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# Complete genome sequence of a rodent polyomaviruses in Hainan Island, China

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**Objective:** Polyomavirus infection is reported in a wide range of mammalian and avian hosts, including asymptomatic infection, acute systemic disease, and tumor induction. This study aims to obtain and characterize the complete genome of rodent polyomaviruses, PyVs-HMU. The host of virus was a *Rattus norvegicus* in the residential areas of Hainan Island, China.

**Methods:** The liver samples of *Rattus norvegicus* were collected from the residential areas of Hainan Island, and then processed with a viral particle-protected, nucleic acid purification method. The extracted RNA and DNA were amplified by sequence-independent PCR. The amplified viral nucleic acid libraries for the samples of *Rattus norvegicus* were then sequenced using an Illumina GAI sequencer for a single read of 100 bp in length. The raw sequence reads were then filtered using previously described criteria to obtain valid sequences.

**Results:** We obtained the complete genome of a novel polyomaviruses, PyVs-HMU. The genomic sequence of PyVs-HMU has been submitted in GenBank under accession number MK372231. The complete genome of PyVs-HMU is 5318 nucleotides (nt) in length with a G+C content of 45.36%. The complete PyV-HMU sequences display the representative genome organization of polyomaviruses. The genome contain antigens of spliced small T (STAg), middle T (MTAg) and large T (LTAg), and a noncoding control region (NCCR) separate the late region of structural VP1, VP2, and VP3 proteins. The STAg, LTAg, VP1, VP2, VP3 and MTAg encoded proteins of 194, 776, 384, 347, 228 and 414 amino acids (aa) respectively. Phylogenetic analyses depend on LTAg amino acid sequence revealed that the PyV-HMU to be a relative lineage beside a cluster comprising RnorPyV1(KR065723).

**Conclusions:** The discovery of PyV-HMU expands the geographic range of polyomavirus and will provide further insights into the ecology and evolution of PyVs in rodents and humans. The identification of the novel rodent PyVs will provide basic data for the control of emerging zoonotic infectious diseases.

**Keywords:** Rodents; Polyomavirus; Genomic analysis

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