

Complete Genomic Sequence of Southern Rice Blacked-Dwarf Virus, a Novel Fijivirus, from Vietnam

Jin Xue,^{a,b} Jing Li,^b Hoang-Anh Ta,^c Heng-Mu Zhang,^b Jian Yang,^a Ming-Fang Lv,^{a,d} Yuan Meng,^a Pei-Pei Li,^a Jian-Ping Chen^a

College of Bio-Safety Science and Technology, Hunan Agricultural University, Changsha, China^a; State Key Laboratory Breeding Base for Zhejiang Sustainable Pest and Disease Control, Key Laboratory of Plant Protection and Biotechnology, Ministry of Agriculture, and Zhejiang Provincial Key Laboratory of Plant Virology, Institute of Virology and Biotechnology, Zhejiang Academy of Agricultural Sciences, Hangzhou, China^b; Plant Protection Research Institute, Hanoi, Vietnam^c; College of Agriculture and Biotechnology (CAB), Zhejiang University, Hangzhou, China^d

J.X., J.L., and H.-A.T. contributed equally to this article.

The nucleotide sequences of the ten genomic segments of a Vietnam isolate of southern rice blacked-dwarf virus were determined. This complete genomic sequence will help to further understand the viral etiology (origin of viral pathogen) and phylogenetic relationships among fijiviruses.

Received 21 March 2013 Accepted 5 April 2013 Published 23 May 2013

Citation Xue J, Li J, Ta H-A, Zhang H-M, Yang J, Lv M-F, Meng Y, Li P-P, Chen J-P. 2013. Complete genomic sequence of southern rice blacked-dwarf virus, a novel fijivirus, from Vietnam. *Genome Announc.* 1(3):e00212-13. doi:10.1128/genomeA.00212-13.

Copyright © 2013 Xue et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](https://creativecommons.org/licenses/by/3.0/).

Address correspondence to Heng-Mu Zhang, zhzhengmu@tsinghua.org.cn, or Jian-Ping Chen, jpchen2001@yahoo.com.cn.

Southern rice black-streaked dwarf virus (SRBSDV) (or rice black-streaked dwarf virus 2) was first reported in China and was identified as a novel putative member of the genus *Fijivirus* within the family *Reoviridae* (1–5). SRBSDV has morphological and serological similarities to rice black-streaked dwarf virus (RBSDV), a recognized member of the genus *Fijivirus*, but it is efficiently transmitted by the white-backed planthopper (*Sogatella furcimer*a Horváth) (3, 6) and only poorly transmitted by the small planthopper (*Laodelphax striatellus* Fallen), the main vector of RBSDV (4, 5).

In Vietnam, a novel dwarf and leaf-twisting syndrome was first observed on rice plants in Nghe An Province in the summer 2009 crop. The disease rapidly spread among diverse agroecological regions in north and central Vietnam and also infected maize after rice was harvested. Although the disease was at first thought to be caused by a mixed infection of rice grassy stunt virus (RGSV) and rice ragged stunt virus (RRSV), transmission experiments and partial genomic data allowed us to identify the causal agent as SRBSDV (7). To date, SRBSDV has been reported from at least 35 provinces and cities in Vietnam (8). The complete sequences of all 10 double-stranded RNA (dsRNA) genome segments of two SRBSDV isolates (SRBSDV-GD and SRBSDV-HN) from China have been determined (9). However, only partial sequences of Vietnamese isolates have been reported (7). To understand the etiology of the viral disease in Vietnam and the phylogenetic relationships among fijiviruses, we have therefore determined the complete genomic sequence of a Vietnam isolate of SRBSDV (SRBSDV-V). Viral dsRNA purification, ligation-dependent RT-PCR amplification, and cloning were performed as described previously (10, 11). The inserts were sequenced using the BigDye Terminator v3.1 cycle sequencing kit on an ABI Prism 3730 DNA sequencer (PerkinElmer Applied Biosystems). The sequences were assembled using the DNAMAN v6.0 program (Lynnon Corporation, Canada).

The total ten-segment genome of SRBSDV-V had 29,115 nucleotides (nt), which is 9 nt shorter than SRBSDV-GD or SRBSDV-HN but similar in organization to these two Chinese isolates and other group 2 fijiviruses that have been sequenced (9–13). Each of the genome segments S1 to S4, S6 and S8, and S10 encodes a single major protein, while S5, S7, and S9 each have two nonoverlapping or partially overlapping open reading frames (ORFs). The extreme 5' and 3' ends of the sense strand of each segment have the sequence 5'-AAGTTTTT...CAGCTA(G)T(C/A)T(C)GTC-3', which is similar to the conserved terminal sequences reported from RBSDV, Mal de Río Cuarto virus (MRCV), and maize rough dwarf virus (MRDV) segments (9–13). The 13 ORFs share the highest homologies (96 to 99%) with those of the corresponding segments of SRBSDV and share some homologies to those of other fijiviruses. In the phylogenetic analyses of their segments, SRBSDV, RBSDV, MRDV, and MRCV were always closely clustered together, supporting the hypothesis that SRBSDV should be a novel species in group 2 of the genus *Fijivirus*, in the family *Reoviridae* (1, 3). The new genomic sequences of SRBSDV-V will be important for determining the taxonomic position of the isolate and the etiology of the viral disease in Vietnam.

Nucleotide sequence accession numbers. The complete genomic sequence of SRBSDV-V has been deposited in the GenBank/EMBL/DBJ databases under the accession no. [HQ731492](https://genbank.ncbi.nlm.nih.gov/GenBank/FASTA/entry.fcgi?acc=HQ731492) to [HQ731501](https://genbank.ncbi.nlm.nih.gov/GenBank/FASTA/entry.fcgi?acc=HQ731501), corresponding to genomic segments 1 through 10, respectively.

ACKNOWLEDGMENTS

This work was funded by the China 973 Program (2006CB708209), the 863 program (2007AA10Z414), the National Science and Technology Support Program (2012BAD19B03), the International Science and Technology Cooperation Project (2007DFB30350), the Special Fund for Agro-Scientific Research in the Public Interest of China (201003031), the Zhejiang Provincial Science and Technology Project (2010C12027), and the

Zhejiang Provincial Foundation for Natural Science (Z305165 and Y3090657).

We thank M. J. Adams, Rothamsted Research, Harpenden, United Kingdom, for help in correcting the English of the manuscript.

REFERENCES

- Zhang HM, Yang J, Chen JP, Adams MJ. 2008. A black-streaked dwarf disease on rice in China is caused by a novel fijivirus. *Arch. Virol.* 153: 1893–1898.
- Zhou GH, Xu DL, Li HP. 2004. Identification of rice black-streaked dwarf virus infecting rice in Guangdong, p 210–212. *In* Peng YL (ed), Proceedings of the conference on Chinese plant pathology. China Agricultural Sciencetech Press, Beijing, China.
- Zhou GH, Wen JJ, Cai DJ, Li P, Xu DL, Zhang SG. 2008. Southern rice black-streaked dwarf virus: a new proposed *Fijivirus* species in the family *Reoviridae*. *Chin. Sci. Bull.* 53:3677–3685.
- Boccardo G, Milne RG. 1984. Plant reovirus group. CMI/AAB descriptions of plant viruses no. 294. Commonwealth Microbiology Institute and Association of Applied Biology, Kew, United Kingdom.
- Attoui H, Mertens PPC, Becnel J, Belaganahalli S, Bergoin M, Brussaard CP, Chappell JD, Ciarlet M, del Vas M, Dermody TS, Dormitzer PR, Duncan R, Fcang Q, Graham R, Guglielmi KM, Harding RM, Hillman B, Makkay A, Marzachi C, Matthijssens J, Milne RG, Mohd Jaafar F, Mori H, Noordeloos AA, Omura T, Patton JT, Rao S, Maan M, Stoltz D, Suzuki N, Upadhyaya NM, Wei C, Zhou H. 2010. Family *Reoviridae*, p 541–637. *In* King AMQ, Adams MJ, Carstens EB, Lefkowitz EJ (ed), *Virus taxonomy: classification and nomenclature of viruses: ninth report of the International Committee on Taxonomy of Viruses*. Academic Press, London, United Kingdom.
- Li YZ, Cao Y, Zhou Q, Guo HM, Ou GC. 2012. The efficiency of southern rice black-streaked dwarf virus transmission by the vector *Sogatella furcifera* to different host plant species. *JIA* 11:621–627.
- Ta HA, Zhang HM, Yang J, Chen JP, Hébrard E, Zhou GH, Ngo VV, Cheng JA. 2011. Identification, characterization, and distribution of southern rice black-streaked dwarf virus in Vietnam. *Plant Dis.* 95: 1063–1069.
- Ta HA, Ngo VV, Nguyen DP, Nguyen VC, Tran TTH, Pham TH, Zhang HM, Yang J, Chen JP, Eugénie H, Zhou GH, Cheng JA. 2012. Southern rice black-streaked dwarf virus and present status of rice viruses in Vietnam, p 23. *In* Chen JA, Lou YG (ed), Proceedings of the international conference on rice planthoppers: ecology, management, socio-economics and policy. The Rice Planthopper Project, Hangzhou, China.
- Wang Q, Yang J, Zhou GH, Zhang HM, Chen JP, Adams MJ. 2010. The complete genome sequence of two isolates of Southern rice black-streaked dwarf virus, a new member of the genus *Fijivirus*. *J. Phytopathol.* 158: 733–737.
- Zhang HM, Chen JP, Lei JL, Adams MJ. 2001. Sequence analysis shows that a dwarfing disease on rice, maize and wheat in China is caused by rice black-streaked dwarf virus (RBSDV). *Eur. J. Plant Pathol.* 107:563–567.
- Zhang HM, Chen JP, Adams MJ. 2001. Molecular characterisation of segments 1 to 6 of Rice black-streaked dwarf virus from China provides the complete genome. *Arch. Virol.* 146:2331–2339.
- Marzachi C, Boccardo G, Nuss DL. 1991. Cloning of the maize rough dwarf virus genome: molecular confirmation of the plant-reovirus classification scheme and identification of two large nonoverlapping coding domains within a single genomic segment. *Virology* 180:518–526.
- Guzmán FA, Distéfano AJ, Arneodo JD, Hopp HE, Lenardon SL, del Vas M, Conci LR. 2007. Sequencing of the bicistronic genome segments S7 and S9 of Mal de Río Cuarto virus (*Fijivirus*, *Reoviridae*) completes the genome of this virus. *Arch. Virol.* 152:565–573.