and New Zealand (*3–5*,*7*). We were unable to confirm the original source of these isolates, and continuous surveillance for carbapenemase producers in our hospital has not uncovered any $bla_{OXA-181}$–positive isolates since 1996. To our knowledge, there are no reports of $bla_{OXA-181}$–positive isolates in Bangladesh. However, this country borders India, which is a source of $bla_{OXA-181}$–positive *Enterobacteriaceae*. These cases highlight potential problems that may arise from medical tourism (the rapidly increasing practice of traveling across international borders to obtain health care) and document the expanding range of a newly emerging mechanism of carbapenem resistance.

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References

1. Nordmann P, Naas T, Poirel L. Global spread of carbapenemase-producing *Enterobacteriaceae*. Emerg Infect Dis. 2011;17:1791–8.
2. Clinical and Laboratory Standards Institute. Performance standards for antimicrobial susceptibility testing. Document M100–S21. 21st informational supplement. Wayne (PA): The Institute; 2011.
3. Williamson DA, Heffernan H, Sidjabat H, Roberts SA, Paterson DL, Smith M, et al. Intercontinental transfer of OXA-181–producing *Klebsiella pneumoniae* into New Zealand. J Antimicrob Chemother. 2011;66:2888–90. http://dx.doi.org/10.1093/jac/dkr396
4. Potron A, Nordmann P, Lafeuille E, Al Maskari Z, Al Rashdi F, Poirel L. Characterization of OXA-181, a carbapenem-hydrolyzing class D β-lactamase from *Klebsiella pneumoniae*. Antimicrob Agents Chemother. 2011;55:4896–9. http://dx.doi.org/10.1128/AAC.00481-11
5. Castanheira M, Deshpande LM, Mathai D, Bell JM, Jones RN, Mendes RE. Early dissemination of NDM-1- and OXA-181–producing *Enterobacteriaceae* in Indian hospitals: report from the SENTRY Antimicrobial Surveillance Program, 2006–2007. Antimicrob Agents Chemother. 2011;55:1274–8. http://dx.doi.org/10.1128/AAC.01497-10
6. Vogel L, Jones G, Triep S, Koek A, Dijkshoorn L. RAPD typing of *Klebsiella pneumoniae*, *Klebsiella oxytoca*, *Serratia marcescens* and *Pseudomonas aeruginosa* isolates using standardized reagents. Clin Microbiol Infect. 1999;5:270–6. http://dx.doi.org/10.1111/j.1469-0691.1999.tb00140.x
7. Kalpoe JS, Al Naiemi N, Poirel L, Nordmann P. Detection of an ambler class D OXA-48-type β-lactamase in a *Klebsiella pneumoniae* strain in the Netherlands. J Med Microbiol. 2011;60:677–8. http://dx.doi.org/10.1099/jmm.0.028308-0

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Dengue Fever in South Korea, 2006–2010

To the Editor: Dengue fever is an acute, febrile disease caused by a flavivirus and is transmitted by *Aedes* spp. mosquitoes (*1*). South Korea is not considered as a region to which dengue virus is endemic because it is located above 35°N latitude and has an isotherm of 10°C in winter, which potentially limits year-round survival of *Aedes aegypti* mosquitoes (*1*,*2*). Thus, dengue fever was seldom recognized as a public health concern in South Korea. However, the first case of dengue fever in South Korea was reported in 1995 in a woman who had traveled to Sri Lanka (*3*). A second case was found in a sailor who had worked in countries in Africa in 2000 (*4*).

Since 2001, dengue fever has been a notifiable infectious disease in South Korea because of concerns about increasing international travel as a source of infection and because the less efficient potential dengue vector, *Ae. albopictus* mosquitoes, were found in this country. All cases reported through the surveillance system should be complemented by thorough epidemiologic investigations to determine whether a case was imported or originated in South Korea. Thus, we analyzed dengue fever–associated data from the Korea Centers for Disease Control and Prevention.

During 2006–2010, a total of 367 suspected cases were reported by physicians through the National Infectious Disease Surveillance System. IgM ELISA and reverse transcription PCR results identified 324 cases as dengue fever. Investigation of 34 cases could not be completed because some cases were in foreigners and in Korean persons who resided in foreign countries, left South Korea after diagnosis, or could not be reached by the contact information that was provided. Investigation of 290 cases was completed by reviewing medical records and by interviews. Interviews were conducted by provincial and Korea Centers for Disease Control and Prevention Epidemic Intelligence Service officers, who used a standardized investigation form.

All 290 case-patients had a history of international travel before onset of dengue fever symptoms.

Destination information was available for all 290 case-patients; 17 countries were identified. Visitors to the Philippines (34.1%) contributed the largest number of cases, followed by visitors to Indonesia, India, Thailand, Vietnam, Cambodia, Laos, Malaysia, Myanmar, Bangladesh, China, East Timor, Maldives, Palau, Sri Lanka, Brazil, and Nigeria (Table). These countries are in areas to which dengue fever is endemic or have reported cases (*1*).

The time interval between the last day of travel and symptom onset was known for 272 (93.8%) of the 290 case-patients. A total of 271 case-patients had traveled within 14 days before symptom onset, and 89 (32.7%) had symptom onset or were given a diagnosis of dengue fever during travel. Symptoms developed within 7 days after travel in 171 (62.9%) persons and 8–14 days after travel in 11 (4.0%) persons. Mean ± SD duration from the last day of travel to symptom onset among 182 case-patients who had symptom onset after travel was 3.20 ± 2.61 days.

Our results indicate that all investigated case-patients had a history of international travel and times of symptom onset during or after travel but within the incubation period for dengue infection. One case-patient had a time to symptom onset of <34 days. This person was eventually given a diagnosis of infection with Epstein-Barr virus but was tested for dengue virus. Because the incubation period exceeded that for dengue virus incubation, this case was classified as an asymptomatic dengue virus infection and an Epstein-Barr virus infection.

Most dengue cases in South Korea are likely imported, and most presumptive countries from which dengue fever originated are in Southeast and southern Asia. These countries are popular holiday destinations for persons from South Korea. Because of distances, few tourists from South Korea travel to Africa and South America (*5*). China is the most popular destination for travelers from South Korea. However, the proportion of persons who acquired dengue infection in China was low (0.7%) because most persons who traveled to China went to Beijing or Shanghai, not to areas in southern China where dengue epidemics have occurred (*5*,*6*).

We report that all dengue fever cases in South Korea during 2006–2010 were imported by persons who had traveled abroad. Global expansion of dengue virus and an increase in international travelers have increased the likelihood of additional cases of dengue fever. In addition, *Ae. albopictus* mosquitoes have been detected in South Korea and can potentially transmit autochthonous dengue infection, as reported in Croatia, France, and Hawaii, USA (*7*–*9*). Thus, more intensified surveillance and investigations should be focused on dengue transmission by *Ae. albopictus* mosquitoes in South Korea.

Table. Presumptive country of origin of imported dengue fever cases, South Korea, 2006–2010

Region, country	No. (%)
Southeast Asia	242 (83.4)
The Philippines	99 (34.1)
Indonesia	37 (12.8)
Thailand	30 (10.3)
Vietnam	24 (8.3)
Cambodia	17 (5.9)
Laos	6 (2.1)
Malaysia	5 (1.7)
Myanmar	5 (1.7)
East Timor	2 (0.7)
Palau	1 (0.3)
Other	16 (5.5)
Southern Asia	40 (13.8)
India	32 (11.0)
Bangladesh	4 (1.4)
Maldives	2 (0.7)
Sri Lanka	1 (0.3)
Other	1 (0.3)
Eastern Asia	
China	2 (0.7)
Africa	
Nigeria	1 (0.3)
South America	
Brazil	1 (0.3)
Other	4 (1.4)
Total	290 (100)

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References

1. World Health Organization. Dengue and dengue hemorrhagic fever. Factsheet no. 117, revised May 2008 [cited 2012 May 15]. http://www.who.int/mediacentre/factsheets/fs117/en/

2. Tabachnick WJ, Powell JR. A world-wide survey of genetic variation in the yellow fever mosquito, *Aedes aegypti*. Genet Res. 1979;34:215–29. http://dx.doi.org/10.1017/S0016672300019467
3. Kim H, Lee C, Kim M. A case of imported dengue hemorrhagic fever [in Korean]. Korean Journal of Infectious Diseases. 1995;27:403–6.
4. Kwon S, Cho B, Yoon S, Cho Y, Kim I, Chung M, et al. A case of dengue hemorrhagic fever imported from Africa [in Korean]. Korean Journal of Infectious Diseases. 2000;32:467–9.
5. Korea Tourism Organization. 2008 Survey for international travel in Koreans [in Korean]. Korean Tourism Organization, 2009 [cited 2012 May 15]. http://korean.visitkorea.or.kr/kor/t2Main.kto?func_name=t2main
6. Wu JY, Lun ZR, James AA, Chen XG. Dengue fever in mainland China. Am J Trop Med Hyg. 2010;83:664–71. http://dx.doi.org/10.4269/ajtmh.2010.09-0755
7. Gjenero-Margan I, Aleraj B, Krajcar D, Lesnikar V, Klobučar A, Pem-Novosel I, et al. Autochthonous dengue fever in Croatia, August–September 2010. Euro Surveill. 2011;16: pii: 19805.
8. La Ruche G, Souarès Y, Armengaud A, Peloux-Petiot F, Delaunay P, Desprès P. First two autochthonous dengue virus infections in metropolitan France, September 2010. Euro Surveill. 2010;15: pii: 19676.
9. Effler PV, Pang L, Kitsutani P, Vorndam V, Nakata M, Ayers T, et al. Dengue fever, Hawaii, 2001–2002. Emerg Infect Dis. 2005;11:742–9.

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Brucellosis in Takins, China

To the Editor: Brucellosis is a highly contagious bacterial disease and one of the world's major zoonoses. It is responsible for enormous economic losses in livestock, and it threatens human health and wildlife populations (*1*). In most host species, brucellosis primarily affects the reproductive system, leading to concomitant loss in productivity of affected animals (*1*). Brucellae have been found in wildlife, such as bison, elk, and wild boar, potentially posing a threat for zoonosis (*2*). Currently, the genus *Brucella* comprises 10 species, which are divided according to host specificity and ability to cause chronic infections in human and animals (*3*,*4*). Most *Brucella* species are associated primarily with certain hosts, presumably the result of evolutionary adaptation to a successful host. *Brucella melitensis* is the species most pathogenic in humans and the species most commonly involved in ovine and caprine brucellosis.

In January 2009, in the nature reserve in Qinling Mountains, China, hygromas were found on the knees, stifles, hocks, haunches, and bursae between the nuchal ligament and the primary thoracic spines of 10 free-ranging takins (*Budorcas taxicolor*). The hygroma contents and tissue samples were collected by using aseptic technique, packed separately, cooled immediately, and stored frozen at -20°C until cultured. The samples were streaked onto blood agar and MacConkey agar and incubated aerobically or anaerobically with 5% CO_2 at 37°C for 4 days.

Tiny gram-negative coccobacilli were isolated. The organism was nonmotile at 20°C and 37°C, and it stained red with the Stamp modification of the Ziehl-Neelsen method. The organism was identified as *B. melitensis* by the Vitek 2 GN identification system (bioMérieux, Marcy l'Étoile, France). The isolate was urease positive, catalase positive, and oxidase positive. It did not require carbon dioxide for growth and did not produce hydrogen sulfide. The isolate could be agglutinated by A-monospecific antiserum but not by M-monospecific antiserum or rough *Brucella*-specific antiserum. It was sensitive to Berkeley and Iz phages at routine test dilution but not sensitive to Tbilisi, Weybridge, Firenze, and R/C phages. According to classical biotyping methods, the isolate was identified as *B. melitensis* biotype 2 (*5*).

Molecular identification by 16S rRNA gene sequencing was used in this study (*6*). According to nucleotide–nucleotide GenBank search by using BLAST (http://blast.ncbi.nlm.nih.gov/), the sequence was 100% identical to the sequences of 16S rDNA of brucellae, especially reference strains including *B. melitensis* 16M (GenBank accession no. NC_003317), *B. abortus* biovar 1 str. 9–941 (NC_006932), *B. suis* 1330 (NC_004310), *B. canis* American Type Culture Collection 23365 (NC_010103), and *B. ovis* American Type Culture Collection 25840 (NC_009505). The isolate was further confirmed as *B. melitensis* according to the 731-bp product by using AMOS-PCR, which discriminates among species by the unique locations of the IS*711* element (*7*,*8*). The restriction pattern of the *omp2b* gene by *Hin*f I was accordant with pattern 3 reported by Cloeckaert et al. (*9*); this finding further indicated that the isolate was *B. melitensis* (*9*).

The takin (*Budorcas taxicolor*) is a ruminant belonging to the family Bovidae, subfamily Caprinae, genus *Budorcas* (Figure). Takins are found in eastern Asia and Southeast Asia and are listed as "vulnerable A2cd" by the International Union for Conservation of Nature (*10*). Brucellosis might pose a major direct or indirect threat to the conservation of endangered species,