SEOV strains, 6 of which were from *R. norvegicus* rodents captured in urban areas of North Vietnam. Phylogenetic analysis showed that this SEOV belonged to the Vietnamese SEOV genotype (Figure).

We describe a clinical case of hantavirus infection and its potential rodent reservoir occurring in Vietnam. The clinical manifestations of the case-patient were compatible with SEOV infection, which is responsible for a moderate form of HFRS (*10*). Also, HFRS caused by SEOV occurs in urban rather than rural areas, unlike other hantavirus infections. Our epidemiologic findings were compatible with other studies indicating the source of infection was the case-patient's home, the only place where she had a history of exposure to rodents. Although viral RNA could not be obtained from the case-patient for genotyping, the genomic comparison of the viral strains from rodents captured in the case-patient's home and elsewhere in Vietnam suggested that the source of infection was local rodents. This report provides additional evidence that hantavirus infection is a worldwide problem and is likely underdiagnosed in Vietnam and other countries where simple standardized laboratory diagnostics are not widely available.

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Vu Thi Que Huong, Kumiko Yoshimatsu, Vu Dinh Luan, Le Van Tuan, Le Nhi, Jiro Arikawa, and Tran Minh Nhu Nguyen

Author affiliations: Pasteur Institute, Ho Chi Minh City, Vietnam (V.T.Q. Huong, V.D. Luan, L. Nhi); Hokkaido University Graduate School of Medicine, Sapporo, Japan (K. Yoshimatsu, J. Arikawa); World Health Organization Technical Office, Ho Chi Minh City (L.V. Tuan); and Vietnam Field Epidemiology Training Program Office, Hanoi, Vietnam (T.M.N. Nguyen)

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Address for correspondence: Tran Minh Nhu Nguyen, Vietnam Field Epidemiology Training Program Office, 63 Hoang Cau St, Hanoi, Vietnam; email: tmnn69@yahoo.com

Origin of Highly Pathogenic Porcine Reproductive and Respiratory Syndrome Virus, China

To the Editor: A highly pathogenic porcine reproductive and respiratory syndrome virus (HP-PRRSV), which affected >2 million pigs, emerged in early 2006 in the People's Republic of China. The disease was characterized by high fever (41°C), high illness rates (50%–100%), and high death rates (20%–100%) for pigs of all ages (*1*). A number of HP-PRRSVs have been isolated from 2006 through 2009 from infected pigs in different provinces of China and confirmed to be the causative agent of the new outbreaks (*1*,*2*). These HP-PRRSVs have a deletion of 30 amino acids in nonstructural protein 2 (NSP-2). However, the evolutionary origin and path of the HP-PRRSV remain unknown.

We analyzed the full-length sequences of 67 PRRSVs: 35 HP-PRRSVs (HuN4 and LNSY-08-1 isolated in our laboratory and 33 viruses isolated in other laboratories), 28 classic PRRSVs (18 viruses isolated from China and 10 viruses representing other Asian countries and North

America), and 4 commercially available attenuated live PRRSV vaccine viruses. Except for the 2 viruses we isolated (HuN4 and LNSY-08-1), the full-length sequences of the other 65 viruses were obtained from GenBank. Nucleotide and deduced amino acid sequences of these PRRSVs were aligned and compared by using previous methods (*3*,*4*).

Whole genome–based phylogenetic analysis showed that these 67 PRRSVs could be divided into 4 subgroups (online Appendix Figure, www.cdc.gov/EID/content/16/2/365-appF.htm). Ten classic PRRSVs from China, together with the North American prototype virus VR-2332 and the vaccine virus RespPRRS/Repro modified live vaccine, were classified into subgroup 1. The first Chinese isolate, CH-1a, and its 3 derivatives (CH2002, CH2003, and CH2004) were classified into subgroup 2. All 35 HP-PRRSVs were classified into subgroup 4, and they shared high homology (>99%) in their genomic sequences. The other 4 Chinese PRRSVs, including HB-1(sh)/2002, HB-2(sh)/2002, Em2007, and SHB, belonged to subgroup 3, an intermediate subgroup between subgroups 2 and 4. Phylogenetically, HP-PRRSVs had a close relationship with subgroups 2 and 3.

Four conserved deletions were shown among all HP-PRRSVs, including an adenosine deletion at position 122 in the 5′-untranslated region, a guanosine deletion at position 15,278 in the 3′-untranslated region, and 2 discontinuous deletions in the NSP-2, including a single amino acid deletion at position 482 (L^{482}) and a second deletion of 29 amino acids between positions 533 and 561 (S^{533}–A^{561}). The presence of these 4 deletions among subgroup 4 viruses is a unique phenomenon, which may be used as a distinctive molecular marker for HP-PRRSVs.

The occurrence of these 4 deletions might be explained as a stepwise accumulation from subgroup 2 to subgroup 4. None of the 4 deletions were found in subgroup 2. Among viruses in subgroup 3, one, 2, or 3 of the 4 deletions occurred. For example, a single deletion was present at 122 nt in Em2007, double deletions at 122 nt and 15,278 nt in HB-1(sh)/2002 and SHB, and triple deletions at 122 nt, 15,278 nt, and 482 aa in GD3-2005 (this sequence was not submitted to GenBank until now). In 2008, Ma et al. compared GD3-2005 with several PRRSVs and reported the homology within them, pointing out that the 2 deletions in NSP-2 were identical to the HP-PRRSV (*5*). After careful analysis, we found the GD3-2005 more interesting than what was reported by Ma et al.; it belongs to an intermediate group, and shares the characteristics of gradual evolution. Eventually, all 4 deletions occurred in subgroup 4. This obvious pattern suggests that these 4 conserved deletions might have evolved step by step.

The primary neutralizing epitope (PNE), which is located on glycoprotein 5 and composed of the residues S^{37}H(F/L)QLIYN with F/L^{39} as the binding site for the neutralizing antibody (*6*,*7*), also displayed similar changes at the 39 position among the 4 subgroups. The PNE residues in subgroups 1 (SHL^{39}QLIYN) and 2 (SHF^{39}QLIYN) were considerably conservative. Subgroup 3 contained either F^{39} or I^{39} (F^{39} in Em2007 and HB-2(sh)/2002, and I^{39} in both HB-1-(sh)/2002 and SHB); subgroup 4 contained I^{39} only. The existence of either F^{39} or I^{39} in subgroup 3 PNE indicates its intermediate position between subgroups 2 and 4 in the evolution of HP-PRRSVs.

Pairwise comparison of subgroups 2, 3, and 4 did not find recombination or large fragment replacement, which suggests that all HP-PRRSVs originated from the same ancestor by gradual evolution. Notably, the recently isolated intermediate PRRSVs mentioned above (SHB, Em2007, and GD3-2005) were isolated in the region of South China where the outbreak of HP-PRRS initially occurred. Furthermore, the epidemiologic data show that the outbreak of HP-PRRSV emerged from 1 particular place and then spread widely. This evidence indicates that all HP-PRRSVs isolated in China likely originated from the same source.

In summary, our findings suggest that the newly emerged HP-PRRSVs originated from the Chinese CH-1a-like PRRSV. Further study is needed to determine what contributes to the increased pathogenicity of HP-PRRSV. Although the 4 deletions are conserved in all HP-PRRVs, the increased pathogenicity of HP-PRRSV may not merely be caused by the deletions; pathogenicity is affected by multigenetic factors.

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Tong-Qing An, Zhi-Jun Tian, Yan Xiao, Ran Li, Jin-Mei Peng, Tian-Chao Wei, Yi Zhang, Yan-Jun Zhou, and Guang-Zhi Tong

Author affiliations: Harbin Veterinary Research Institute, Harbin, People's Republic of China (T.-Q. An, Z.-J. Tian, Y. Xiao, R. Li, J.-M. Peng, T.-C. Wei, Y. Zhang, G.-Z. Tong); and Shanghai Veterinary Research Institute, Shanghai, People's Republic of China (Y.-J. Zhou, G.-Z. Tong)

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Address for correspondence: Guang-Zhi Tong, Shanghai Veterinary Research Institute, CAAS, No. 518, Ziyue Rd, Minhang District, Shanghai 200241, People's Republic of China; email: gztong@shvri.ac.cn

Evidence-based Tool for Triggering School Closures during Influenza Outbreaks

To the Editor: I read with interest the recent article by Sasaki et al., "Evidence-based Tool for Triggering School Closures during Influenza Outbreaks, Japan" (*1*), which describes an algorithm for determining the optimal timing of school closures to control influenza outbreaks. The published information is a helpful guide for predicting influenza outbreaks in school settings. However, no data are presented to show the efficacy of school closures after the detection of such outbreaks. As such, the title "Evidence-based Tool for Predicting Influenza Outbreaks, Japan" would more accurately describe the article.

The findings presented by Sasaki et al. (*1*) could be used to help make a decision for school closure or dismissal in places like Japan, but no information is provided on whether this approach is effective in preventing further influenza virus transmission. This is an important distinction and should not change the current school response guidance published by the Centers for Disease Control and Prevention (CDC) (*2*). In general, CDC guidance suggests that during an influenza outbreak, policymakers should weigh the advantages and disadvantages of school dismissals or school closures before making a decision.

Richard L. Vogt

Author affiliation: Tri-County Health Department, Greenwood Village, Colorado, USA

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Address for correspondence: Richard L. Vogt, Tri-County Health Department, 7000 E Belleview, Ste 301, Greenwood Village, CO 80111-1628, USA; email: rvogt@tchd.org

In Response: Vogt (*1*) correctly points out that our article (*2*) did not present data on the effectiveness of school closures to control influenza outbreaks. However, public health agencies continue to support school closure as a nonpharmaceutical response to the ongoing outbreak of pandemic (H1N1) 2009 (*3*) despite little evidence for the appropriate timing of closures, even though it is known that timely action is critical. As the title of our article reflects, our algorithm was designed as an evidence-based tool for supporting the timing of school closures.

In our article, we pointed out that evaluating the impact of school closures is a critical research question. Before April 2009, decision-making regarding school closure in Japan was left to individual schools, 98% of which are public. Since then, recommendations for public school closure have been made according to standardized rules set by the Japanese School Health and Safety Law, leaving final decision-making authority up to local education boards. Our next study will evaluate the effectiveness of this early, standardized timing of school closure in Japan.

On September 24, 2009, the Japanese Ministry of Health, Labor and Welfare presented a school closure plan for use in the different stages of an influenza outbreak; the plan is based on World Health Organization