



SDI FINAL EVALUATION FORM 1.1

PART 1:

Journal Name:	British Journal of Medicine and Medical Research
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

PART 2:

FINAL EVALUATOR'S comments on revised paper (if any)	Authors' response to final evaluator's comments
<p>To my requested comments "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>The author's answer has been "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> <p>Well I suggest the authors to consult the book entitle "The phylogenetic handbook" by Philippe Lemey, Marco Salemi and Anne-Mieke Vandamme</p> <p>To better understand the principle of phylogeny</p> <p>Mega 4 is not appropriate for Maximum Likelihood analysis because this program does not have ML</p> <p>Composite is another thing another concept If the author used or confirmed their analysis with PAUP why they do not put in material and methods and in results section this??</p> <p>No mention again has been about how they choose the Kimura 2 has evolutionary model</p> <p>Anyway no experience they have on phylogeny and evolution methods</p> <p>"</p>	<p>We are very grateful to the reviewer for the important insight on the phylogenetic methodologies. We have confirmed the earlier analysis using more robust considerations. Besides the preliminary analysis on REGA, we have employed MEGA version 5.0 for Maximum Likelihood (ML) analysis with a bootstrap of 1000 replicates for assessment of the strength of the phylogenetic tree and values above 70% were considered significant. An out-group HIV subtype was used to root the tree and Hasegawa-Kishino-Yano model (+G+I) selected for the analysis based on the Bayesian Information Criterion (BIC) scores of 24 different nucleotide substitution models. Nearest-Neighbour-Interchange (NNI) method was used as the ML Heuristic option for tree inference. We have made this clarification in section 2.3 of the write-up.</p>