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GENOME ANNOUNCEMENT

Complete Genome Sequence of a Reovirus Isolated from Grass Carp, Indicating Different Genotypes of GCRV in China

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A widespread grass carp hemorrhagic disease (GCHD) caused by grass carp reovirus (GCRV) has been known in China since 1983. A virulent reovirus strain, HZ08, was isolated from diseased grass carp in Zhejiang Province, China. We sequenced and analyzed the complete genome of strain HZ08 and compared it with published GCRV genome sequences, contributing to the evidence of several genotypes of GCRV in China.

Grass carp reovirus (GCRV) was first isolated in 1983. The virus causes severe hemorrhagic disease with approximately 85% mortality in fingerling and yearling grass carp, *Cyenopharyngodon idellus*, in China (4). It was assigned to the genus *Aquareovirus* because of its morphology and its genome, which is composed of 11 segments of double-stranded RNA (dsRNA) (7). Seven genetic groups were established, designated aquareovirus A to G (AQRV-A to AQRV-G), and GCRV 873 is considered to belong to AQRV-C (1, 6). In order to understand the genetic diversity and molecular epidemiology of this virus, we report here the complete sequence of all 11 segments of GCRV strain HZ08, from Zhejiang Province, China, that was isolated in 2008.

cDNA copies of the dsRNA genome segments from HZ08 were synthesized, cloned, and sequenced according to a single-primer amplification technique described previously (2). The complete genome of HZ08 is 24,707 bp, and the size of the genome segments typically ranged from 1,027 to 3,927 bp. The 11 segments code for 9 proteins with putative functions and 2 unknown proteins. The lengths of these proteins (in amino acid residues) are 1,294 (VP1), 1,274 (VP2), 1,232 (VP3), 716 (NS79), 726 (VP5), 650 (VP4), 512 (σ1-like protein), 361 (unknown), 418 (VP6), 345 (NS38), and 310 (unknown).

In the family *Reoviridae*, the polymerase is a highly conserved protein (5). The complete segment 2 of HZ08, which codes for polymerase, shares 96.4%, 51.7%, 51.3%, 50.9%, 50.6%, and 49.7% nucleotide sequence identity with GCRV GD108 (AQRV), GCRV 873 (AQRV-C), golden shiner reovirus (GSRV, AQRV-C), American grass carp reovirus (AGCRV, AQRV-G), chum salmon reovirus (CSRV, AQRV-A), and GCRV 104 (unclassified). Although GCRV 873, HZ08, GD108, and 104 were isolated from diseased grass carp in China and GCRV 873 is confirmed to belong to AQRV-C, the classification of these isolates, with the obvious differences in the highly conserved polymerase gene, needs to be further determined.

Except for GCRV 873, HZ08, GD108, and 104, whose whole-genome sequences have been completed, most GCRV isolates have been partially sequenced. The sequence of the VP6 gene has been determined in most submitted isolates and functions in the formation of a continuous capsid shell by clamping with VP3 (3). The phylogenetic relationship of these isolates displayed 3 groups based on VP6. The similarity was less than 20% among the 3 groups, with representative isolates GCRV 873 (group I), HZ08 (group II), and 104 (group III). In group I, the identity among 5 GCRV isolates, 873, 096, 875, 876, and 991, varied from 72.5% to 99.7%, whereas in group II, the identity in isolates HZ08, GD108, and HA-2011 varied from 72.6 to 98.7%. Only one strain of GCRV 104 was in group III; it shared 19.2% and 16.5% identity to GCRV 873 and HZ08, respectively, indicating that several genotypes exist simultaneously in China. The present study will promote a better understanding of the molecular epidemiology and genetic diversity of GCRV field isolates in China.

Nucleotide sequence accession numbers. The complete genome sequence of GCRV HZ08 has been deposited in GenBank under accession numbers GQ896334, GQ896335, GU350742, GU350743, GQ896336, GQ896337, GU350744, GU350745, GU350746, GU350747, and GU350748.

ACKNOWLEDGMENTS

This work was supported in part by the National Special Research Programs for Non-Profit Trades (Agriculture) (grant no. 200803013) and Special Scientific Research Funds for Central Non-profit Institutes, Chinese Academy of Fishery Sciences (grant 2012A0506).

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Received 28 August 2012 **Accepted** 28 August 2012

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doi:10.1128/JVI.02333-12