Author's response to reviews

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

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Author's response to reviews: see over
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

1) The authors' main conclusion in the abstract and the main text that the level of epidemiological clustering is high (and therefore ongoing TB transmission is high) in Cameroon is not supported by the data presented. Using the current gold standard for molecular epidemiological investigation of TB transmission, which is the combination of both spoligotyping plus at least 15-loci MIRU-VNTR (see Ref. 15 in the text), clustering is in fact 0% as acknowledged by the authors. Hence, based on their data alone (i.e. spoligotyping plus MIRU-VNTR), one would conclude that there is no transmission at all. Obviously, this is very unlikely and just an artifact of the fact that the authors have not included enough patient samples. Nevertheless, the conclusion as it stands is wrong and needs to be deleted from the manuscript.

Answer 1
We agree that although the spoligotyping data suggests some clustering, the more sensitive MIR-VNTR analysis does not confirm this. Therefore we have deleted this conclusion form the MS as suggested by the reviewer,

2) It should also be highlighted in the text that this was a convenience sample which therefor a) might not be representative of the overall genetic diversity of Mtb complex in Cameroon and b) that conclusions about ongoing transmission cannot be drawn based on these data alone.

Answer 1
We agree and this has been mentioned in the text