

# Complete Genome Sequence of Seoul Virus Isolated from *Rattus norvegicus* in the Democratic People's Republic of Korea

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**Seoul virus (SEOV) is responsible for 25% of cases of hemorrhagic fever with renal syndrome in Asia. Here we report the complete genome of strain DPRK08. The sequence information provided here is useful for understanding the molecular character of SEOV in the Democratic People's Republic of Korea (DPRK) and the circulation of SEOV in East Asia.**

Seoul virus (SEOV), a member of the genus *Hantavirus* in the family *Bunyaviridae*, is carried by *Rattus rattus* and *Rattus norvegicus* (4). It has been reported to cause milder disease compared to Hantaan virus and Dobrava-Belgrade virus and is responsible for 25% of cases of hemorrhagic fever with renal syndrome in Asia (3). As *Rattus* species are cosmopolitan, SEOV has the potential to cause human disease worldwide. In East Asia, SEOV was found in China, Far East Russia, South Korea, and Japan, among others (2); however, there is no information in the Democratic People's Republic of Korea (DPRK).

Here we report the complete genome of strain DPRK08. SEOV was isolated from lung tissue by use of the Vero-E6 cell line of *Rattus norvegicus* in Hyesan, DPRK. Standard reverse transcription-PCR was performed with primers specific for SEOV (1). All sequencing was carried out using an ABI 3730 Sanger-based genetic analyzer, and one contig containing a high-quality trace file was assembled using DNASTAR version 7.0.

The genome of SEOV strain DPRK08 is composed of three negative-stranded RNA segments referred to as S, M, and L. The full lengths of the segments are 1,771, 3,651, and 6,530 nucleotides (nt), respectively. The three genes encode proteins with the following amino acid lengths: nucleocapsid, 429; glycoprotein precursor, 1,134; transcriptase protein, 2,152, respectively. A sequence analysis of L, M, and S segments shows that DPRK08 has 95.9%, 96.2%, and 96.8% nucleotide identities to SEOV strain 80-39, isolated in South Korea, and 97.3%, 97.5%, and 96.8% to strain ZT10 in China, respectively. Phylogenetic analysis, which was performed by the neighbor-joining method and maximum likelihood method using MEGA5.05, based on a partial M (nt 2001 to 2301) segment shows that DPRK08 belongs to the S3 subtype (5).

The sequence information provided here is useful for under-

standing the molecular character of SEOV in DPRK and the circulation of SEOV in East Asia.

**Nucleotide sequence accession numbers.** The nucleotide sequence of the SEOV strain DPRK08 genome has been lodged within the GenBank sequence database under the accession numbers [JX853574](#) for the L segment, [JX853576](#) for the M segment, and [JX853575](#) for the S segment.

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