Province enjoy eating frog meat, particularly from wild frogs, many frogs have been sold in the market, including a substantial number of wild frogs. The results of our survey show that infection of wild frogs with spargana reached 27.3% in western Guangdong Province; hence, consumption of wild frogs (and use as poultices) poses a high risk for sparganum infection. Therefore, public officials, epidemiologists, health medical practitioners, parasitologists, veterinarians, and the general public should be aware of such risks and should implement strategies to reduce or eliminate them.

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References

- Wiwanitkit V. A review of human sparganosis in Thailand. Int J Infect Dis. 2005;9:312–6. DOI: 10.1016/j. ijid.2004.08.003
- Pampiglione S, Fioravanti ML, Rivasi F. Human sparganosis in Italy. Case report and review of the European cases. APMIS. 2003;111:349–54. DOI: 10.1034/j.1600-0463.2003.1110208.x

- Gray ML, Rogers F, Little S, Puette M, Ambrose D, Hoberg EP. Sparganosis in feral hogs (Sus scrofa) from Florida. J Am Vet Med Assoc. 1999:215:204–8.
- Yoon KC, Seo MS, Park SW, Park YG. Eyelid sparganosis. Am J Ophthalmol. 2004;138:873–5. DOI: 10.1016/j. ajo.2004.05.055
- Cho JH, Lee KB, Yong TS, Kim BS, Park HB, Ryu KN, et al. Subcutaneous and musculoskeletal sparganosis: imaging characteristics and pathologic correlation. Skeletal Radiol. 2000;29:402–8. DOI: 10.1007/s002560000206
- Zhou P, Chen N, Zhang RL, Lin RQ, Zhu XQ. Food-borne parasitic zoonoses in China: perspective for control. Trends Parasitol. 2008;24:190–6. DOI: 10.1016/j. pt.2008.01.001
- Ooi HK, Chang SL, Huang CC, Kawakami Y, Uchida A. Survey of *Spirometra erinaceieuropaei* in frogs in Taiwan and its experimental infection in cats. J Helminthol. 2000;74:173–6.
- Fukushima T, Yamane Y. How does the sparganosis occur? Parasitol Today. 1999;15:124. DOI: 10.1016/S0169-4758 (99)01405-2
- Nithiuthai S, Anantaphruti MT, Waikagul J, Gajadhar A. Waterborne zoonotic helminthiases. Vet Parasitol. 2004;126:167–93. DOI: 10.1016/j.vetpar.2004.09.018

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Letters

Letters commenting on recent articles as well as letters reporting cases, outbreaks, or original research are welcome. Letters commenting on articles should contain no more than 300 words and 5 references; they are more likely to be published if submitted within 4 weeks of the original article's publication. Letters reporting cases, outbreaks, or original research should contain no more than 800 words and 10 references. They may have 1 Figure or Table and should not be divided into sections. All letters should contain material not previously published and include a word count.

Human Rhinovirus Group C in Hospitalized Children, Singapore

To the Editor: Human rhinovirus (HRV) is a common etiologic agent of upper respiratory tract infections and is associated with symptoms such as asthma and wheezing. HRV has >100 serotypes, and recently, several groups reported a new HRV group C (HRV-C) in children that is associated with more severe respiratory infections (1-5). We examined the incidence of respiratory viruses in children hospitalized in Kandang Kerbau Women's and Children's Hospital, Singapore (6, 7). These studies also identified human metapneumovirus and human bocavirus (HBoV) among children in Singapore. We recently performed a retrospective study by using PCR-based testing (8) to identify HRV, in particular HRV-C, in these patients. From October 2005 through March 2007, a total of 500 nasopharyngeal swab specimens from pediatric patients (age range 1 month through 12 years) were collected and tested for HRVs.

PCR-based testing identified HRV with an incidence rate of 12.8% (64/500), the highest incidence rate in Singapore, compared with incidence rates of other respiratory viruses reported in the same study (7). Of the HRV-positive patients, 31 (48.4%) of 64 had symptoms of lower respiratory tract infections (LRTIs) and 16 (25%) of 64 had symptoms of upper respiratory tract infections. Ten patients infected with HRV were co-infected with a second respiratory virus, HBoV (8/10) or respiratory syncytial virus (RSV) (2/10).

HRV-C was detected by molecular serotyping as described (3). Briefly, the first PCR was performed with the forward primer P1–1 (5'-CAA GCA CTT CTG TYW CCC C-3') and the reverse primer P3–1 (5'-ACG GAC ACC CAA AGT AG-3'). A second

heminested PCR was performed with forward primer P1-1 but with 3 different reverse primers, P2-1 (5'-TTA GCC ACA TTC AGG GGC-3'), P2-2 (5'-TTA GCC ACA TTC AGG AGC C-3'), and P2-3 (5'-TTA GCC GCA TTC AGG GG-3'). PCR amplicons were sequenced by using the P1-1 primer. DNA sequences were blasted by using the National Center for Biotechnology Information database (Bethesda, MD, USA) and aligned with available sequences by using Clustal X version 1.83 software (www. bips.u-strasbg.fr/fr/documentation/ clustalx). All protocols are available on request.

A phylogenetic tree (GenBank accession nos. FJ645828-FJ645771) was constructed by using neighborjoining method with 1,000 bootstrap replicates and MEGA version 4 software (9). The tree showed similar branching of known HRVs into serogroups (HRV-A, HRV-B, and HRV-C) as described (3). Forty-seven (73%) of the 64 HRV specimens from Singapore were grouped into HRV-A, 9 (14%) into HRV-B, and 2 (3%) into HRV-C. We also found a cluster of 10 HRV-A strains (Figure) diverging from the reference HRV-A strains. This finding suggests that these strains could be new strains of the HRV-A, as reported (3). We could not determine virus subtype for 6 specimens, possibly because of low virus load.

Our results confirm that HRV infections in Singapore are caused mainly by HRV-A. An increase in HRV-C infections with the onset of winter has been reported in the People's Republic of China (26%) (5) and the Hong Kong Special Administrative Region of China (80%) (2). These findings indicate that the incidence of HRV-C infections is seasonal, which may account for the apparent low rates of HRV infection in Singapore. However, the incidence rate for HRV-C infections in Singapore was higher than that for HRV-C infections in Australia

(1.4%) (4), which has a clearly defined winter season.

The 2 patients in which HRV-C was detected had asthma (virus strain SING-06–263) and bronchiolitis (virus strain SING-06–291). These ob-

servations are consistent with reports of HRV-C in patients with severe wheezing (2,4,10). We also detected co-infection with another virus in 10 patients infected with HRV. Of these 10 co-infections, HRV-A was detect-

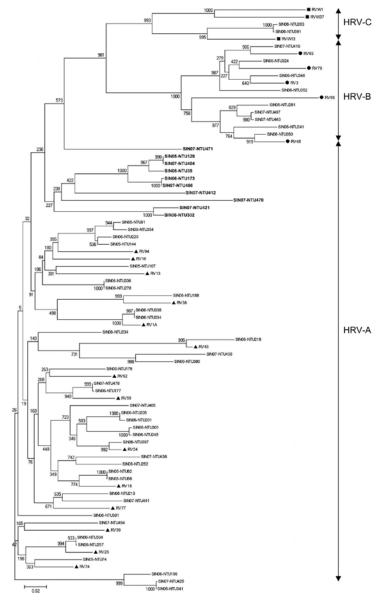


Figure. Phylogenetic analysis of human rhinoviruses (HRVs) from Singapore based on nucleotide sequences of the 5' noncoding region. The tree was constructed by using the neighbor-joining method with 1,000 bootstrapped replicates generated by MEGA version 4 software (9). Sequences (GenBank accession nos. FJ645828–FJ645771) of viruses from Singapore (SIN) are indicated, where the 2 numbers represent the year the specimen was collected, and NTU (Nanyang Technological University) followed by 3 numbers represents the specimen number. Representative strains of HRV-C are indicated by squares, HRV-B by circles, and HRV-A by triangles. RV indicates rhinovirus strains, followed by the serotype no. These sequences were obtained from the report by Lee et al. (3). **Boldface** indicates a cluster of 10 HRV-A strains that diverged from reference HRV-A strains. Scale bar indicates nucleotide substitutions per site.

ed in 7 patients; 5 were co-infected with HBoV (2 patients had LRTIs, 2 had upper respiratory tract infections, and 1 had undefined symptoms), and 2 were co-infected with RSV (both patients had symptoms of LRTIs). Of the other 3 patients co-infected with HRV and HBoV, 1 was infected with HRV-B (had LRTI), 1 with HRV-C (had LRTI), and 1 with an untypeable HRV (had undefined symptoms). Co-infections with HRV and RSV (4,5) and HRV and HBoV (4) have been reported.

Although the clinical role of these co-infections needs to be clarified, these studies suggest that co-infections may result in more severe disease symptoms. The role of HRV-C in causing illness among the children of Singapore will require further study.

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References

Lamson D, Renwick N, Kapoor V, Liu Z, Palacios G, Ju J, et al. MassTag polymerase-chain-reaction detection of respiratory pathogens, including a new rhinovirus genotype, that caused influenza-like illness in New York State during 2004–2005. J Infect Dis. 2006;194:1398–402. DOI: 10.1086/508551

- Lau SK, Yip CC, Tsoi HW, Lee RA, So LY, Lau YL, et al. Clinical features and complete genome characterization of a distinct human rhinovirus (HRV) genetic cluster, probably representing a previously undetected HRV species, HRV-C, associated with acute respiratory illness in children. J Clin Microbiol. 2007;45:3655-64. DOI: 10.1128/JCM.01254-07
- Lee WM, Kiesner C, Pappas T, Lee I, Grindle K, Jartti T, et al. A diverse group of previously unrecognized human rhinoviruses are common causes of respiratory illnesses in infants. PLoS One. 2007;2:e966. DOI: 10.1371/journal.pone.000966
- McErlean P, Shackelton LA, Lambert SB, Nissen MD, Sloots TP, Mackay IM. Characterisation of a newly identified human rhinovirus, HRV-QPM, discovered in infants with bronchiolitis. J Clin Virol. 2007;39:67–75. DOI: 10.1016/j. jcv.2007.03.012
- Xiang Z, Gonzalez R, Xie Z, Xiao Y, Chen L, Li Y, et al. Human rhinovirus group C infection in children with lower respiratory tract infection. Emerg Infect Dis. 2008;14:1665–7. DOI: 10.3201/ eid1410.080545
- Loo LH, Tan BH, Ng LM, Tee NW, Lin RT, Sugrue RJ. Human metapneumovirus in children, Singapore. Emerg Infect Dis. 2007;13:1396–8.
- Tan BH, Lim EA, Seah SG, Loo LH, Tee NW, Lin RT, et al. The incidence of human bocavirus infection among children admitted to hospital in Singapore. J Med Virol. 2009;81:82–9. DOI: 10.1002/jmv.21361
- Hayden FG, Turner RB, Gwaltney JM, Chi-Burris K, Gersten M, Hsyu P, et al. Phase II, randomized, double-blind, placebo-controlled studies of ruprintrivir nasal spray 2-percent suspension for prevention and treatment of experimentally induced rhinovirus colds in healthy volunteers. Antimicrob Agents Chemother. 2003;47:3907–16. DOI: 10.1128/ AAC.47.12.3907-3916.2003
- Tamura K, Dudley J, Nei M, Kumar S. MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. Mol Biol Evol. 2007;24:1596–9. DOI: 10.1093/molbev/msm092
- Miller EK, Edwards KM, Weinberg GA, Iwane MK, Griffin MR, Hall CB, et al. New Vaccine Surveillance Network. A novel group of rhinoviruses is associated with asthma hospitalizations. J Allergy Clin Immunol. 2009;123:98–104. DOI: 10.1016/j.jaci.2008.10.007

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Nondominant Hemisphere Encephalitis in Patient with Signs of Viral Meningitis, New York, USA

To the Editor: Herpes simplex virus (HSV) is the most common cause of sporadic fatal encephalitis across the globe and for all ages. HSV is the etiologic agent of 10%–20% of the 20,000 cases of encephalitis per year in the United States (1); >50%of untreated cases are fatal. Of the 2 types of HSV, HSV-1 and HSV-2, HSV-1 most commonly affects persons 20-40 years of age, whereas HSV-2 commonly affects neonates. This rapidly progressive disease is a common cause of fatal encephalitis in the United States. Signs and symptoms include fever and headache for a few days, followed by confusion, focal deficits, seizures or hemiparesis, hallucinations, and altered levels of consciousness (2). One third of all HSV encephalitis cases afflict children and adolescents. Lumbar puncture typically shows lymphocytic pleocytosis, increased erythrocytes, and elevated protein (2); glucose level is typically within normal limits. Serologic assays often show prior infection. Brain imaging frequently indicates unilateral frontal or temporal lobe abnormalities with edema or hematoma (3,4). The involvement of the nondominant brain hemisphere is associated with atypical signs and symptoms (5). Diagnosis is usually made by using PCR to examine viral DNA in cerebrospinal fluid (CSF) (6). This method of finding DNA in CSF is highly sensitive (98%) and specific (94%-100%). Without therapy, 70% of patients die; with therapy, 20%–30% die (6). Illness includes behavioral sequelae.

A 43-year-old female immigrant from China was admitted to Flushing