Reviewer’s report

Title: Recent-Transmission of Mycobacterium tuberculosis (MTB) strains among Iranian and Afghan Treatment failure Cases: Use of IS6110-Fingerprinting

Version: 2 Date: 21 February 2008

Reviewer: Christophe Sola

Reviewer’s report:

1. Is the question posed by the authors well defined?

The goal of the study was to distinguish real relapses from recent transmission (reinfection) cases in a total of 258 cases recruited during 2006-2007 and considered as retreatment cases. However, there is no definition of new cases versus retreatment cases nor any initial genotyping data (first sample).

2. Are the methods appropriate and well described?

Yes and No. There are much more efficient methods (association of spoligotyping to MIRU-VNTR typing to get a better discrimination on 258 cases. IS6110-RFLP should not be considered as a golden standard anymore since more than 5 years. There are internationally agreed standardized methods that suggests that IS6110-RFLP should only be performed on a limited amount of DNAs that remain identical after VNTR5+MIRU12+spoligo (english standard, see Hawkey et al. JCM 2004) or on MIRU24+spoligo (Supply et al. standard JCM 2006)

3. Are the data sound?

Yes, but of limited value.

4. Does the manuscript adhere to the relevant standards for reporting and data deposition?

Yes

5. Are the discussion and conclusions well balanced and adequately supported by the data?

No. Any study wishing to consider the relapse versus reinfection (recent transmission) in a retreatment population should first focus on the statistics of IS6110 genetic diversity and genotype families prevalence in the setting, linked to MDR phenotype (and Rif and inh genotype if possible through a rapid Hain-diagnostics or Inno Lipa test). If we try to relate this study and the once published by the same authors in 2004 (Farnia et al. 2004) 5 genotypes families were found (Figure 1) and no mention of these 5 genotypes family is made anymore. The dendrogram and figure presented in this article suggests a much wider genetic diversity without reference to the previous work. Indeed, It would
have been better to go from the last (spoligotyping) to the most (VNTR-MIRU or IS6110-RFLP) discriminative markers to study this retreatment population to be able to compare this work and the previous one. Was spoligotyping done for these isolates, if yes, include the results. The Bionumerics analysis looks as being sub-optimal.

6. Are limitations of the work clearly stated?

No, the authors do not discuss their genotyping strategy within a larger scientific technological environment. They refer to South-Africa, whose demographic and Public health context is very different from the one found in Iran.

7. Do the authors clearly acknowledge any work upon which they are building, both published and unpublished?

Yes

8. Do the title and abstract accurately convey what has been found?

Yes

9. Is the writing acceptable?

Yes

What next?: Unable to decide on acceptance or rejection until the authors have responded to the major compulsory revisions

Level of interest: An article of limited interest

Quality of written English: Acceptable

Statistical review: Yes, but I do not feel adequately qualified to assess the statistics.

Declaration of competing interests:

I have no competing interests