Accepted Manuscript

Title: Identification and genomic characterization of a novel CRESS DNA virus from a calf with severe hemorrhagic enteritis in China

Authors: Zijing Guo, Qifu He, Cheng Tang, Bin Zhang, Hua

Yue

PII: S0168-1702(18)30376-9

DOI: https://doi.org/10.1016/j.virusres.2018.07.015

Reference: VIRUS 97452

To appear in: Virus Research

Received date: 25-6-2018 Revised date: 20-7-2018 Accepted date: 20-7-2018

Please cite this article as: Guo Z, He Q, Tang C, Zhang B, Yue H, Identification and genomic characterization of a novel CRESS DNA virus from a calf with severe hemorrhagic enteritis in China, *Virus Research* (2018), https://doi.org/10.1016/j.virusres.2018.07.015

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.



ACCEPTED MANUSCRIPT

Identification and genomic characterization of a novel CRESS DNA virus from a calf with severe hemorrhagic enteritis in China

Zijing Guo, Qifu He, Cheng Tang, Bin Zhang and Hua Yue*

College of Life Science and Technology, Southwest University for Nationalities, Chengdu, China.

*Corresponding author:

College of Life Science and Technology, Southwest University for Nationalities, No.16, South 4th Section 1st Ring Road, Chengdu, 610041, China, Phone: (86)-28-85528276; Fax: (86)-28-85528276, E-mail: yhua900@163.com (H. Yue)

Highlights

- A complete genome of a novel CRESS DNA virus with six putative ORFs was determined in diarrheic sample of a calf with severe hemorrhagic enteritis.
- First report of a CRESS DNA virus genome with more than 2 ORFs in bovine.
- The CRESS DNA virus may represent a new virus in the proposed family *Kirkoviridae*.

Depositories: the raw sequence reads from the viral metagenomic libraries have been deposited into as BioProject, Biosample and SRA at NCBI, the accession number were PRJNA389792, SAMN07208491 and SRP108885, respectively. The complete genome

Download English Version:

https://daneshyari.com/en/article/8751681

Download Persian Version:

https://daneshyari.com/article/8751681

<u>Daneshyari.com</u>