viruses showed high nucleotide identities, which suggested that the outbreak viruses in domestic ducks and Baikal teals might have an identical origin. Although research on the epidemiologic features of this outbreak is currently underway, it seems likely that on the basis of reassortant sequence features of the 8 genome segments, these 3 distinct viruses originated in eastern China. These influenza viruses are a potential threat to the poultry population in South Korea, including gallinaceous birds during movement of domestic ducks through the distribution network of live bird markets.

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Possible Misidentification of *Mycobacterium yongonense*

To the Editor: Tortoli et al. (*1*) reported pulmonary disease caused by *M. yongonense* strains isolated from patients in Italy; these strains were identified by sequencing the 16S rRNA, *hsp65*, *rpoB*, and *sodA* genes and the internal transcribed spacer 1 (ITS1) region. The 16S rRNA gene sequence of these isolates showed 100% similarity with those of *M. yongonense* and *M. marseillense*. The isolates were more closely related to *M. yongonense* than to *M. marseillense* in terms of the *hsp65* gene and ITS1 region; however, the *rpoB* gene sequence showed a higher degree of similarity to that of *M. intracellulare* (99.4%) than to that of *M. marseillense* (97.4%). The authors did not mention the similarity of the isolates with *M. intracellulare* in these sequences except for the *rpoB* gene. However, because these sequences showed high similarity to *M. yongonense*, a high degree of similarity to *M. intracellulare* could be inferred.

The initial description of *M. yongonense* highlighted its unique molecular character (*2*). The 16S rRNA and *hsp65* genes and ITS1 region are closely related to those of *M. intracellulare* ATCC 13950^T; however, the *rpoB* gene is closely related to that of *M. parascrofulaceum* ATCC BAA-614^T (99.4%). No consensus guidelines are available for mycobacterial identification, but the *rpoB* gene has been used widely as a target gene; multilocus sequence analysis also has been used recently (*3*,*4*). Although the authors suggest that a variant of *M. yongonense* preceded the acquisition of the *rpoB* gene from *M. parascrofulaceum* by a lateral gene transfer event (*3*), the isolates described are more similar to *M. intracellulare* than to *M. yongonense* on the basis of the *rpoB*

gene sequence and multilocus sequence analysis. It is also possible that the isolates are a *M. yongonense* strain that preceded the acquisition of the *rpoB* gene but that are not the same as the initially described *M. yongonense*.

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etymologia

Zika Virus

Zika [zēk′ ə] Virus

Zika virus is a mosquito-borne positive-sense, single-stranded RNA virus in the family *Flaviviridae*, genus *Flavivirus* that causes a mild, acute febrile illness similar to dengue. In 1947, scientists researching yellow fever placed a rhesus macaque in a cage in the Zika Forest (*zika* meaning "overgrown" in the Luganda language), near the East African Virus Research Institute in Entebbe, Uganda. A fever developed in the monkey, and researchers isolated from its serum a transmissible agent that was first described as Zika virus in 1952. It was subsequently isolated from a human in Nigeria in 1954. From its discovery until 2007, confirmed cases of Zika virus infection from Africa and Southeast Asia were rare. In 2007, however, a major epidemic occurred in Yap Island, Micronesia. More recently, epidemics have occurred in Polynesia, Easter Island, the Cook Islands, and New Caledonia.

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