



SDI Review Form 1.6

Journal Name:	International Journal of TROPICAL DISEASE & Health
Manuscript Number:	Ms_IJTDH_31517
Title of the Manuscript:	Molecular Identification of Plasmodium Species in Malaria in Zimbabwe by Mitochondrial DNA Sequencing
Type of the Article	Short Research 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	Ln 68 Change 3'-TCG... to 5'-TCG... also, last three nucleotides should be changed from ACC to AAC (see reference 11). Ln 69 Change 3'-AAT... to 5'-AAT... Ln 84. Phylogenetic tree was produced in Geneious Basic, but the algorithm used needs to be specified (e.g. was it Neighbor-joining, Bayesian, Maximum Likelihood, etc?) Ln 148 and 149. The statement that sequence identity to <i>P. falciparum</i> was 96 to 100% is vague and needs to be clarified. Fig. 3 shows that only one sample (M2) is not 100% identical. If this is the case, it should be specifically stated and the percent identity given. It would also be informative to know the nucleotide site(s) that differ between M2 and the other samples of <i>P. falciparum</i> shown in Fig. 3.	The section (lines 68-69) has been corrected to "(5'-TCG CTT CTA ACG GTG AAC-3' and 5'-AAT TGA TAG TAT CAG CTA TCC ATA G-3')" Line 84 has been corrected to: "A phylogenetic tree was drawn using the Geneious Basic program using the Juke-Cantor genetic distance model and UPGMA (Unweighted Pair Group Method with Arithmetic mean) algorithms". The section has been corrected to: "The pairwise identity of 59 out of the 60 sequences was 100% with Plasmodium falciparum. Only 1 sequence (M2) was 99.4% similar to Plasmodium falciparum sequence. There was a single base difference in M2 at nucleotide position 56 of the sequence where there was base A instead of base T which was present in Plasmodium falciparum. A further sequence searches in the Genbanks failed to find sequences which were 100% similar with M2".
Minor REVISION comments	Ln 33. Since only a very small part of the mitochondrial genome was sequenced, suggest changing last part of sentence to read: "...sequencing a short segment of the <i>Plasmodium</i> mitochondrial genome." It would also be useful to know what specific mitochondrial gene(s) is included in the 220 bp segment.	The section has been modified to: "The aim of this study was to identify the Plasmodium species circulating in Zimbabwe by amplifying and sequencing a short hypervariable segment of the Plasmodium mitochondrial genome within the cytochrome c oxidase gene".



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	Ln 73 and 74 Suggest deleting "of the <i>Plasmodium</i> mitochondrial genome" Ln 100 Insert "which" following "samples" Ln 148 Change "majorities" to "majority" Suggest shortening the Discussion, especially in the first paragraph. Much of this information was already included in the Introduction and Materials and Methods.	The statement "of the Plasmodium mitochondrial genome:" was deleted. "which were" has been added to Line 100. Section with Line 148 has been re-written and the word "majorities" has been deleted. The first paragraph of the Discussion section has been shortened.
<u>Optional/General</u> comments	The authors should consider depositing the distinct haplotypes obtained in their study in GenBank or other public database.	The sequences will definitely be deposited into the Genbank once the manuscript has been published.