Author's response to reviews

Title: Genotyping and clinical characteristics of multidrug and extensively drug-resistant tuberculosis from a tertiary care tuberculosis hospital in China

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Author's response to reviews: see over
Dear Editor:

We thank you and the Reviewers for re-reviewing of our manuscript (MS: 1204211201862874), entitled “Genotyping and clinical characteristics of multidrug and extensively drug-resistant tuberculosis in a tertiary care tuberculosis hospital in China”. Please find enclosed the revised manuscript, which has been changed in response to the Reviewers comments. Our answers (in black text) on Reviewers comments (in blue text) are listed below.

Sincerely Yours,

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1. The authors need to indicate clearly how this work is different from their own work published in J Clin Microbiol 2012; 50:2404 and what is the new information included in this work.

In our previous work (J Clin Microbiol 2012;50:2404), we investigated the prevalence and pattern of mutations occurred to the drug target loci ($rpoB$, $katG$, $mabA-inhA$, $gyrA$, $gyrB$, and $rrs$) among the 77 multidrug-resistant and extensively drug-resistant (MDR and XDR, respectively) strains of *Mycobacterium tuberculosis* from Jiangxi province, China. In addition, we identified the genetic lineage of the 77 isolates using the 15-locus MIRU-VNTR genotyping method. About this, Please see Page 4, lines 85-87 in the revised manuscript.

Of the 123 strains used in this work, 69 strains (59 MDR and 10 XDR) were also used in our previous work (J Clin Microbiol 2012; 50: 2404). About this, Please see Page 9, lines 189-190 in the revised manuscript.

In the present work, we have investigated the clinical features of 123 patients with MDR or XDR TB diagnosed at the Jiangxi Chest Hospital, and further evaluated the discriminatory power of 15-locus MIRU-VNTR method for genotyping the 123 MDR or XDR strains (including 59 MDR and 10 XDR strains used in our previous work).

Based on a hospital-based survey of drug-resistant cases, we found that the rate of MDR TB was 19.8% and that 10.6% of MDR cases were XDR. Although data from a specialised TB hospital is not representative of Jiangxi Province as a whole, our data suggest that the emergence of MDR and XDR TB may be a severe problem and that TB control is a major concern for the region. We also found that most MDR and XDR TB patients were between 20 and 59 years old, with a peak frequency between 40 and 59 years old, and that diabetes mellitus was the most common comorbidity in both
MDR (16/110, 14.5%) and XDR (2/13, 15.4%) tuberculosis patients. In addition, the discriminatory power of the 15-loci MIRU-VNTR method was very high for genotyping the 123 MDR and XDR strains from Jiangxi Province. Furthermore, 14 of the 15 loci investigated in this work (excluding ETR-C) showed relatively moderate or high discrimination ($h>0.3$). These results indicate that ETR-C may not suitable for the genotyping of the *M. tuberculosis* strains circulating in Jiangxi province. The 123 strains investigated in this work showed great genetic diversity and a low clustering percentage. However, we noted that more than one-fifth of the MDR and XDR TB patients were new cases, which may have been caused by the active transmission of drug-resistant TB. Thus, decisive measures are urgently needed to effectively prevent and manage MDR and XDR tuberculosis in this province.

2. Quality of written English: Needs some language corrections before being Published.

We have re-modified our manuscript in response to the comments and suggestions from the reviewers. Please note that many of the changes in revised manuscript were made to reduce wordiness and improve the flow of the paper. We would like to thank Adane Mihret for his (her) suggestions.

**Reviewer:** Dhammika Magana-Arachchi

1. Discretionary Revisions

We agree with this revision and the sentence was rewritten. Please see Page 5, lines 94-97 in the revised manuscript. Thank you!