Study Letters

Failure to detect *Mycobacterium lepromatosis* as a cause of leprosy in 85 Chinesepatients

Sir,

Leprosy was long believed to be caused by a single pathogenic agent, *Mycobacterium leprae* until 2008, when a new species named *Mycobacterium lepromatosis* was identified to cause diffuse lepromatous leprosy (DLL) in a Mexican population.[1] *M. lepromatosis* has also been reported in other forms of leprosy, or as a dual infection with *M. leprae*.[2] Apart from Mexico, there are also reports of the new species from Singapore and Canada.[3] This study aimed to identify the existence of *M. lepromatosis* in Chinese leprosy patients.

We performed genetic analysis of the organism in 85 Chinese leprosy cases in Shandong province (tuberculoid leprosy [TT] $n = 2$; borderline tuberculoid leprosy [BT] $n = 5$; borderline lepromatous leprosy [BL] $n = 34$ and lepromatous leprosy [LL] $n = 44$). DNA was extracted from archived formalin-fixed and paraffin-embedded skin biopsy specimens. The 16S rRNA gene of *Mycobacterium* was selected as the polymerase chain reaction (PCR) target. Two rounds of semi-nested PCRs were performed. The amplicons were examined by electrophoresis, then products were purified and directly sequenced.

Of the 85 skin biopsies of leprosy patients, 72 (84.7%) were confirmed to be infected by mycobacteria by the first-round PCR analyses. All of the mycobacteria-positive samples were identified to be infected with *M. leprae*, while the other 13 patients were PCR-negative. The PCR-negative result might be due to DNA fragmentation that occurs during formalin fixation and paraffin embedment of tissue which may not allow successful amplification if DNA is insufficient. We could not identify any sample infected with *M. lepromatosis* in the second-round PCR analyses.

One reason for the negative result may be related to the geographic variability of species. The regional difference in the distribution of *M. lepromatosis* and *M. leprae* may be a reason for the remarkable geographic variation of different forms of leprosy. For example, in Africa, nearly 90% of cases are tuberculoid (TT) leprosy, in North America 90% of cases are lepromatous leprosy (LL); whereas in Southeast Asia, the two forms are equally distributed.[4] Because there is a marked variation in clinical types of leprosy between China and Mexico, it is possible that *M. lepromatosis* might not exist in China. Moreover, *M. lepromatosis* was first discovered in diffuse lepromatous leprosy (DLL), which manifests as a diffuse cutaneous infiltrate with no nodule or plaque formation. It is believed that *M. lepromatosis* specifically causes diffuse lepromatous leprosy, an uncommon form of leprosy with only occasional cases reported worldwide, including Asia, Africa, North America, and South America. In our study, we failed to include this form of leprosy which may be responsible for our inability to identify the species. This is a major limitation of our study.

To conclude, we have not been able to identify the new species *M. lepromatosis* in Chinese leprosy cases.

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