disease in an immunocompromised patient. However, most cases of *M. fortuitum* pneumonia were reported before the use of molecular technology for species identification. Newer species such as *M. mageritense* resemble *M. fortuitum* and would not have been differentiated without this method.

Our patient met the criteria for diagnosing nontuberculous mycobacterial lung disease as established by the American Thoracic Society and the Infectious Diseases Society of America (*9*). Her therapeutic response also supports a cause-and-effect relationship.

The identity of an RGM isolate as *M. mageritense* may be suspected by its unusual antimicrobial drug susceptibility pattern, which showed an intermediate MIC to amikacin and resistance to clarithromycin at 3 days (Table). However, definitive identification requires molecular methods. Previous studies have shown that *M. mageritense* contains an inducible erythromycin methylase gene (*erm* 40) that confers macrolide resistance (*10*). The use of molecular studies and greater attention to susceptibility patterns should enable increased recognition of *M. mageritense* as a human pathogen.

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Extensively Drug-Resistant Tuberculosis, China

To the Editor: The prevalence of drug-resistant tuberculosis (TB) is a serious problem in the People's Republic of China. China is 1 of 22 countries with the highest incidence of TB (*1*). It is also 1 of 27 countries with the highest incidence of multidrug-resistant TB (MDR TB) and extensively drug-resistant TB (XDR TB). According to the national baseline survey on TB in 2007 and 2008, the frequency of MDR TB among pulmonary TB patients in China was 8.3%. We estimate that there are 120,000 new cases of MDR TB in China per year, which accounts for 24.0% of new cases worldwide (510,000) per year.

XDR TB has recently emerged as a global public health problem (*2*). It is defined as TB with resistance to at least isoniazid, rifampin, a fluoroquinolone, and 1 of 3 injectable second-line drugs (amikacin, kanamycin, or capreomycin). XDR TB is a type of MDR TB that shows resistance to isoniazid and rifampin. Recent reports on current prevalence of XDR TB (*3,4*) indicate that China now has the second highest incidence of MDR TB worldwide. However, there is no information available on XDR TB in China.

To obtain information on XDR TB in China, we conducted a study

at Shanghai Pulmonary Hospital. It is the only specialized hospital for TB in Shanghai and plays a major role in treating TB patients and providing state-of- the-art treatment. Most patients referred to this hospital have been previously treated or have recurrent TB. Therefore, higher rates of MDR TB and XDR TB are expected in this setting, which is not comparable to community or multicenter-based studies.

Patients with culture-proven MDR TB during January 2008–June 2009 were retrospectively evaluated. All patients were HIV negative. Drug susceptibility testing was conducted for culture-positive isolates by using the BACTEC 960 System (Becton Dickinson, Franklin Lakes, NJ, USA) at concentrations of 0.1 μg/mL for isoniazid, 1 μg/mL for rifampin, 5 μg/mL for ethambutol, 1 μg/mL for streptomycin, 2.5 μg/mL for capreomycin, 1μg/mL for amikacin, and 2 μg/mL for ofloxacin.

Among 518 strains that were culture positive for *Mycobacterium tuberculosis*, 350 (67.6%) were drug resistant and 168 (32.4%) were drug sensitive. A total of 217 (41.9%) of 518 strains were classified as MDR and accounted for 62.0% of drug-resistant strains. Among 217 MDR strains, 45 (20.7%) were from patients who had a new diagnosis of TB, and 172 (79.3%) were from patients whose medical history included treatment for TB for ≥4 weeks. A total of 65 (12.6%) strains were XDR, of which 51 were from patients previously treated. These strains accounted for 18.6% of drug-resistant strains and 30.0% of MDR strains.

Of 217 MDR isolates, 217 (100.0%), 217 (100.0%), 172 (79.3%), 175 (80.6%), 170 (78.3%), 68 (31.3%), and 69 (31.8%) were resistant to isoniazid, rifampicin, streptomycin, ethambutol, ofloxacin, capreomycin, and amikacin, respectively. Of 65 XDR isolates, 65 (100.0%), 65 (100.0%), 61 (93.9%), 60 (92.3%), 65 (100.0%), 60 (92.3%), and 60 (92.3%) were resistant to isoniazid, rifampicin, streptomycin, ethambutol, ofloxacin, capreomycin, and amikacin, respectively.

Our results indicate that 30.0% of MDR strains were XDR strains. Although our study was conducted in only 1 hospital, this prevalence of XDR strains indicates that XDR TB in China is a serious concern. A total of 78.3% of MDR isolates were resistant to ofloxacin, which is higher than rates reported for South Korea (42.8%) (*5*) and Taiwan (16.6%) (*6*). Population-based studies have reported lower frequencies of XDR strains among MDR strains; 9.9% for 14 qualified reference laboratories (*7*), 5.3% for South Korea (*8*), and 23.9% for South Africa among patients co-infected with HIV and TB (*9*).

In our study, 2 factors may have contributed to high drug-resistance rates. First, fluoroquinolones have been widely used for treatment of respiratory tract bacterial infections because of their efficacy and mild adverse reactions. Second, we also prescribed fluoroquinolones for treatment of patients with drug-resistant TB and some patients with drug-sensitive TB who could not tolerate first-line anti-TB drugs. More than 90% of patients with XDR TB had strains resistant to streptomycin, ethambutol, capreomycin, and amikacin, which was higher than rates reported in other studies (*5,9,10*). Currently, anti-TB medications in China for treatment of patients with XDR TB are scarce. This scarcity has resulted in poor treatment outcomes in patients with XDR TB.

One limitation of our study is that we investigated patients at only 1 specialized TB hospital in Shanghai. Therefore, data are not representative for the general population. A community-based multicenter study is needed to determine the true prevalence of XDR TB in China. Nevertheless, our study confirms that the prevalence of MDR TB and XDR TB is high in some areas. It also emphasizes the need to increase TB prevention and therapy, educate society about TB, implement modern TB control strategies, and strengthen basic and clinical research to curb the spread of MDR TB and XDR TB.

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Clade 2.3.2 Avian Influenza Virus (H5N1), Qinghai Lake Region, China, 2009–2010

To the Editor: In 2005, a large population of wild migratory birds was infected with highly pathogenic avian influenza (HPAI) virus (H5N1) in the Qinghai Lake region of western People's Republic of China, resulting in the death of ≈10,000 birds (*1,2*). On the basis of phylogenetic analysis of the hemagglutinin (HA) gene, the virus was classified as clade 2.2 according to the World Health Organization guidelines. Subsequently, viruses from this clade were found in Mongolia, Russia, Europe, and Africa along the migratory flyways of birds (*3,4*). This unique distribution of the same clade of HPAI virus (H5N1) through different migratory routes indicates that migratory birds might play a global role in virus dissemination (*3,4*).

In 2006, viruses from the same clade were isolated in the Qinghai Lake region (*3*). Analysis of viral outbreaks along migratory flyways demonstrated a similar outbreak pattern for the past 4 years (2006–2009) (*5*). During that period, clade 2.2 avian influenza virus (H5N1) was isolated in China, Mongolia, Russia, Germany, Egypt, and Nigeria; all viruses were closely related to the Qinghai Lake virus. Despite the broad distribution of clade 2.2 viruses in migratory flyways, few isolates of clade 2.2 viruses in local domestic poultry were reported, especially in China (*6*). Outbreaks of these viruses were reported in poultry in Africa (*7*). The reason these viruses rarely cause outbreaks in poultry is unknown.

During May–June 2009 and 2010, several dead migratory birds were found in the Qinghai Lake region. Nine HPAI viruses (H5N1) were isolated in 2009 and 2 were isolated in 2010 from great cormorants (*Phalacrocorax*

carbo), brown-headed gulls (*Chroicocephalus brunnicephalus*), great black-headed gulls (*Ichthyaetus ichthyaetus*), great-crested grebes (*Podiceps cristatus*), and bar-headed geese (*Anser indicus*) and serotyped as described (*3*). HA genes from all 11 isolates were subsequently amplified by using reverse transcription–PCR and sequenced.

Phylogenetic analysis of HA sequences and an additional HA gene sequence from the 2009 Qinghai Lake subtype H5N1 virus isolate from a great crested grebe (from the National Avian Influenza Virus Reference Laboratory, Harbin, China) (GenBank accession no. CY063318) showed that HA genes from all 12 viruses clustered as clade 2.3.2 (Figure); none clustered with clade 2.2 viruses. Additionally, the HA cleavage site in the new isolates is PQRERRRKRG, which is identical to that of clade 2.3.2 viruses. In clade 2.2, the cleavage site is PQRERRRKKRG.

A bootstrap (1,000×) maximum likelihood tree (*8*) also demonstrated that Qinghai 2009 and 2010 virus isolates are closely related to those isolated in Mongolia and Uvs Nuur Lake in 2009, as reported by Sharshov et al. (*5*). Qinghai Lake and Uvs Nuur Lake, which are found along the migratory flyway in central Asia, are major lakes for bird migration and breeding. Many birds fly from Qinghai Lake to Uvs Nuur Lake in the spring.

If one considers isolation date and bird species infected, viruses isolated in Mongolia and Russia and our isolates were likely transmitted between the 2 lake regions by bird migration. Moreover, HA sequences are closely related to viruses isolated from wild birds in Hong Kong and Japan during 2007–2008, which are the most recent isolates of clade 2.3.2 viruses before isolation of 2009 Qinghai Lake viruses. These results indicate that viruses in the Qinghai Lake region may be transmitted by wild birds along the migratory flyway in eastern