Urban Rodent Surveillance, Climatic Association, and Genomic Characterization of Seoul Virus Collected at U.S. Army Garrison, Seoul, Republic of Korea, 2006–2010

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Abstract. Rodent-borne pathogens pose a critical public health threat in urban areas. An epidemiological survey of urban rodents was conducted from 2006 to 2010 at the U.S. Army Garrison (USAG), Seoul, Republic of Korea (ROK), to determine the prevalence of Seoul virus (SEOV), a rodent-borne hantavirus. A total of 1,950 rodents were captured at USAG, Yongsan, near/in 19.4% (234/1,206) of the numbered buildings. Annual mean rodent infestation rates were the highest for food service facilities, e.g., the Dragon Hill Lodge complex (38.0 rodents) and the Hartell House (18.8 rodents). The brown rat, *Rattus norvegicus*, accounted for 99.4% (1,939/1,950) of all the rodents captured in the urban area, whereas only 0.6% (11/1,950) of the rodents was house mice (*Mus musculus*). In November 2006, higher numbers of rats captured were likely associated with climatic factors, e.g., rainfall and temperatures as rats sought harborage in and around buildings. Only 4.7% (34/718) of the rodents assayed for hantaviruses was serologically positive for SEOV. A total of 8.8% (3/34) *R. norvegicus* were positive for SEOV RNA by reverse transcription polymerase chain reaction, of which two SEOV strains were completely sequenced and characterized. The 3' and 5' terminal sequences revealed incomplete complementary genomic configuration. Seoul virus strains Rn10-134 and Rn10-145 formed a monophyletic lineage with the prototype SEOV strain 80-39. Seoul virus Medium segment showed the highest evolutionary rates compared with the Large and Small segments. In conclusion, this report provides significant insights into continued rodent-borne disease surveillance programs that identify hantaviruses for analysis of disease risk assessments and development of mitigation strategies.

INTRODUCTION

Emerging or reemerging RNA viruses, e.g., Ebola virus in West Africa, Middle East Respiratory Syndrome virus in East Asia, Zika virus in South America, and Seoul virus (SEOV) in the United States, pose significant worldwide public health threats.^{1–4} The recent outbreaks of these viruses originated from zoonoses and have significantly impacted global economies and public health.^{5,6} Rodents are known to carry a variety of pathogens including viruses, bacteria, and arthropod-associated vectors.^{7–11} The surveillance of rodents in urban areas is critical for the identification and prevention of zoonotic viral outbreaks affecting human health. A recent study identified potential urban threats of viruses and bacteria from rats, *Rattus norvegicus*, in New York City.¹² However, the epidemiological survey of urban threats transmitted by *R. norvegicus* in Seoul, Republic of Korea (ROK), remained to be investigated.

Seoul virus belongs to the genus *Orthohantavirus*, family *Hantaviridae*, order *Bunyavirales* and poses a major public health threat to military personnel, civilians, and family members residing in urban environments.^{13,14} The genome of SEOV consists of negative-sense single-stranded RNA tripartite genomes, including Large (L), Medium (M), and Small (S) segments.¹⁵ The L segment encodes for an RNA-dependent RNA polymerase (RdRp), whereas the M segment encodes for two membrane glycoproteins, Gn and Gc. The S segment of SEOV encodes for a nucleoprotein (N). Seoul virus, harbored by *R. norvegicus* and *Rattus rattus*,

causes hemorrhagic fever with renal syndrome (HFRS) with significant mortality and morbidity in the absence of good medical care. In humans, SEOV infections usually present with a mild to moderate form of HFRS with < 1% fatality and make up about 20% of the clinical HFRS cases reported in the ROK.¹⁶

The incidence of HFRS was shown to be associated with environmental factors, e.g., temperatures, rainfall, and changes in vegetation.^{17–19} Climatic factors influenced the rodent populations as a result of changes in available habitat and food that impact reproduction and numbers of young naive rodents.^{20,21} For example, the El Niño–Southern Oscillation (ENSO) led to outbreaks of hantavirus pulmonary syndrome (HPS) caused by Sin Nombre virus (SNV) as a result of increased densities of *Peromyscus maniculatus*.^{22,23} Higher temperatures that resulted in increased vole populations correlated with an outbreak of Puumala virus (PUUV) infection in Scandinavia and Belgium.^{24,25} By contrast, warmer temperatures during the winter season negatively impacted vole populations by decreasing protective snow cover that resulted in increased predation.²⁶ In China, it was shown that heavy rains decreased rodent populations as a result of habitat reduction, resulting in decreased numbers of HFRS cases.²⁷ Thus, the association of HFRS cases, rodent populations, and climatic factors was applied to the development of models for disease surveillance and the prediction of outbreaks of hantaviruses.^{28–30}

To investigate a biothreat of a rodent-borne hantavirus in an urban environment, the surveillance of small mammals was conducted from 2006 to 2010 at the U.S. Army Garrison (USAG), Seoul, ROK. The prevalence and whole-genome sequences of SEOV were determined and characterized in the rat population. Thus, this report provides a better understanding for characteristics of rat populations and SEOV in the urban area, ROK.

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MATERIALS AND METHODS

Ethics statement. Animal trapping was approved by the U.S. Forces Korea (USFK) in accordance with USFK Regulation 40-1 "Prevention, Surveillance, and Treatment of HFRS" at the U.S. military installations and U.S. and ROK operated military training sites. Captured animals were treated in accordance with the Korea University Institutional Animal Care and Use Committee (KU-IACUC, #2010-212) protocol.

Rodent trapping and climatic data. Rodent trapping was conducted from 2006 to 2010 at buildings on USAG, Yongsan, Seoul, ROK, where rodent infestations were reported to the Pest Control Section, Department of Public Works (DPW), Korea Regional Office, Installation Management Agency (Figure 1). Rodents were captured using live-capture Tomahawk® (Tomahawk Live Trap, Hazelhurst, WI) traps baited with saltine crackers and GOT'CHA™ glue boards (Stone Gotcha Laboratories, Inc., Cicero, IL). Trap index (TI) is the annual mean number of rodents collected for each of the buildings surveyed and was determined as the total number of rodents trapped/5 years. Poison bait stations were routinely placed and serviced quarterly along the perimeter of installation residences and worksites, whereas outdoor (building perimeter) and indoor rodent trapping was conducted when rodent infestations were reported to DPW. The climatic data (rainfall and temperatures)

were provided by Korean Meteorological Administration (www.kma.go.kr).

Rodent handling. Rodents captured in live-capture traps and glue boards were provided to the 5th Medical Detachment/Medical Command Activity-Korea and then transported in secure containers to the Department of Microbiology, College of Medicine, Korea University, Seoul, where the live rodents were maintained in laboratory cages in a biosafety level 3 laboratory until processed. Live rodents were euthanized by cardiac puncture under isoflurane anesthesia in accordance with the approved KU-IACUC protocol and then identified to species by morphological criteria and polymerase chain reaction (PCR) using universal primers, L14115F (5'-CGA AGC TTG ATA TGA AAA ACC ATC GTT G-3') and L14532R (5'-GCA GCC CCT CAG AAT GAT ATT TGT CCA C-3'), for mitochondrial DNA *cytochrome b* gene.³¹ Serum, lung, spleen, kidney, and liver tissues were collected aseptically and frozen at -70°C until used.

Indirect immunofluorescent antibody test (IFAT) for SEOV. Vero E6 cells infected with SEOV strain 80-39 were fixed on 10-well slides with cold acetone for 10 minutes. A total of 25 µL of 1:32 diluted rodent sera in phosphate buffered saline (PBS) were added to each well, followed by incubation at 37°C for 30 minutes. Antigen slides were washed twice with PBS, and 25 µL of fluorescein isothiocyanate-conjugated anti-rat immunoglobulin G (IgG) (ICN Pharmaceuticals, Laval, Canada) were added to each well. After incubating at 37°C for 30

FIGURE 1. Survey area of the U.S. Army Garrison, Yongsan, Seoul, Republic of Korea (ROK). (A) A black circle indicates ROK. (B) A black square indicates Seoul. (C) Building infestation rates; black circles (> 15 rodents/year) and squares (≤ 8–15 rodents/year). Numbers are building number sectors.

minutes and washing, the slides were mounted with glycine-buffered glycerol under cover slips and examined for cytoplasmic fluorescent patterns under a fluorescence microscope (Axio Scope; Zeiss, Berlin, Germany).

RT-PCR for SEOV. Total RNA was isolated from lung tissues of seropositive *R. norvegicus* using the RNA-Bee™ isolation kit (Tel-Test, Inc., Gaithersburg, MD) and then reverse transcribed using Moloney-Murine leukemia virus reverse transcriptase (Promega, Madison, WI). Polymerase chain reaction was performed in 50-μL reactions, containing 10 mM dNTP, 0.5U of Super-Therm Taq polymerase (JMR Holdings, London, United Kingdom) and 5 μM of forward and reverse primers. Oligonucleotide primer sequences for nested PCR were G2F1 (5'-TGG GCT GCA AGT GC-3'), OSS34 (5'-CCA TCA GGG TCT YTC CA-3'), and OSS36 (5'-GCA AAG TTA CAT TTY TTC CT-3') for SEOV M segment. The primer sequences of SEOV S segment were OSV844 (5'-CCG ATG TCC ACC AAC ATG-3'), OSV846 (5'-ATC TAT RTT GCA GGG ATG GC-3'), and OSM55 (5'-TAG TAG TAG AC TCC-3'). For the PCR program, initial denaturation was at 95°C for 5 minutes; followed by six cycles of denaturation at 94°C for 30 seconds, annealing at 37°C for 30 seconds, and elongation at 72°C for 1 minute; and then 32 cycles of denaturation at 94°C for 30 seconds, annealing at 42°C for 30 seconds, and elongation at 72°C for 1 minute, in a Mastercycler ep gradient S (Eppendorf AG, Hamburg, Germany). Polymerase chain reaction products were then purified by QIAquick PCR purification kit (QIAGEN Inc., Chatsworth, CA), and DNA sequencing performed in both directions using each PCR product with the BigDye® Terminator v3.1 cycle sequencing kit (Applied Biosystems Inc., Foster City, CA) on an automated sequencer (Model 3730; Applied Biosystems).

Whole-genome sequencing of SEOV. cDNA was synthesized using random hexamers or OSM55 (5'-TAG TAG TAG ACT CC-3') using a high-capacity RNA-to-cDNA kit (Applied Biosystems). First and nested PCR were performed using primer sets and ProFlex PCR System (Life Technology, Carlsbad, CA) (the primer lists are shown in the Supplemental Tables 1–3). The PCR program was described as mentioned previously (ProFlex PCR System; Life Technology). To complete 3' and 5' terminal genomic sequences, 3' rapid amplification of cDNA ends (RACE) and 5' RACE PCR were performed using 3'-Full RACE Core Set and 5'-Full RACE

Core Set (Takara, Shiga, Japan) according to manufacturer specifications, respectively. The genomic sequences of SEOV were deposited in GenBank (Accession numbers; JF693879–JF693880, JF693882–693885, and MF149936–149937).

Analyses of phylogeny and evolutionary rate. Genomic sequences were aligned and trimmed using the ClustalW tool in the Lasergene program, version 5 (DNASTAR, Inc., Madison, WI) and the multiple sequence alignment with high accuracy and high throughput MUSCLE algorithm in MEGA 6.0.^{32,33} Phylogenetic trees were generated by maximum likelihood method based on the GTR+G model according to the best fit substitution model. Support for the topologies was evaluated by bootstrapping for 1,000 iterations. Evolutionary rates were evaluated as previously described.³⁴

RESULTS

Epidemiological surveillance of rodents captured at USAG, Seoul, ROK.

A total of 1,950 rodents were captured in/near 234 of the buildings surveyed at USAG, Seoul, ROK, from 2006 to 2010 (Table 1). Annual infestation rates were classified as high (> 15 rodents per year), moderate (> 8–15 rodents per year), low (1–8 rodents per year), and very low (< 1 rodent per year). The TI was the highest for 0.9% (2/234) facilities, e.g., Dragon Hill Lodge complex (38.0 rodents per year) and the Hartell House (senior officer's mess hall) (18.8 rodents per year), and accounted for 9.7% (190/1,950) and 4.8% (94/1,950) of all rodents collected in this study, respectively. Although direct exposure to rats may be limited, because of the overall numbers collected, rodent infestation rates for these areas were considered to be high. Trap index for 3.4% (8/234) of the facilities, including dining facilities/snack bars, Seoul Civilian Personnel Advisory Center (adjacent to USAG Yongsan perimeter with Yongsan district of metropolitan Seoul), finance headquarters (adjacent to bus terminal and eating establishment), and family housing that provided harborage and food sources, had moderate annual rodent infestation rates that ranged from 8.4 to 12.2 and accounted for 20.3% (395/1,950) of small mammals captured in the area. A TI < 2.4 for 35.9% (84/234) of the buildings was considered low risk for rodent infestations. About 59.8% (140/234) of the buildings were considered very low risk for rodent infestations where the TI was < 0.4.

TABLE 1

Infestation categories and mean number of rodents captured annually at selected facilities, Yongsan Garrison, Seoul, Republic of Korea, 2006–2010

Category	Total number of Bldgs	Bldgs number	Total number of collected rodents	TI*	Building name
High	2	4050	190	38.0	Dragon Hill Lodge complex
		3724	94	18.8	Hartell House
Moderate	8	2667	61	12.2	KATUSA snack bar
		1435	55	11.0	PX (AAFES)
		4314	53	10.6	Seoul CPAC
		2524	52	10.4	Shappette
		5211	48	9.6	KATUSA snack bar
		1657	42	8.4	Navy club
		2254	42	8.4	Finance HQ near bus terminal
		4610	42	8.4	Family housing
Low	84	NA	1,018	2.4	Various
Very low	140†	NA	253	0.4	Various
Total	234	NA	1,950	1.7	NA

AAFES = Army, Air Force Exchange Services; Bldgs = buildings; CPAC = Civilian Personnel Advisory Center; DPW = Department of Public Works; HQ = headquarter; KATUSA = Korean Augmentation Troops to U.S. Army; NA = not applicable; PX = post exchange; TI = trap index.

* TI = total number of rodents collected for the building surveyed/5 years.

† 11 *Mus musculus* (the house mouse) were captured in #4728 including in the category of Very low.

FIGURE 2. The monthly total number of rodents collected by Tomahawk live cage traps baited with crackers, glue traps, and rat poison (observed dead rodents) at the U.S. Army Garrison, Yongsan, Seoul, Republic of Korea from 2006 to 2010, and monthly environmental data, rainfall, and temperatures, during 2006–2010.

The monthly numbers of *R. norvegicus* captured were highly variable (Figure 2). The total number of captured rodents per month was the highest with 78 *R. norvegicus* during November 2006, corresponding to higher amount of rainfall in July and warmer temperatures in November of that year. In general, the overall rodent TI was the highest in the fall (August–September) and early winter (November) (Figure 3).

Prevalence and genomic characterization of SEOV. A total of 1,939 (99.4%) *R. norvegicus* and 11 (0.6%) *Mus musculus* were captured, respectively (Table 2). Among them, 36.5% (707/1,939) *R. norvegicus* and 11/11 (100%) *M. musculus* were examined for IgG antibodies against SEOV by IFAT. The serological prevalence of *R. norvegicus* was

4.8% (34/707) for anti-SEOV IgG, whereas none of the 11 *M. musculus* were positive. The partial sequences of SEOV M and S segments were identified from 8.8% (3/34) seropositive *R. norvegicus*, including SEOV Rn06-162, Rn10-134, and Rn10-145. Based on the 697 nt-length M segment (coordinates 2,020–2,716 nt) and 619 nt-length S segment (coordinates 1,135–1,753 nt) of SEOV strains, phylogenetic trees demonstrated that SEOV strains from *R. norvegicus* captured at USAG Yongsan in Seoul formed a monophyletic group with SEOV strains 80-39 and Tchoupitoulas, as supported by a high bootstrap probability (Figure 4). The nucleotide identity of SEOV strains for the M and S segments varied ranging from 94.3% to 100% and 93.8% to 100%, respectively, compared with SEOV 80-39.

Whole-genome sequences of SEOV tripartite RNA were determined from two of three SEOV strains, SEOV Rn10-134 and Rn10-145, using conventional RT-PCR and dideoxy-chain termination sequencing according to Sanger et al. The 3' and 5' terminal sequences were determined for SEOV L, M, and S segments by RACE PCR. The 3' and 5' end sequences of SEOV tripartite RNA were 5'-GGAGUCUACUACUA-3' and 5'-UAGUAGUAUGCUCC-3', respectively, showing the incomplete complementarity due to a mismatch at position 9 and a noncanonical U-G pair at position 10 in all three segments. The whole-genome sequences of SEOV Rn10-134 and Rn10-145 consistently formed a phylogenetic lineage with SEOV strains 80-39 and Tchoupitoulas (not shown). The genomic sequences of SEOV L, M, and S segments from SEOV Rn10-134 and Rn10-145 showed 98.1–98.2%, 98.0%, and 98.4% similarities, and the amino acid sequence identity for RdRp, Gn and Gc, and N proteins was 99.4%, 99.4%, and 99.8% with respect to SEOV 80-39. The evolutionary rate of

FIGURE 3. Mean monthly number of rodents collected by three different collecting methods (Tomahawk live cage traps baited with crackers, glue traps, and rat poison [observed dead rodents]) at the U.S. Army Garrison, Yongsan, Seoul, Republic of Korea, from 2006 to 2010.

TABLE 2

Epidemiological survey for SEOV in *Rattus norvegicus* and *Mus musculus* collected at the U.S. Army Garrison, Yongsan, Seoul, Republic of Korea, 2006–2010

Species	Year	Total no. collected	No. (%) tested	IFAT for SEOV (%)*	RT-PCR for Seoul virus (%)
<i>R. norvegicus</i>	2006	447	160 (35.8)	12 (7.5)	1 (0.6)
	2007	403	140 (34.7)	9 (6.4)	0
	2008	411	102 (24.8)	11 (10.8)	0
	2009	314	137 (43.6)	0	0
	2010	364	168 (46.2)	2 (1.2)	2 (1.2)
	Subtotal	1,939	707 (36.5)	34 (4.8)	3 (0.4)
<i>M. musculus</i>	2010	11	11 (100.0)	0	0
Total		1,950	718 (36.8)	34 (4.8)	3 (0.4)

IFAT = indirect immunofluorescent antibody test; SEOV = Seoul virus.

* (Number of positive samples/Number of tested samples) × 100.

whole-genome sequences of SEOV L, M, and S segments, recovered in 2010, was 5.3–5.4E10–04, 6.7E–04, and 5.8E–0.4 (substitution/nucleotide/year), respectively, for 30 years since SEOV was first identified in 1980 (Table 3).

DISCUSSION

Lee et al.³⁵ isolated SEOV from *R. norvegicus* and reported infection rates of 15–30% among rats caught in urban areas of Seoul and Incheon, ROK. The prevalence rate of antibodies by IFAT to Hantaan-like virus (assumed to be SEOV) among 1,986 U.S. Army Soldiers stationed in South Korea during 1982–1983 was 1.2%, similar to that of Seoul residents and ROK Army Soldiers.³⁶ In addition, 5.8% (3/52) of *R. norvegicus* were positive for the Hantaan-like virus at

USAG, Yongsan in 1983. These results coincide with our seroepidemiological survey that showed a 4.8% (34/707) infection rate of SEOV for *R. norvegicus* collected at USAG Yongsan in this study.

Environmental factors, e.g., flooding, rainfall, and temperatures, may impact rodent densities, prevalence of hantaviruses in rodent populations, and incidence of HFRS cases.^{17,27,29,37} Heavy rainfall (precipitation) was associated with the HPS outbreak in the four corners region, southwestern United States.²² The ENSO likely resulted in increased rainfall, leading to the grass seed production and higher densities of *P. maniculatus*, a natural host for SNV. Higher temperatures were correlated with the increased incidence of HFRS caused by PUUV infections that resulted from increased seed production and bank vole densities in

FIGURE 4. Maximum-likelihood phylogenetic cladogram based on a 697 nt-length of the Medium (M) segment and 619 nt-length of the Small (S) segment of Seoul viruses (SEOVs) amplified from *Rattus norvegicus* captured at the U.S. Army Garrison, Yongsan, Seoul, Republic of Korea (GenBank accession numbers; JF693879–JF693885). Branch lengths are proportional to the number of nucleotide substitutions, although vertical distances are for clarity only. The numbers at each node are bootstrap probabilities (expressed as percentages), as determined for 1,000 iterations by MEGA 6.0. The phylogenetic positions of SEOV are shown in relationship to SEOV strains (SEOV 80-39, M: NC_005237, S: NC_005236; SEOV Tchoupitoulas/POR, M: KU204959, S: KU204960; SEOV B1, M: AB457794; SEOV Sapporo rat virus, M: M34882; SEOV 5CSG, M: AB618130; SEOV CSG5, S: AB618112; SEOV LY0852, M: KF387724, S: KF387725; SEOV L99, M: AF035833; SEOV SC106, S: GU361893; SEOV PI26, S: AY006465; SEOV LongwanRn581, M: GU592930, S: GU592946; SEOV ZT10, M: DQ159911, S: AY766368; SEOV Z37, M: AF187081, S: AF187082; SEOV ZT71, M: EF117248, S: AY750171; SEOV Cherwell, M: KM948593, S: KC626089; SEOV Humber, M: JX879768, S: JX879769; SEOV CSG11, S: AB618113; SEOV Singapore06 RN41, S: GQ274944 and other rodent-borne hantaviruses, including Hantaan virus (HTNV 76-118, M: NC_005219, S: NC_005218), Soochong virus (SOOV SOO-1, M: AY675353, S: AY675349), Muju virus (MUJV 11-1, M: JX028272, S: JX028273), Puumala virus (PUUV Sotkamo, M: NC_005223, S: NC_005224), Sin Nombre virus (SNV NMH10, M: NC_005215, S: NC_005216), Tula virus (TULV M5302v, M: NC_005228, S: NC_005227), Prospect Hill virus (PHV PH-1, M: X55129, S: Z49098), Thottapalayam virus (TPMV VRC66412, M: DQ825771, S: NC010704), and Imjin virus (MJNV 05-11, M: EF641798, S: EF641804).

TABLE 3

Percentage of nucleotide and amino acid sequence similarities and evolutionary rates of SEOV identified in *Rattus norvegicus* collected at the U.S. Army Garrison, Yongsan, Seoul, Republic of Korea, 2010

Strains	Percentage of nucleotide and amino acid sequence similarities in SEOV (compared with SEOV 80-39)						Evolutionary rate (substitution/nucleotide/year)		
	L segment		M segment		S segment		L segment	M segment	S segment
	Nucleotide (%)	Amino acid (%)	Nucleotide (%)	Amino acid (%)	Nucleotide (%)	Amino acid (%)			
Rn10-134	98.2	99.4	98.0	99.4	98.4	99.8	5.3E-04	6.7E-04	5.8E-04
Rn10-145	98.1	99.4	98.0	99.4	98.4	99.8	5.4E-04	6.7E-04	5.8E-04

L = large; M = medium; S = small; SEOV = Seoul virus.

Belgium.²⁵ In China, the occurrence of HFRS in humans was shown to be associated with the ENSO, temperatures, and increased vegetation.^{28,38,39} This study showed that the number of *R. norvegicus* captured at USAG Yongsan, Seoul, was the highest in November 2006. Higher rainfall during the dry monsoon season might cause increased densities of the rats and higher numbers of the rats captured. In addition, the unusual high temperatures in November 2006 (8.4°C compared with 6.5–7.6°C of the following years) might have been associated with the high numbers of *R. norvegicus* captured during that 1-month period, which may have been because of an extended breeding season that resulted in higher than average numbers of rodents seeking harborage during the less favorable winter months. The relationship between HFRS incidences and rat populations influenced by climatic factors remains to be further investigated through continued surveillance of the natural hosts and hantaviruses.

In this study, SEOV Rn10-134 and Rn10-145 were completely sequenced, characterized, and compared with the prototype SEOV 80-39. The whole-genome sequences of SEOV obtained from rats collected at USAG formed a phylogenetic group with SEOV strain 80-39 and Tchoupitoulas, demonstrating a high degree of similarity of nucleotide and amino acid levels, respectively. However, the termini of SEOV L, M, and S segments showed incomplete complementarity similar to other hantaviruses.^{40,41} The 3' and 5' terminal sequences in the SEOV tripartite RNA contained a mismatch at position 9 and a noncanonical U–G pair at position 10. The whole-genome sequences of SEOV Rn10-134 and 10-145 were recovered after 30 years since SEOV was first identified in 1980. The evolutionary rate of SEOV L, M, and S segments was 5.3–5.4E-04, 6.7E-04, and 5.8E-04 (substitution/nucleotide/year), respectively, suggesting the M segment was most divergent with respect to SEOV 80-39.

Trap indices provide a baseline for advance warning of potential changes in rodent populations, identify requirements for an active rodent-borne disease surveillance and control programs, and may lead to early diagnosis and interventions through education and awareness of zoonotic diseases, e.g., SEOV-induced HFRS, that significantly reduce morbidity and mortality.⁴² Thus, routine rodent surveillance programs that identify rodent population changes, partially due to man-made activities, in association with the prevalence and distribution of zoonotic pathogens that affect human health should be conducted at urban areas. In addition, rodent-borne disease surveillance identifies harborage areas and provides for developing strategies to reduce rodent infestations

through harborage reduction, proper food storage and waste removal, and sealing outside entrances to prevent entry and exposure of personnel in family housing, food handling facilities, and worksite areas that reduce exposure to zoonotic rodent-borne diseases.

In conclusion, an increased knowledge for the prevalence of SEOV in rodent populations in urban environments provides the need for comprehensive rodent-borne hantavirus surveillance and control programs to prevent a critical public health threat and to develop early diagnosis and interventions that significantly reduce morbidity and mortality due to urban hantavirus infections.

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