Review Form 1.7

Journal Name:	**International Journal of TROPICAL DISEASE & Health**
Manuscript Number:	**Ms_IJTDH_98453**
Title of the Manuscript:	**Characterization and Profiling of Gut Bacterial Microbiome and Pathobionts among HIV-negative and HIV-infected individuals in Cameroon**
Type of the Article	Original research paper

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:

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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		
1. **Is the manuscript important for scientific community?** (Please write few sentences on this manuscript)	**Yes, the manuscript provides new data on the taxonomic composition of the gut microbiome of Cameroonians, including those with HIV infection. To date numerous surveys of the HIV gut microbiota matched for lifestyle factors suggest consistent shifts in gut microbiota among HIV-infected subjects. Although changes in the gut microbiota are not directly linked to the development of HIV infection, dysbiosis plays an important role in chronic inflammation in HIV patients and thus may affect the severity of the disease. It is therefore important to identify the differences in the gut microbiota of HIV-infected and uninfected people and to understand how these differences may affect the immune state and the disease progression.**	
2. **Is the title of the article suitable?** (If not please suggest an alternative title)	**Yes, partially. Which of the results do the authors refer to as microbiota characterisation and which as microbiota profiling, and why should both terms be used in the title?**	
3. **Is the abstract of the article comprehensive?**	**The abstract should be corrected. The abstract should clearly reflect the new data obtained in current study concerning gut microbiome composition of HIV-infected persons.**	
4. **Are subsections and structure of the manuscript appropriate?**	**Generally, yes**	
5. **Do you think the manuscript is scientifically correct?**	**The manuscript should be revised.** **1. Why the authors performed the HIV screening of the people engaged in the study? Did they collect a medical history for the HIV-infected patients? How homogeneous was the group of participants in terms of duration/severity of the disease?** **2. The Table 1 contains description of only 10 faecal samples purposely selected for 16S rRNA sequencing. Where is the information about other 15 HIV-infected and 15 HIV-negative samples?** **3. Why the raw sequence data was not deposited in GenBank NCBI? It is a generally accepted practice. The information on sequence data quality also should be provided.** **4. The gender / age composition of each of HIV-infected and HIV-negative groups should be specified in Table 2.** **5. The general and distinctive features of the gut microbiome composition (including names of shared taxa and taxa, specific for each of study groups) should be presented in the section "Gut Bacterial Microbiome Composition in studied population".** **6. The data, summarized in Table 1, is not clear for interpretation. Foe examples, what does it mean "Kingdom 1 (n=50%) in HIV-positive group"? It means that the representatives of only 1 kingdom were detected in 50% of studied HIV-positive individuals? And other 50% did not contain any kingdom?** **Why do the authors suggest that they have discovered an unknown kingdom of prokaryotes (what were the criteria for this determination)? Could the low level of similarity be the result of poor sequence quality or incorrect taxonomic classification of the sequences?** **7. Metagenomic analysis using NGS sequencing is not powerful enough to identify strains (OTUs up to species level only). Therefore it is incorrect to use the name "Taxonomy abundance variation....abundant microbial strains", this needs to be checked and corrected in the text and in the figure names. May be the authors mean microbial species.** **8. Concerning the microbiome structure and diversity, the "core" OTUs of the HIV-negative and HIV-positives individuals should be identified and the indices of diversity (Shannon, Simpson's, Chao 1) should be compared.** **9. The data represented on figures 6, 7-13 need to be summarized (or combined).** **9. Which method (or criterion) was used to identify the pathobionts in the metagenomic sequences of HIV-positive and HIV-negative individuals? What was the relative abundance of different pathobionts in the microbiome of infected and non-infected people? The figure 14 needs additional comments for its interpretation.** **10. The conclusion should be revised. The statement that "The gut microbiome OTU**	

6. Are the references sufficient and recent? If you have suggestion of additional references, please mention in the review form. **(Apart from above mentioned 6 points, reviewers are free to provide additional suggestions/comments)**	**diversity for HIV-negative individuals was abundant with less enrichment of butyrate-producing flora as compared to those of HIV-positive…" does not have any proves in the "Results" section. The same unproven information presents in the abstract. To make such statement, the authors should identify the butyrate-producing bacteria and their relative abundance.** **11. The specific termed should be checked through the text. Sometimes the authors use "16S gene" instead of "16S rRNA gene", "microflora/flora" instead of "microbiota", etc.** **The references are adequate**	
Minor REVISION comments **1. Is language/English quality of the article suitable for scholarly communications?**	**The manuscript needs language, grammar and syntactic editing.**	
Optional/General comments	**Data should be presented in a more informative way. The general and distinctive features of the gut microbiome composition of HIV-positive and HIV-negative individuals should be presented, including names of shared taxa and taxa, specific for each of study groups. The relative abundance of different taxa, including pathobionts, should be compared.**	

PART 2:

	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)*
Are there ethical issues in this manuscript?	*(If yes, Kindly please write down the ethical issues here in details)*	

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