Complete Genome Sequence of Porcine Reproductive and Respiratory Syndrome Virus Isolated from Piglet Stool Samples

Tao Song,a Liurong Fang,a Songlin Zeng,a Bin Li,a Huanchun Chen,a and Shaobo Xiao*a

Division of Animal Infectious Diseases, State Key Laboratory of Agricultural Microbiology, College of Veterinary Medicine, Huazhong Agricultural University, Wuhan, People's Republic of China,a and Institute of Veterinary Medicine, Jiangsu Academy of Agricultural Sciences, Nanjing, People's Republic of China

WUH4 is a highly pathogenic North American porcine reproductive and respiratory syndrome virus (PRRSV). Unlike previous PRRSV isolates, which were mainly recovered from sera or tissues, WUH4 was isolated from a piglet stool sample. Here we announce its complete genome sequence.

Porcine reproductive and respiratory syndrome (PRRS) is an emerging viral infectious disease characterized by severe reproductive failure in sows and respiratory distress in piglets and growing pigs (6, 9). The causative agent, PRRS virus (PRRSV), is a single-stranded positive-sense RNA virus classified within the family Arteriviridae (3). Since its emergence in the late 1980s, PRRS has continuously been a threat to the global swine industry, causing high economic losses (6, 11, 15). Because PRRSV has a strong tropism for monocyte/macrophage lineages in vivo (4, 12) and PRRSV infection results in persistent viremia (1), previous PRRSV isolates were mainly recovered from serum, lung, or brain (2, 7, 8, 13, 14). PRRSV strain WUH4 was accidentally isolated from a piglet stool sample in China in 2011. An obvious cytopathic effect (CPE), characterized by clumping, shrinkage, and detachment, could be observed in WUH4-infected porcine alveolar macrophages (PAMs). To understand the diversity and the evolutionary characteristics of WUH4, we determined its complete genome sequence.

Fourteen pairs of oligonucleotide primers were designed based on the sequences of PRRSV strains VR-2332 (2) and JXA1 (13) to amplify the different regions of WUH4 genome. The PCR products were cloned into pMD18-T vector (TaKaRa) and sequenced with an ABI3730XL genome sequencer. The terminal sequences were acquired by using a kit for rapid amplification of cDNA ends (RACE) (Clontech, Japan). The sequence data of strain WUH4 were assembled into one contiguous sequence of 15,339 nucleotides, including the poly(A) tail. The genome of WUH4 shared 89.6% and 99.7% sequence identity with the representative North American isolates VR-2332 and VR-2332, respectively. However, compared with the European prototype Lelystad virus (LV) (10), indicating that WUH4 may possess the potential to circumvent immune responses induced by currently used vaccines.

The availability of the genome sequence of WUH4 will facilitate future investigations of the transmission of PRRSV via the fecal-oral route. Furthermore, PRRSV can be recovered from stool samples, which raises the issue of how well PRRSV replicates in the gastrointestinal tract.

Nucleotide sequence accession number. The genome sequence of PRRSV strain WUH4 has been deposited in GenBank under accession number JQ326271.

ACKNOWLEDGMENTS

This work was supported by the “863” project (2011AA10A208) and the National Natural Sciences Foundation of China (30972189 and 31001066).

REFERENCES

8. Li B, et al. 2011. Epidemiology and evolutionary characteristics of the


