

Complete Genomic Sequence of Maize Rough Dwarf Virus, a Fijivirus Transmitted by the Small Brown Planthopper

Mingfang Lv, Li Xie, Jian Yang, Jianping Chen, Heng-Mu Zhang

State Key Laboratory Breeding Base for Zhejiang Sustainable Pest and Disease Control, Key Laboratory of Plant Protection and Biotechnology, Ministry of Agriculture, Zhejiang Provincial Key Laboratory of Plant Virology, Institute of Virology and Biotechnology, Zhejiang Academy of Agricultural Sciences, Hangzhou, China

The nucleotide sequences of the 10 genomic segments of an Italian isolate of maize rough dwarf virus (MRDV) were determined. This first complete genomic sequence of MRDV will help understand the phylogenetic relationships among group 2 fijiviruses and especially the closely related rice black-streaked dwarf virus, which is also found to naturally infect maize.

Received 5 November 2015 Accepted 18 December 2015 Published 4 February 2016

Citation Lv M, Xie L, Yang J, Chen J, Zhang H-M. 2016. Complete genomic sequence of maize rough dwarf virus, a fijivirus transmitted by the small brown planthopper. *Genome Announc* 4(1):e01529-15. doi:10.1128/genomeA.01529-15.

Copyright © 2016 Lv 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 Jianping Chen, jpcchen2001@yahoo.com.cn, or Heng-Mu Zhang, zhengmu@tsinghua.org.cn.

Maize rough dwarf virus (MRDV) was first described in Italy in the late 1940s (1) and is one of four recognized species in group 2 of the genus *Fijivirus*, family *Reoviridae* (2). MRDV naturally infects maize and causes a severe and economically important disease primarily in Europe and the Middle East (1, 3). Infected maize plants are typically stunted, with swellings along the veins on the undersides of leaves and on the sheaths of leaves and ears, and they are far less productive compared to healthy maize plants. MRDV shares many features with rice black-streaked dwarf virus (RBSDV), another group 2 fijivirus. Both viruses can be transmitted to maize by the planthopper *Laodelphax striatellus* in a persistent manner and induce similar severe growth abnormalities (4). They have a close serological relationship, but there are important biological differences. RBSDV naturally infects rice, but MRDV does not, and while MRDV is transmitted through the eggs of the vector insect, RBSDV is not (4).

The nucleotide sequences of each of the 10 genomic RNAs of RBSDV have been determined (5, 6) but sequence information from MRDV is more limited (7). We have therefore determined the complete genomic sequence of an Italian isolate of MRDV to improve our understanding of the relationship between the two viruses and to assist in studies to correlate genome structure and function. Viral double-stranded RNA purification, reverse transcription-polymerase chain reaction (RT-PCR) amplification, cloning, and sequencing were performed, as previously described (6, 8). The inserts were sequenced using the BigDye Terminator version 3.1 cycle sequencing kit on an ABI PRISM 3730 DNA sequencer (PerkinElmer Applied Biosystems, USA). Sequences were assembled using the DNAMAN version 6.0 program (Lynnon Corporation, Canada).

The total 10-segment genome of MRDV was composed of 29,144 nucleotides (nt), which is 3 nt longer than the RBSDV genome and is similar in organization to RBSDV and the other group 2 fijiviruses that have been sequenced (Mal de Rio Cuarto virus [MRCV] and southern rice black-streaked dwarf virus [SRBSDV]). The extreme 5' and 3' ends of the sense strand of each segment had the sequence 5'-AAGTTTTTTT...CAGCTA(G)T(C/A)T(C)GTC-3', which is similar to the conserved terminal se-

quences reported from RBSDV, MRCV, and SRBSDV segments (7–9). A perfect or imperfect 6- to 10-bp inverted repeat was identified immediately adjacent to the conserved terminal sequences in each genomic segment. Each of the genome segments S1 to S4, S6, S8, and S10 encodes a single major protein, while S5, S7, and S9 each had two nonoverlapping or partially overlapping open reading frames (ORFs). The 13 ORFs share the highest homologies (81 to 97%) with those of the corresponding segments of RBSDV. S1 contained the major motifs characteristic of an RNA-dependent RNA polymerase (RdRp) (10), which can be aligned with those from the RdRp proteins of other reoviruses and which is thought to be a minor component of the core particle. RBSDV, MRDV, RBSDV-2, and MRCV were always closely clustered together in phylogenetic analyses of their segments, and the new sequences of MRDV will be important for determining the appropriate taxonomic positions of these viruses, which sometimes have been considered isolates of a single species (11).

Nucleotide sequence accession numbers. The complete genomic sequence of MRDV has been deposited in the GenBank/EMBL/DDBJ databases with the accession numbers [HQ637550](https://www.ncbi.nlm.nih.gov/nuccore/HQ637550) to [HQ637559](https://www.ncbi.nlm.nih.gov/nuccore/HQ637559) corresponding to genomic segments 1 to 10, respectively.

ACKNOWLEDGMENTS

This work was funded by the National Science and Technology Support Program (grant 2012BAD19B03), the China 973 Program (grant 2010CB126203), the Special Fund for Agro-Scientific Research in the Public Interest of China (grant 201003031), and the Zhejiang Provincial Science and Technology Project (grant 2010C12027).

We thank Piero Caciagli, Istituto di Virologia Vegetale—CNR, Turin, Italy, for generously providing maize plant samples infected by MRDV, and M. J. Adams, Rothamsted Research, Harpenden, United Kingdom, for help in correcting the English of the manuscript.

FUNDING INFORMATION

This work was funded by the National Science and Technology Support Program (2012BAD19B03), the China 973 Program (2010CB126203), the Special Fund for Agro-scientific Research in the Public Interest of China

(201003031), and the Zhejiang Provincial Science and Technology Project (2010C12027).

REFERENCES

1. Boccardo G, Milne RG. 1984. Plant reovirus group. CMI/AAB description of plant. Viruses no. 294. <http://www.dpvweb.net/dpv/showdpv.php?dpvno=294>.
2. 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.
3. Dovas CI, Eythymiou K, Katis NI. 2004. First report of maize rough dwarf virus (MRDV) on maize crops in Greece. *Plant Pathol* 53:238. <http://dx.doi.org/10.1111/j.0032-0862.2004.00973.x>.
4. Milne RG, Lovisolo O. 1977. Maize rough dwarf and related viruses. *Adv Virus Res* 21:267–341. [http://dx.doi.org/10.1016/S0065-3527\(08\)60764-2](http://dx.doi.org/10.1016/S0065-3527(08)60764-2).
5. 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. <http://dx.doi.org/10.1023/A:1011204010663>.
6. Zhang HM, Chen JP, Adams MJ. 2001. Molecular characterization of segments 1 to 6 of rice black-streaked dwarf virus from China provides the complete genome. *Arch Virol* 146:2331–2339. <http://dx.doi.org/10.1007/s007050170006>.
7. 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. [http://dx.doi.org/10.1016/0042-6822\(91\)90065-J](http://dx.doi.org/10.1016/0042-6822(91)90065-J).
8. Wang Q, Yang J, Zhou GH, Zhang HM, Chen JP, Adams MJ. 2010. The complete genome sequence of two isolates of a new rice-infecting fijivirus from China. *J Phytopathol* 158:733–737. <http://dx.doi.org/10.1111/j.1439-0434.2010.01679.x>.
9. 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. <http://dx.doi.org/10.1007/s00705-006-0864-2>.
10. Zhang HM, Yang J, Xin X, Chen JP, Adams MJ. 2007. Molecular characterization of the largest and smallest genome segments, S1 and S12, of rice gall dwarf virus. *Virus Genes* 35:815–823. <http://dx.doi.org/10.1007/s11262-007-0142-8>.
11. Isogai M, Azuhata F, Uyeda I, Shikata E, Kimura I. 1995. Genomic relationships between rice black-streaked dwarf and maize rough dwarf fijiviruses detected by nucleic acid hybridization. *Ann Phytopath Soc Jpn* 61:513–518. <http://dx.doi.org/10.3186/jjphytopath.61.513>.