

(97% bootstrap value). The sequence L47 clustered with *L. borgpetersenii* DQ286415 with a high bootstrap value (82%). These results are in accordance with those obtained by Haake et al. (9) based on *lipL32*. Finally, *L. santarosai* sequences formed the third separate clade (100% bootstrap) (data not shown).

Although the method we used does not enable specific identification, determining the most similar species by BLAST is needed for control programs. *L. interrogans* serovar Copenhageni is the predominant infecting serovar among patients with severe leptospirosis (7), and *L. borgpetersenii* is also commonly acquired from mice.

On the basis of these findings, the global distribution of *Leptospira* spp. must be revised to include the Canary Islands, with rodents as natural hosts. Because pathogenic *Leptospira* spp. were detected on every island studied and in both analyzed species, *R. rattus* and *M. domesticus*, the distribution of this pathogen likely extends to even the islands not studied. The high incidence found suggests that rodents play a role in transmission of human leptospirosis. Further studies are needed to identify other possible reservoir hosts and to determine the risk areas for acquiring pathogenic leptospires in the Canary Islands.

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Highly Pathogenic Porcine Reproductive and Respiratory Syndrome Virus, Asia

To the Editor: Recently, the novel and highly virulent variant of porcine reproductive and respiratory syndrome virus (PRRSV), which first emerged in the People's Republic of China and Vietnam in 2006 (1), has rapidly spread in pigs in Southeast Asia. The affected countries include Bhutan, Cambodia, Laos, Malaysia, Myanmar, the Philippines, Thailand, and Singapore. In eastern and northern Asia, South Korea and Russia were also reported to be affected (2) (Figure). The epidemic affected not only large commercial farms but also the backyard industry, which created a serious problem for the global swine industry and for food safety. In February 2011, the Veterinary and Animal Breeding Agency in Ulaanbaatar, Mongolia, confirmed an outbreak of porcine reproductive and respiratory syndrome (PRRS) (3). Nearby neighbors, such as Japan, North Korea, Indonesia, and other Asia-Pacific countries, are also at risk.

PRRS was first reported in the United States in 1987. The disease causes reproductive failure during late-term gestation in sows and respiratory disease in pigs of all ages. In 2006, a new, highly pathogenic PRRS emerged, characterized by high fever (41°C–42°C), skin discoloration/reddening, high incidence of illness (50%–100%), and high proportion of deaths (20%–100%) in pigs of all ages. This new PRRS has spread throughout the swine industry in China, resulting in the culling of an estimated 20 million pigs annually in 2006–2007 in China (4). PRRSV is a member of the family *Arteriviridae* in the order *Nidovirales*, which also



Figure. Areas in Asia where outbreaks of highly pathogenic porcine reproductive and respiratory virus syndrome occurred. The countries or regions affected (North Asia, East Asia, Asia, and South Asia) are indicated. A color version of this figure is available online (www.cdc.gov/EID/content/17/9/110411-F.htm).

includes severe acute respiratory syndrome coronavirus.

PRRSV is a single-stranded positive sense RNA virus that shows high rates of genetic diversity. In the genome of the novel highly pathogenic PRRSV mutant, 4 deletions (2 deletions in nonstructural protein 2, one deletion in the 5' untranslated region, and one deletion in the 3' untranslated region), and some other point mutations, have occurred, which were markedly different from those found in any other previous virus isolate.

After a surveillance study of the epidemic and an analysis of >300 novel highly pathogenic PRRSVs were conducted, the highly pathogenic PRRSV from China was considered to have gradually evolved from CH-1a, a local PRRSV isolate. The evolutionary path could be traced through intermediate PRRSV strains (5). Moreover, we found that highly pathogenic PRRSV has a further enlarged deletion in nonstructural protein 2.

Highly pathogenic PRRSV first emerged in China and Vietnam almost simultaneously in 2006, and

the epidemic focus was in the area between southern China and northern Vietnam (6,7). Although no evidence has shown that the highly pathogenic PRRSV isolate from China or Vietnam has spread in other areas, highly pathogenic PRRS has spread throughout the Malaysian Peninsula to southern Russia.

In addition, all highly pathogenic PRRSV isolates share high sequence identity and have the same deletions as the highly pathogenic PRRSV isolated from China or Vietnam. PRRSV can spread through a variety of routes, including direct contact between pigs, droplet contact through nasal secretions, direct contact with saliva and feces, and indirect contact.

PRRS has spread rapidly around the world through pig sales, semen, and airborne transmission, including from airline passengers who carry the virus on their clothing, shoes, or equipment while traveling (8). In the global market, any virus emerging in the highly pathogenic form is a threat. The risk of highly pathogenic PRRS spreading to other countries is increasing.

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Etymologia: *Pseudoterranova* *azarasi*

To the Editor: Regarding the March 2011 Etymologia on *Pseudoterranova azarasi* (1), we think that someone literally missed the boat on the derivation of *Pseudoterranova*. Although the Greco-Latin amalgam, *Pseudoterranova*, translates to “false new earth,” the generic name of the organism refers to the ship, the *Terra Nova*, which Robert Falcon Scott captained en route to Antarctica exactly 100 years ago in his ill-fated attempt to be the first person to reach the South Pole.

During the Antarctic summer of 1911–12, while Scott and 4 companions trudged toward the South Pole, the ship's surgeon, Edward Leicester Atkinson, who remained with the *Terra Nova*, dissected polar fish, birds, and sea mammals, looking for parasites. Atkinson found an unusual nematode in a shark, and in 1914, he, along with parasitologist Robert Thomson Leiper of the London School of Tropical Medicine, commemorated the ship by conferring the name *Terranova antarctica* upon this newly discovered creature (2).

The genus *Pseudoterranova* was established by Aleksei Mozgovi in 1951 for a somewhat similar nematode obtained from a pygmy sperm whale. *Pseudoterranova azarasi*, the subject of the Etymologia, was originally described in 1942 as *Porrocecum azarasi*, but recent molecular work, as described by Arizono et al. (3) and Mattiucci and Nascetti (4), showed that this nematode is part of a large species complex within *Pseudoterranova*. Thus, it has been transferred to this genus as part of the *P. decipiens* species complex.

The nomenclatural specifics are complex and arcane. However, in this centennial year of the *Terra Nova* expedition, we think it is worthwhile

to remember the historic origins of these names.

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Corrections

Vol. 16, No. 2

Some data were listed incorrectly in Table 1 and the text in the article Epidemiology of *Cryptococcus gattii*, British Columbia, Canada, 1999–2007 (E. Galanis et al.). The article has been corrected online (www.cdc.gov/eid/content/16/2/251.htm).

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References were misnumbered in the Appendix Table of the article *Mycobacterium lentiflavum* in Drinking Water Supplies, Australia (H.M. Marshall et al.). The article has been corrected online (www.cdc.gov/eid/content/17/3/395.htm).

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Vol. 17, No. 6

The abstract of the article Wild Birds and Increased Transmission of Highly Pathogenic Avian Influenza (H5N1) among Poultry, Thailand (Juthatip Keawcharoen et al.) incorrectly referred to the swab samples collected. The article has been corrected online (www.cdc.gov/eid/content/17/7/1202.htm).

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Vol. 17, No. 7

In the article Hansen Disease among Micronesian and Marshallese Persons Living in the United States (P. Woodall et al.), the first paragraph of the Results section should reference 686 total cases of Hansen disease in the United States. The article has been corrected online (www.cdc.gov/eid/content/17/7/1202.htm).

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