



SDI FINAL EVALUATION FORM 1.1

PART 1:

Journal Name:	British Microbiology Research Journal
Manuscript Number:	2013_BMRJ_3708
Title of the Manuscript:	Detection of Mycobacterium tuberculosis Complex in Lung Specimen of Slaughtered Cattle and Goats By a DNA Based multiplex- Polymerase Chain Reaction and Ziehl-Neelsen Methods In Jos, Nigeria.

PART 2:

FINAL EVALUATOR'S comments on revised paper (if any)	Authors' response to final evaluator's comments
Abbreviation should be the same throughout the text, M-PCR or m-PCR. However, the most serious problem of this study is the difference in the sequence of the primer JB22 previously described (Rodriguez <i>et al</i>, Microbiology 141:2131-2138. 1995) The primer JB22 described by Rodriguez was (5'CGTCCGCTGACCTCAAGAAG3'). In the study of Chukwu <i>et al</i> the sequence of JB22 is 5'CGTCCGCTGACCTCAAGAAAG3'. But also I would like to clarify that these primers described by Rodriguez in 1995 are not updated to differentiate <i>M. bovis</i> from other mycobacterium from <i>M. tuberculosis</i> complex. The complete genome sequence of <i>M. bovis</i> showed that these primers are not suitable for this differentiation. In lines 320-321 the author suggest "it is possible that members of the MTBC responsible for TB in the animals tested, lacked the 500bp fragment" It is true, but this is because <i>M. bovis</i> strains have not exactly the sequence of these primers. The authors should mention something about it.	Authors' response to final evaluator's comments This has been corrected through out the text. The additional adenine to the JB22 primer sequence was a typographical error We have effected the correction. We actually used these sets of primers because it had been successfully used by other authors to amplify the 500bp fragments meant for <i>M.bovis</i>. Rodriguez et al., 1995 and Sechi et al., 2000. This research is still ongoing, in this part of the world, we still have a lot to do in disease diagnosis. We are a developing country. We were not able to confirm this because, we were interested in the species <i>M.bovis</i>, not all the strains. We are trusting that one day we will be able to have all it takes to detect the strains.