Beijing/W
Mycobacterium tuberculosis in Italy

To the Editor: Molecular typing of Mycobacterium tuberculosis strains isolated in several countries in recent years has shown that a group of strains known as “Beijing” is widespread around the world (1). The Beijing group of M. tuberculosis has been associated with drug resistance; one multidrug-resistant strain, designated “W,” was found in New York City in the early 1990s and caused large institutional outbreaks of tuberculosis (TB) in the United States (2). M. tuberculosis strains of Beijing/W genotype are mostly prevalent in Asia (1), but recent data suggest that they have been spreading in Indochina and are prevalent among younger persons in Vietnam (3). Beijing/W strains are also widespread in Eastern Europe (1); during the last decade, the Beijing/W genotype of M. tuberculosis, with more prevalent drug-resistant mutations than non-Beijing strains, has been identified in 40% to 50% of clinical isolates studied in Russia (4).

We studied a total of 245 M. tuberculosis strains collected during a 1-year period, from January to December 2002, from the same number of TB patients hospitalized in Tuscany, Italy. All the isolates were typed by the standardized IS6110 restriction fragment length polymorphism (RFLP) and the spoligotyping (spacer oligonucleotide typing) techniques. A total of 216 distinct IS6110 RFLP patterns were found among the 245 isolates; 51 isolates (20.8%) occurred in 23 clusters, each constituting strains with an identical IS6110 RFLP and spoligotype pattern; 19 clusters contained two isolates each, 3 contained three isolates, and 1 contained four isolates. Spoligotype analysis showed seven isolates with the typical Beijing/W pattern of probe hybridization only to spacer sequences 35–43. The Beijing/W isolates yielded distinct IS6110 RFLP profiles with similarity coefficient >57.8%. Characteristics of the Beijing/W strains and respective patients, obtained from clinical records, are reported in the Table. Although the overall prevalence of Beijing/W strains was low (7/245, 2.9%), five of the seven strains were from recent immigrants to Italy from China who live in the same area; the other two strains were from Italian citizens also living in that area. Recent immigration from high-prevalence areas is therefore likely to be associated with the occurrence of the Beijing/W genotype in Italy. None of the Beijing/W strains isolated in Tuscany were susceptible to rifampin, ethambutol, pirazinamide, and streptomycin (tested only in two strains), and all but one were susceptible to isoniazid.

Although we detected only a few cases, our data do not show a trend of Beijing/W strains being associated with infection in young people, as has been observed in other settings (3). The age of immigrants with Beijing/W TB (mean 33.2 years, standard deviation [SD] 8.2 years) did not significantly differ from that of immigrants infected with non-Beijing/W strains (30.7 years, SD 7.4 years), a find that indicates that, at least in our setting, immigrant status, rather than M. tuberculosis genotype, is associated with infection in young people. The few cases of Beijing/W infections in Italian-born patients do not allow us to draw conclusions regarding non-immigrant patients.

In conclusion, M. tuberculosis strains of Beijing/W genotype are becoming widespread worldwide, including in countries with a low prevalence of TB. Their association with drug resistance and infection in young people, clearly shown in certain settings, remains to be defined. Further molecular epidemiologic surveillance is needed to monitor trends in prevalence and spread of these strains.

Table. Characteristics of Mycobacterium tuberculosis strains of Beijing/W genotype isolated in 2002 in Tuscany, Italya

| Strain no. | Patient’s country of birth | Sex | Age | HIV status | Years in Italy | Site of TB     | Drug resistanceb |
|-----------|---------------------------|-----|-----|------------|----------------|----------------|-----------------|
| 669       | China                     | M   | 40  | –          | 1              | Pulmonary      | S S S S S      |
| 763       | China                     | M   | 42  | –          | <1             | Pulmonary      | S S S S S      |
| 804       | China                     | F   | 23  | –          | 4              | Pulmonary      | NT S S S S     |
| 836       | China                     | M   | 34  | –          | 1              | Pulmonary      | NT S S S S     |
| 884       | Italy                     | F   | 39  | +          | NA             | Extrapulmonary | NT S S S S     |
| 952       | Italy                     | F   | 28  | –          | NA             | Pulmonary      | NT R S S S     |
| 974       | China                     | F   | 27  | –          | 1              | Pulmonary      | NT S S S S     |

aTB, tuberculosis; Str, streptomycin; Inh, isoniazid; Rif, rifampin; Eth, ethambutol; Pza, pirazinamide; S, susceptible; R, resistant; M, male; F, female; NA, not applicable; NT, not tested.
bDrug resistance was assessed by the radiometric BACTEC system (Becton Dickinson, Towson, MD) according to the proportion method.
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References
1. Glynn JR, Whiteley J, Bifani PJ, Kremer K, van Soolingen D. Worldwide occurrence of Beijing/W strains of Mycobacterium tuberculosis: a systematic review. Emerg Infect Dis 2002;8:943–9.
2. Bifani PJ, Mathema B, Liu Z, Moghazeh SL, Shopsin B, Tempalski B, et al. Identification of a W variant outbreak of Mycobacterium tuberculosis via population-based molecular epidemiology. JAMA 1999;282:2321–7.
3. Anh DD, Borgdorff MW, Van LN, Lan NT, van Gorkom T, Kremer K, et al. Mycobacterium tuberculosis Beijing genotype emerging in Vietnam. Emerg Infect Dis 2000;6:302–5.
4. Mokrousov I, Otten T, Vyazovaya A, Limeschenko E, Filipenko ML, Sola C, et al. PCR-based methodology for detecting multidrug-resistant strains of Mycobacterium tuberculosis Beijing family circulating in Russia. Eur J Clin Microbiol Infect Dis 2003;22:342–8.
5. Diaz R, Kremer K, de Haas PE, Gomez RI, Marrero A, Valdivia JA, et al. PCR-based methodology for detecting multidrug-resistant strains of Mycobacterium tuberculosis Beijing family circulating in Russia. Eur J Clin Microbiol Infect Dis 2003;22:342–8.
6. Stavrinides J, Guttman DS. Mosaic evolution of infectious diseases. Nature 2003;425:915.

To the Editor: Martina et al. reported that domestic cats and ferrets are susceptible to infection by severe acute respiratory syndrome (SARS)-associated coronavirus (SARS-CoV) isolated from a patient infected with SARS. These infected animals could efficiently transmit the virus to uninfected animals housed with them (1). This finding is similar to that of SARS transmission in humans in which SARS-CoV can be quickly spread from person to person through close contact. Ferrets and domestic cats not only can be infected by SARS-CoV in the laboratory, but also can shed SARS-CoV from the pharynx at 2 days postinfection and continuing through 10 and 14 days postinfection, respectively (1). No clinical signs were observed in six cats that were injected with SARS-CoV, whereas three of six ferrets that were injected with SARS-CoV became lethargic within 2 to 4 days postinfection, and one of the three ferrets died at day 4 postinfection (1,2). This finding indicates that domestic cats may not only be a useful animal model for evaluating candidate vaccines and drugs against SARS (1) but also may be good reservoirs of SARS-CoV. Domestic cats living in the Amoy Gardens in Hong Kong, where >100 residents contracted SARS in the spring of 2003, were infected with SARS-CoV (1,3). This fact suggests that domestic cats can be naturally infected with SARS-CoV from humans infected with SARS, although how this SARS-CoV transmission occurs is unclear. Unfortunately, however, the transmission capability of the SARS-CoV strain transmitting from domestic animal to human, despite the widely accepted hypothesis of the animal origin of SARS-CoV (4–6), cannot be ascertained. If the transmission of SARS-CoV from animal to human is as easy as that from humans to domestic cats, the speculation that the outbreak of SARS in the Amoy Garden in Hong Kong was caused by environmental sources, such as U-traps in bathrooms contaminated with SARS-CoV (3), we should reevaluate, because this outbreak of SARS in these apartments might also be caused by infected cats or other mammalian hosts.

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References
1. Martina BE, Haagmans BL, Kuiken T, Fouchier RA, Rimmelzwaan GF, Van Amerongen G, et al. SARS virus infection of cats and ferrets. Nature 2003;425:915.
2. Kuiken T, Fouchier RA, Schutten M, Rimmelzwaan GF, Van Amerongen G, van Riel D, et al. Newly discovered SARS-CoV coronavirus as the primary cause of severe acute respiratory syndrome. Lancet 2003;362:263–70.
3. World Health Organization. Severe acute respiratory syndrome (SARS)—multi-country outbreak [monograph on the Internet]. [cited 2003 Apr 18] Update 33. Available from: http://www.who.int/csr/don/2003_04_18/en/
4. Huang Z, Wang X, Nie J, Xu L, Zhang XZ, Cheung CL, et al. Isolation and characterization of SARS virus from animals in southern China. Science 2003;302:276–8.
5. Antia R, Regoes RR, Koella JC, Bergstrom CT. The role of evolution in the emergence of infectious diseases. Nature 2003;426:658–61.
6. Stavrinides J, Gutman DS. Mosaic evolution of severe acute respiratory syndrome coronavirus. J Virol 2004;78:76–82.

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