast of Iran. Proc 2nd Asian Plant Pathol Cong, Singapore.
- Omidi M, Hosseini-Pour A, Rahimian H, Massumi H, Saillard C. 2011. Identification of *Circulifer haematoceps* (Hemiptera:Cicadellidae) as vector of *Spiroplasma citri* in the Kerman Province of Iran. J Plant Pathol 93:167–172.
- Schubert J, Habekuss A, Kazmaier K, Jeske H. 2007. Surveying cereal-infecting geminiviruses in Germany—diagnostics and direct sequencing using rolling circle amplification. Virus Res 127:61–70. https://doi.org/10.1016/j.virusres.2007.03.018.
- Lotfipour M, Behjatnia SAA, Afsharifar A, Izadpanah K. 2013. Surveying cereal-infecting geminiviruses in Germany—diagnostics and direct sequencing using rolling circle amplification. Iran J Plant Pathol 49:17–31.
- Ng TF, Willner DL, Lim YW, Schmieder R, Chau B, Nilsson C, Anthony S, Ruan Y, Rohwer F, Breitbart M. 2011. Broad surveys of DNA viral diversity obtained through viral metagenomics of mosquitoes. PLoS One 6:e20579. https://doi.org/10.1371/journal.pone.0020579.

Volume 5 Issue 8 e01674-16 genomea.asm.org 2