Hemorrhagic Fever with Renal Syndrome in 4 US Soldiers, South Korea, 2005

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Four US soldiers acquired hemorrhagic fever with renal syndrome while training near the Demilitarized Zone, South Korea, in 2005. Hantaan virus sequences were amplified by reverse transcription–PCR from patient serum samples and from lung tissues of striped field mice (Apodemus agrarius) captured at training sites. Epidemiologic investigations specified the ecology of possible sites of patient infection.

Hantaan virus (HTNV), the etiologic agent for hemorrhagic fever with renal syndrome (HFRS), accounts for ≈70% of all HFRS cases in South Korea and is the most severe of the 4 rodent-borne hantaviruses (Seoul virus, Soochong virus, and Muju virus) found there (1–3). Recently, a shrew-borne hantavirus, Imjin virus, was isolated from Ussuri white-toothed shrews (Crocidura lasiura) captured near the Imjin River in South Korea (4). The reservoir host of HTNV, the striped field mouse (Apodemus agrarius), is the most abundant field rodent found in South Korea. We conducted an epidemiologic investigation for rodents at 6 training sites near the Demilitarized Zone after 4 US soldiers acquired HFRS in 2005, because no evidence of rodent activity was found where the soldiers worked or resided at their base camp (Camps Hovey and Casey).

The Study

On October 27, 2005, a US soldier (patient 1) assigned to Camp Hovey, Dongducheon, exhibited signs and symptoms of HFRS and so were sent to the BAACH where they received a diagnosis of HFRS (Table 1). Patient 4 from the same unit sought treatment at the Camp Casey Troop Medical Clinic on November 13 with low-grade fever, decreased appetite, abdominal pain, chills, low back pain, nausea, and vomiting, and was provided fluids and assigned to quarters (home bed rest). On November 14, laboratory results indicated a nonspecific proteinuria characteristic of HFRS infections, and the patient was transported to the BAACH, where HFRS was diagnosed. Blood samples from all 3 patients were positive for HTNV by IFA and RT-PCR. All 3 patients had trained at Twin Bridges Training Area (TBTA) with potential incubation periods that ranged from 16 to 35 days, and 2 (patients 2 and 4) had trained together at Rodriguez and Watkins Ranges 3 days before conducting a tactical move to TBTA (Table 1; Figure 1). Patients 2 and 4 conducted training at TBTA-North (N) and TBTA-South (S), and patient 3 only conducted training at TBTA-N.

Small mammal trapping was conducted at US and South Korea–operated training sites where the HFRS patients had previously trained within 60 days. Preseasonal (September) A. agrarius mice trapping rates were relatively low at both FP-60 (11.4%) and Rodriguez Range (7.6%), and although postseasonal trapping rates were high at FP-60...
(42.3%), they remained relatively low at Rodriguez Range (15.7%) (Table 2). During the fall, hantavirus seropositive rates were high at FP-60 (20.0%) and Rodriguez Range (31.3%). During the winter, seropositive rates increased at FP-60 (25.8%), but decreased at Rodriguez Range (12.1%). During the winter, seropositive rates at TBTA-N (26.3%) and TBTA-S (37.8%) were high, but were relatively low at other training sites (LTA320/36/37) surveyed.

Blood samples from each of the 4 patients and lung tissues of seropositive rodents were assayed by RT-PCR. RNA extracted by using RNA-Bee isolation kit (TEL-TEST Inc., Friendswood, TX, USA) was reverse transcribed by using the superscript II RNase H-reverse transcriptase kit (GIBCO-BRL, Gaithersburg, MD, USA). Primers (outer primer set, 5′-TGGGCTGCAAGTGC-3′, 5′-ACATGC TGTACGCTGTGCC-3′; inner primer set, 5′-TGGGCTGCAAGTGCATCAGAG-3′, 5′-AT GGATTACAACCCCAGCTCG-3′) amplified a 373-nt region of the hantavirus G2-encoding medium (M) segment (1,5,6). Amplified products were fractionated according to size by electrophoresis on 1.5% agarose gels containing ethidium bromide (0.5 mg/mL). DNA sequencing was performed in both directions, by using the dye primer cycle sequencing ready reaction kit (Applied Biosystems, Foster City, CA, USA) on an automated sequencer (Model 3730XL; Applied Biosystems).

Phylogenetic analysis, both neighbor-joining and maximum-parsimony methods, based on the 320-nt region of the G2 glycoprotein–encoding M segment of the 4 HFRS patients, and HTNV sequences amplified from the A. agrarius mice captured at FP-10, FP-60, TBTA-N, and TBTA-S demonstrated that the HTNV sequence amplified from patient 1 was identical to sequences from A. agrarius HTNV strain (04–1325) at FP-60. The analyses also demonstrated that the HTNV sequences from patients 2 and 4 were identical to A. agrarius HTNV sequence (05–1437) at TBTA-S, and the HTNV sequence from patient 3 was identical to A. agrarius HTNV sequences (07–196 and 05–1465) at TBTA-N. These data demonstrate the most likely site of infection for the 4 HFRS patients (Figure 2).

### Conclusions

The relationships between rodent density, the proportion of hantavirus-seropositive rodents, and incidence of human infection are complex and poorly understood (7,8). Previous literature indicates that a prevalence of hantavirus seropositivity >20% among A. agrarius mice greatly increased the risk for transmission (9–11). Although monitoring rodent populations may provide some warning, the most effective means of controlling hantavirus infections is
limiting human contact with rodents and the inhalation of dust with virus-laden rodent excreta (12).

The large patches of tall dense grasses narrowly separated by barren ground where artillery firing is conducted at FP-60 provide harborage for A. agrarius mice and, during the winter trapping period, yielded ≈20% capture rates (10). Eliminating these large grassy islands, and thus the rodents that inhabit these areas, and cutting the tall grasses and scrub vegetation to <10 cm along the training site perimeter would decrease hantavirus infection risks by re-

Table 2. Results of rodent-borne disease surveillance at FP 60 and LTAs 36, 37, and 320, Rodriguez Range and Twin Bridges Training Area (South and North Bowls), Gyeonggi Province, South Korea, 2005

<table>
<thead>
<tr>
<th>Location</th>
<th>Spring Trapping rate (%)</th>
<th>Seropositive rate (%)</th>
<th>Summer Trapping rate (%)</th>
<th>Seropositive rate (%)</th>
<th>Fall Trapping rate (%)</th>
<th>Seropositive rate (%)</th>
<th>Winter Trapping rate (%)</th>
<th>Seropositive rate (%)</th>
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</thead>
<tbody>
<tr>
<td>FP 60</td>
<td>21/220 (9.5)</td>
<td>12/89 (13.5)</td>
<td>25/220 (11.4)</td>
<td>5/25 (20.0)</td>
<td>93/220 (42.3)</td>
<td>24/93 (25.8)</td>
<td>26/90 (28.9)</td>
<td>2/26 (7.7)</td>
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<tr>
<td>LTA 36/37</td>
<td>ND</td>
<td>ND</td>
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<td>ND</td>
<td>ND</td>
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<tr>
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<td>ND</td>
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</tr>
<tr>
<td>Rodriguez</td>
<td>38/180 (21.1)</td>
<td>7/29 (24.1)</td>
<td>16/210 (7.6)</td>
<td>5/16 (31.3)</td>
<td>33/210 (15.7)</td>
<td>4/33 (12.1)</td>
<td>19/180 (10.6)</td>
<td>5/19 (26.3)</td>
</tr>
<tr>
<td>TBTA-N</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
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</tr>
<tr>
<td>TBTA-S</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>45/180 (25.0)</td>
<td>17/45 (37.8)</td>
</tr>
</tbody>
</table>

*FP, firing point; LTAs, local training area; ND, not determined; TBTA, Twin Bridges Training Area; N, north; S, south.
†Trapping rate, total number of rodents trapped/number of traps.

Figure 2. Phylogenetic tree by maximum parsimony method, rooted at the midpoint, based on the 320-bp region of G2 glycoprotein—encoding medium segment of 4 hemorrhagic fever with renal syndrome patients who were US soldiers in South Korea (patients 1–4), 2005 (GenBank accession nos. FJ561275–FJ561278) and field mice (Apodemus spp.)–borne Hantaan viruses (HTNV). HTNV sequence amplified from patient 1 was identical with a HTNV sequence (Aa04–1325) from A. agrarius mice captured at firing point (FP) 60. HTNV sequences from patients 2 and 4 were the same as 3 HTNV sequences (Aa05–1437, Aa06–119, Aa06–171) from A. agrarius mice captured at Twin Bridge Training Area—South (TBTA-S), and the HTNV sequence from patient 3 was identical to 11 HTNV sequences (Aa05–1465, Aa07–2, Aa07–21, Aa07–196, Aa07–223, Aa07–280, Aa07–284, Aa07–288, Aa07–306 and Aa07–318) from A. agrarius mice at Twin Bridge Training Area-North (TBTA-N). Branch lengths are proportional to the number of nucleotide substitutions, while vertical distances are for clarity only. The numbers at each node are bootstrap probabilities (expressed as percentages), as determined for 100 iterations by using PAUP version 4.0b (http://paup.csit.fsu.poly). The colors indicate patients and corresponding training sites.
ducing the rodent populations. Efforts to mitigate disease risks through modernization of training sites, cutting of vegetation that increases predation of small mammals, and habitat reduction within 50 m of military operations, where possible, are being instituted at selected US-operated training sites as a result of consolidation and modernization of large, multipurpose range complexes.

Previously, phylogenetic analysis of a 324-nt region of the G2 glycoprotein-encoding M genomic segment has been shown to be representative of the entire M segment (6). This region may be useful for classifying newly identified hantaviruses (when cross-neutralization data are unavailable) or for further analysis of molecular phylogeny of hantaviruses spatially. The genome of HTNV sequences obtained from patient 1 was identical to a viral sequence from an A. agrarius field mouse captured at FP-60 and those from patients 2 and 4 were identical to 3 viral sequences from A. agrarius at TBTA-South, and patient 3 was identical to 11 viral sequences from A. agrarius field mice at TBTA-North. These data showed the epidemiologic link between US soldier patients and rodent hosts at the training sites near the Demilitarized Zone in South Korea.

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Dr Jin-Won Song is a professor of microbiology at Korea University. He has had a long-term interest in the global epizootiology and epidemiology of hantaviruses.

References


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