Mycobacterium tuberculosis and nontuberculous mycobacteria isolates from HIV-infected patients in Guangxi, China

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Guangxi Zhuang Autonomous Region is located in the southern of China.
Location

- Guangxi shares the border with Vietnam
- Area is 236,000 square kilometers.
- The mountains and hills areas account for around 70% of total area.
Population

• Total population 50 millions.

• 38% are minorities.

• Most minorities live in mountains and hill areas.
BACKGROUND

• China is one of the 22 countries with a high Tuberculosis (TB) burden recognized by the WHO, and has a growing epidemic of HIV.

• The No. of Guangxi HIV(+) arranges the second in China. Guangxi has a high burden of TB and HIV/AIDS.

• The prevalence of infection with *Mycobacterium tuberculosis* (*M. tuberculosis*) and nontuberculous mycobacteria (NTM) in HIV-infected patients in China is unknown.
OBJECTIVE

• Estimate the prevalence of *M. tuberculosis* and NTM in HIV-infected patients in the Guangxi province

• Determine the drug resistance profiles of *M. tuberculosis*

• Evaluate the genotype patterns of strains of *M. tuberculosis*. 
DESIGN

• The sample was collected from two HIV designated hospitals in Guangxi from 2005 to 2008.

• HIV-infected patients with mycobacterial culture positive were included. All isolates were cultured on a BacT/Alert 3D Microbial Detection System (bioMerieux) and on Lowenstein-Jensen (L-J) medium. Drug susceptibility testing was performed by proportion method.

• NTM species was identified by sequencing of the 16SrRNA and *M. tuberculosis* isolates were genotyped by the VNTR method.
RESULTS

Study patients and isolates

• From 2005 to 2008, 1233 HIV-infected patients were screened for TB infection. Eighteen percent (n=219) of these had a clinical specimen that was culture positive for *Mycobacterium* species.

• *M. tuberculosis* was identified in 117 (53%) patients, NTM was isolated in 102 (47%) patients. Most of the isolates (96%) were of pulmonary origin. There was no significant difference in the demographic characteristics of patients with *M. tuberculosis* and NTM.
RESULTS
Species identification

• CD4 counts was available for 154 (70%) patients: the median count was 35 cells/mm³, patients with NTM strains were more likely to be associated with lower CD4 counts ($P = 0.01$).

• 12 NTM species were identified from the 102 NTM isolates. The most frequent organism was *M. avium* complex (MAC, 54%).
RESULTS

Drug resistance profiles of M. tuberculosis isolates

- 111 (95%, 111/117) M. tuberculosis isolates with available DST results, 30 (27%) were resistant to at least one first-line anti-TB drug, of which 67% (n=20/30) of patients were new TB cases.

- 12 (11%) patients had MDR-TB. MDR-TB was diagnosed in 40% (n=8/20) of previously treated TB cases and in 4% (n=4/91) of new TB cases.

- 12 MDR-TB patients were younger than 45 years of age.
RESULTS

Genotype patterns of *M. tuberculosis* isolates

- 117 *M. tuberculosis* isolates, 105 different VNTR genotype patterns were identified.

- 97 (83%) isolates had unique genotype patterns and 20 (17%) isolates were identified as cluster strains which belonged to 8 different clusters.

- Beijing family strains accounted for 67% (n=78/117) of *M. tuberculosis* isolates.

- 74% (n=58/78) of isolates from patients aged <40 years were of Beijing genotype.
CONCLUSION

• High frequency of NTM among HIV-infected patients raised concerns about the accurate species identification before treatment.

• The high rate of MDR-TB in previously-treated HIV-infected patients indicates the need for effective management and treatment of patients with both TB and HIV.
Thank you!
Welcome to Guangxi!