



SDI Review Form 1.6

Journal Name:	<u>British Journal of Medicine and Medical Research</u>
Manuscript Number:	2013_BJMMR_7449
Title of the Manuscript:	High frequency of non-B HIV-1 subtypes specific mutations at the protease gene among treatment-naïve HIV-1 infected individuals in Jos, Nigeria
Type of the Article	

General guideline for Peer Review process:

This journal's peer review policy states that **NO** manuscript should be rejected only on the basis of '**lack of Novelty**', provided the manuscript is scientifically robust and technically sound.

To know the complete guideline for Peer Review process, reviewers are requested to visit this link:

(<http://www.sciencedomain.org/page.php?id=sdi-general-editorial-policy#Peer-Review-Guideline>)



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PART 1: Review Comments

	Reviewer's comment	Author's comment (if agreed with reviewer, correct the manuscript and highlight that part in the manuscript. It is mandatory that authors should write his/her feedback here)
Compulsory REVISION comments	<p>In line 51 : patients were recruited between October 2011 and April 2011 so time period (7 months) is very short.</p> <p>In line 52: it was said that demographic data collected but there is not any demographic data was given in the article. Also collection dates of the samples should have been represented.</p> <p>In line 87: the method for sequencing was conventional sequencing. Because of the quasispecies nature of HIV this type of method is not enough the determination of point mutations, deeper method is needed.</p> <p>In line 98: downloading references and reference including criteria was not given.</p> <p>In line 101: software MEGA 4.0 was performed for phylogenetic analysis but it is an old version of MEGA. At least MEGA 5.0 should have been used. Because this version of MEGA 4.0 could not use a maximum likelihood criteria but it uses a composite of maximum likelihood. With an unrooted tree, it is not possible to give a direction to the tree and it is not possible to estimate the cluster distance. It is not clear that which evolutionary model was choosed for evolutionary analysis.</p>	<p>We have corrected this in the ms saying that it was a cross-sectional study.</p> <p>There is demographic data which is only age and sex and mentioned in table 1 and under results/ Discussion in the ms</p> <p>The conventional sequencing methods approved by CDC and WHO are worldwide accepted, and deep sequencing is mainly for a particular research but not readily used for public health approach</p> <p>MEGA 4.0 is not obsolete even though there is a newer version (5.0). The composite maximum likelihood estimates cluster distances which can be confirmed by other software such as PAUP V4.0. The use this version can also be verified from several others studies on the web page</p>



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	<p>In line 123: statistical analysis was performed but which kind of statistical analysis was performed? There is no result about this analysis in the article.</p> <p>In line 211: given results were not statistically supported, even if the results couldn't be support statistically, it must be indicated as unsupported.</p> <p>In line 212: the phylogenetic tree was mentioned but there is not a tree figure in the article.</p> <p>In line 213: a recombinant subtype was mentioned but recombination analysis is also needed to prove a sequence as a recombinant form.</p> <p>Conclusion is very short</p>	<p>The statistical analysis performed was mainly descriptive (percentages and medians with their IQR); and this was mentioned under stat. analysis in the ms. Here we did not give any p value because we did not have any comparison groups. We have modified the language – 'as evidenced', in the ms to show lack of any statistical significance.</p> <p>The tree is available and the focus was not detailed description of the evolutionary relationships but on mutations</p> <p>Recombination identification program (RIP) of Stanford HIV sequence program was used to confirm recombinants, and sample of it is available.</p> <p>Conclusion edited sentences inserted</p>
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<u>Minor</u> REVISION comments		
<u>Optional/General</u> comments		