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Genome sequencing and analysis of SFTSVs isolated from patients in South Korea during 2013

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Severe fever with thrombocytopenia syndrome (SFTS) is a new emerging infectious disease in China, Japan, and South Korea. It is caused by SFTS virus (SFTSV), in the genus of Phlebovirus (family Bunyaviridae). The major clinical symptoms and laboratory parameters of SFTS are fever, thrombocytopenia, leukopenia, and elevated serum hepatic enzymes, and SFTS patients usually die due to multiple organ failure. In this study, we conducted the complete or draft genome sequencing of SFTSVs which were isolated from patients in South Korea during 2013. The single-stranded RNA genome comprised of three segments: L, M, and S. All coding sequences for five complete SFTSV sequences (L, M and S segment) and ten draft sequences (M and S) from Korean strains were nearly identical, with sequence similarities of 93.9%–100% for the S segment, 93.2%–99.8% for the M segment, and 96.2-97.6% for the L segment. These strains were compared to strains from two neighboring Asian countries, China and Japan. In phylogenetic analysis, the five Korean SFTSV sequences clustered with all of eight Japanese and three of 102 Chinese (KF374682, KJ597825, JQ670934) strains on the L segment. On the M segment, 12 of 15 Korean sequences grouped with all of eight Japanese and two of 106 Chinese (KF374684, KJ597824) isolates. All coding sequences will be studied further to determine the precise phylogenetic features and the transmission pattern.

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