Virus Genes (2013) 46:375–376
DOI 10.1007/s11262-012-0861-3

Identification and characterization of a novel subgenotype of bovine viral diarrhea virus isolated from dairy cattle in Northwestern China

Xiaowei Gong · Xiaoan Cao · Fuying Zheng · Qiwei Chen · Jizhang Zhou · Hong Yin · Lihong Liu · Xuepeng Cai

Received: 7 August 2012 / Accepted: 1 December 2012 / Published online: 11 December 2012

Abstract Bovine viral diarrhea virus (BVDV) was detected by RT-PCR in 105 out of 391 samples which were collected from five dairy farms in Ningxia, China during 2010–2011. Non-cytopathogenic BVDV was isolated from 13 samples and a 230-bp fragment of the 5′-untranslated region was amplified and sequenced. While the predominant subgenotypes were BVDV-1b and BVDV-1d, a potentially novel subgenotype was identified by phylogenetic analysis, which may have implications for vaccine development.

Keywords BVDV-1 · Genotyping · Phylogeny · Molecular epidemiology

Bovine viral diarrhea virus (BVDV) is a ubiquitous pathogen that infects domestic animals such as cattle, goats, sheep, and pigs, as well as many wild and captive animals [1]. To date, the BVDV circulating in the Chinese cattle population is mainly BVDV-1b, -1c, -1m, -1p, and BVDV-2a [2–4]. To investigate the prevalence of BVDV in Ningxia Hui Autonomous Region of China, a total of 391 blood samples were collected from five dairy farms, without vaccination history, during 2010–2011, and tested by an RT-PCR method targeting the 5′-untranslated region (5′-UTR).

One hundred and five samples were found positive for BVDV infection. Virus isolation was successful in 13 samples and all isolated viruses were of non-cytopathogenic biotype. Comparative analysis of the 230-bp fragment of the 5′-UTR showed that the 13 isolates shared an identity of 85.2–100 % and had an identity of 85.7–99.6 % between the isolates and BVDV-1 reference strains. The newly determined sequences have been deposited in GenBank under accession numbers JX437146-JX437158. Phylogenetic analysis clustered the 13 isolates into three subgenotypes: BVDV-1b, BVDV-1d, and a potentially novel subgenotype, tentatively designated as "BVDV-1*" (Fig. 1). While BVDV normally causes subclinical infection or mild disease, the cattle which were infected with "BVDV-1*" were characterized by fevers and oral lesions. Further studies are required to confirm an association between these clinical signs and BVDV-1*. This is the first report describing the detection of subgenotypes BVDV-1d and BVDV-1* in the Chinese cattle population, which may have important implications for developing effective BVDV vaccines against the newly identified subgenotypes in China.

X. Gong · X. Cao · F. Zheng · Q. Chen · J. Zhou (✉) · H. Yin · X. Cai (✉)
State Key Laboratory of Veterinary Etiological Biology, Key Laboratory of Veterinary Public Health of Ministry of Agriculture, Lanzhou Veterinary Research Institute, Chinese Academy of Agricultural Sciences, No. 1 Xujiaping, Chengguan, Lanzhou 730046, People's Republic of China
e-mail: zhoujizhang@126.com

X. Cai
e-mail: caixp@vip.163.com

L. Liu
Department of Virology, Immunobiology and Parasitology, National Veterinary Institute, Uppsala 75189, Sweden

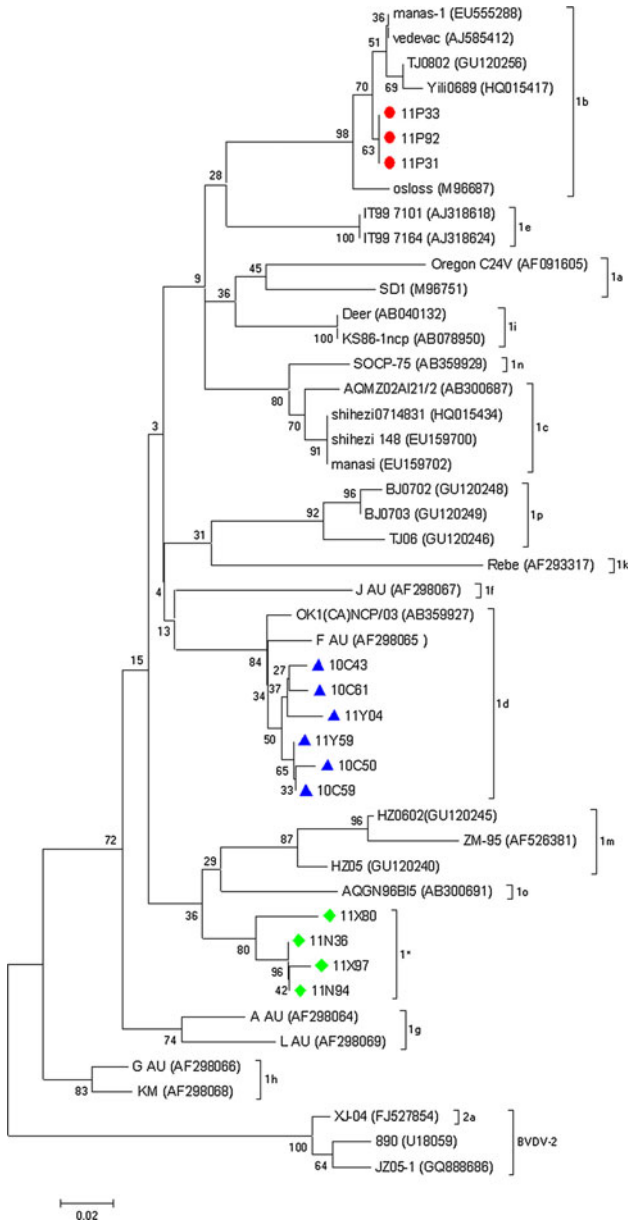

Fig. 1 The phylogenetic tree was generated based on comparison of nucleotide sequences of the 5′-UTR of 13 BVDV isolates with sequences downloaded from the GenBank database. The tree was constructed by the neighbor-joining (NJ) method and a bootstrap test by means of MEGA version 4.1. The *numbers* at the phylogenetic branches indicate the *bootstrap values* (1,000 replicates) in percentage supporting each group. Subgenotype BVDV-1b included three isolates and is indicated in *red*; subgenotype BVDV-1d included six isolates and is indicated in *light blue*; subgenotype BVDV-1* included four isolates and is indicated in *green* (Color figure online)

Acknowledgments This work was supported by the Grants from NBCITS, MOA (CARS-38).

References

1. N. Mishra, S. Vlicek, K. Rajukumar, R. Dubey, A. Tiwari, V. Galav, H.K. Pradhan, Res. Vet. Sci. **84**(3), 507–510 (2007)
2. F.G. Zhong, N. Li, X. Huang, Y. Guo, H.X. Chen, X.H. Wang, C.Q. Shi, X.Y. Zhang, Virus Genes **42**(2), 204–207 (2011)
3. F. Xue, Y.M. Zhu, J. Li, L.C. Zhu, X.G. Ren, J.K. Feng, H.F. Shi, Y.R. Gao, Vet. Microbiol. **143**(2–4), 379–383 (2010)
4. Y.Q. Lin, L.Q. Zhu, J. Tao, H.J. Sun, X.S. Meng, J.Y. Wang, G.Q. Zhu, Chin. J. Prev. Vet. Med. 33(1), 23–27 (2011) (in Chinese)