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GENOME ANNOUNCEMENT

Complete Genomic Sequence of a Muscovy Duck-Origin Reticuloendotheliosis Virus from China

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The complete proviral sequence of a Muscovy duck-origin reticuloendotheliosis virus (REV) associated with spontaneously occurring neoplastic disease in 2011 in Zhejiang province, China, was determined. Comparative sequence analyses indicate that the present REV is most closely related to the chicken-origin REV isolate HLJR0901 and the goose-origin isolate Goose/3410/06. These findings suggest that chickens or geese may transmit the REV to Muscovy ducks.

Reticuloendotheliosis virus (REV) is a member of the genus *Gammaretrovirus* in the family *Retroviridae* (7). The virus can cause immunosuppression, runting disease, and lymphoma in a variety of avian hosts, including chickens, turkeys, ducks, geese, pheasants, peafowl, and some other bird species (3). An epidemiological investigation involving PCR detection of tissue samples from sick or dead ducks randomly selected demonstrated a higher prevalence (55%) of REV infection in duck populations in Shandong province, China (4). In recent years, the occurrence of neoplastic disease was occasionally observed in Muscovy ducks in China.

To date, only one complete genomic sequence of duck-origin REV (GenBank accession number DQ003591) has been reported. The virus, namely, Trager duck spleen necrosis virus (TDSNV), was isolated by Trager from ducks infected with a malaria organism (*Plasmodium lophurae*) (8). To our knowledge, there is no report of a complete sequence of REV associated with the spontaneously occurring neoplastic disease of Muscovy duck.

In the present study, we determined the complete genomic sequence of a Muscovy duck-origin REV isolate (designated 1105) from naturally occurring neoplastic disease in 2011 in Zhejiang province, China. DNA extracted from a liver sample exhibited neoplastic lesions using a tissue DNA rapid-extraction kit (Aidlab, Beijing, China). Most of the proviral genome sequence was generated by nine overlapping DNA fragments amplified using PCR with primers described previously (6) and designed in this study. Sequences of the extreme 5′ and 3′ ends of the REV 1105 proviral DNA were deduced from the 3′-end U3 (unique sequence from the 3′ end of the viral RNA) and the 5′-end U5 (unique sequence from the 5′ end of the viral RNA), respectively.

The complete proviral genome of REV isolate 1105 comprises 8,284 bp. The genes and nucleotide locations are as follows: long terminal repeat (LTR), 1 to 543; primer binding site, 544 to 933; *gag*, 934 to 2,433; *pol*, 2,434 to 6,015; *env*, 5,952 to 7,712; polypurine tract, 7,713 to 7,741; and LTR, 7,742 to 8,284. The precursor proteins predicted from the *gag*, *pol*, and *env* genes are as follows: gag protein, 499 amino acid (aa); pol protein, 1,193 aa; and env protein, 586 aa.

Comparative sequence analyses indicate that the REV 1105 isolate is most closely related to the chicken-origin REV isolate HLJR0901 from mainland China and the goose-origin isolate Goose/3410/06 from Taiwan (2, 3). The most divergent sequence to Muscovy duck-origin REV 1105 is the duck-origin REV TDSNV. These findings suggest that chickens or geese may transmit the REV to Muscovy ducks.

REV, Marek's disease virus (MDV), and avian leukosis virus (ALV) are the main causes of neoplastic diseases in avian hosts. The presence of MDV and ALV in the liver sample was excluded by the methods described by Davidson et al. (1) and Ottiger (5), respectively. It is therefore suggested that the tumor formation in the tissues of Muscovy duck is associated with REV infection.

Nucleotide sequence accession number. The complete genomic sequence of the Muscovy duck-origin REV isolate 1105 has been deposited into GenBank under accession number JQ804915.

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