Reviewer’s report

Title: Genetic analyses revealed Mycobacterium tuberculosis as the causative agent of TB in the southern ecological zones of Cameroon

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Reviewer: Sebastien Gagneux

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This paper reports the genotyping results of 169 M. tuberculosis complex (MTBC) patient isolates from 3 regions in Cameroon analyzed using spoligotyping and 24-loci MIRU-VNTR typing. The authors found that the 3 regions harbour essentially the same MTBC genotype families with the “Cameroon family”, the T1 and Haarlem spoligotypes being the most dominant. Based on MIRU-VNTR typing, the authors found essentially no evidence of epidemiological clustering among the TB patients included in the study.

I have several comments which the authors should address:

Major Compulsory Revisions:

1) There was no genotypic clustering based on the MIRU data; yet, the authors argue that there is a lot of “ongoing transmission” of TB in Cameroon. This is likely to be the case in reality, but the MIRU data reported in this paper do not support this conclusion! Most likely, this is because the samples included are a convenience sample (i.e. this is not a population-based study!). This limitation needs to be addressed and discussed in the manuscript.

2) The authors refer to a “correlation” between phenotypic drug resistance profiles and strain genotype as determined by spoligotyping. I don’t see any correlation in these data, much less any which might be statistically supported. Hence, this section should be deleted from abstract, results and discussion.

3) There are many grammatical errors, typos and style issues throughout the paper. Please have the manuscript checked by someone with appropriate English writing skills.

4) In the results section, make to to appropriately differentiate between “strain/isolate” and the “spoligotypes”. E.g. on page 1 of Results, it states” the 17 spoligotypes were compared with those contained….And it was found that 61 (!) of them (of what?) were already described……”. This is very confusing and should be clarified.. Please refer to the spoligotypes of 61 strains were compared” or something similar. Similar sections in the Results suffer from the same problem.

5) The authors argue that based on their data, MIRU-VNTR was “100% sensitive and specific” fro MTBC isolates. How do they know this given they have not tested any MTBC-negative samples (includzing non-MTBC mycobacteria)?
Minor Essential Revisions:

6) The introduction refers to “10 million cases” and “3 million deaths” causes by TB yearly. According to the latest WHO report (2012) these numbers are ~9 million and 1.4 million, respectively. (…and please add the relevant reference!)

7) A reference is missing in the introduction when referring to the study performed “30 years ago”.

8) Be consistent when reporting % values (e.g. use just on decimal) across the manuscript (including tables):

9) When reporting the MIRU-VNTR data, there is no need to give so many details by region as none of the strains are clustered in any of the regions.

10) The authors found a low prevalence of M. africanum, particularly compared to the older literature. Can they speculate about why M. africanum in Cameroon might be so rare by now?

Level of interest: An article of limited interest

Quality of written English: Needs some language corrections before being published

Statistical review: No, the manuscript does not need to be seen by a statistician.

Declaration of competing interests:

I declare that I have no competing interests.