Dear Editor, We appreciate the reviewers suggestion for the improvement of the quality of this manuscript. The manuscript has been revised according to the suggestions and comments of the reviewers. Below is a point by point rebuttal to suggestions.

Review report 2

Comments and Suggestions for Authors

An interesting account of HPAIV epidemiology in Nigeria is presented. A lot of sequencing data have been established to allow following the spread of virus within the country and to speculate about possible incursion routes. While the overall design of the study is sound, there are some conflicts as regards the validity of some of the conclusions.

1. Has there really been "extensive" HPAIV evolution and diversity in Nigeria? This reviewer wouldn't opt for this phrase based on the data shown. Compared to Europe 2020-2 and the Amercian continents after 2021 variation of viruses might at best be called "substantially" divers.
2. 2. Merely three genotypes have been detected, one represented only by a single virus.
3. 3. HA variation within those genotypes seems limited and most of the variation is shown to be due to incursions from abroad.

4. This also challenges the designation of Nigeria as a "hot spot" of HPAIV evolution. Rather, from the data shown here, it seems to be a sink with very little dynamics within the country. Also, comparable surveillance data from neighboring countries is missing to allow for comparisons.

This criticism is not meaning this would not be a good paper; just the interpretation of data should be reconsidered and the conclusions re-directed.

We thank the reviewer for these comments. Despite the identification of multiple evidences of the ongoing evolution of H5 viruses in Nigeria reported throughout the study (e.g. emergence of “local” molecular changes across the viral genomes, intersubtype reassortment between viruses circulating in poultry), we do agree that the use of terms such as “extensive genetic diversity” may be misleading in a global perspective. Therefore, according to the reviewer’s request, we revised the title, discussion and conclusions accordingly, avoiding placing emphasis on diversity and focusing on the different introductions in Nigeria and the occurrence of the reassortment event (H5N2).

Minor suggestions:

Title: Should be re-phrased The title has been changed with: Evolution of Highly Pathogenic Avian Influenza A (H5) in poultry in Nigeria, 2021-2022

96 - pers. comm. It is strange to see this essential and central information as a pers. comm. Shouldn't the owners of these data be included as co-authors to fully validate their findings?. Both the Federal Ministry of Agriculture and the National Reference Laboratory (owners of the data) are included co-authors

202 - The genotype groups named here, how do they fit into the European nomenclature system (of which several colleagues are co-authors here)? The HPAI H5N1 viruses belong to the H5N1 A/Eurasian_Wigeon/Netherlands/1/2020- like genotype, while the HPAI H5N8 viruses belong to the H5N8 A/duck/Chelyabinsk/1207-1/2020-like genotype. The H5N2 virus is a new reassortant virus never identified in Europe.

211 - Is it possible H5N8 has been replaced by H5N1 by greater fitness of the latter? Any indications? It is possible because less of H5N8 viruses are detected ecologically

233 - The bootstrap values play an important here to distinguish HA clusters. For each meaningful cluster they should be shown at an enlarged font size while the other values should be omitted completely. The tree has been modified accordingly. As we think that all bootstrap values are important, we maintained visible all the significant ultrafast bootstrap values higher than 80.

248-50 - Mentioning of the glycosilation pattern and its importance: but what exactly are the changes observed with the Nigerian viruses, if any? Thank you for this comment, we modified the sentence specifying the mutation which causes the loss of a potential glycosylation site.

253 - Which viruses did not show the NA stalk deletion and how do the authors think the stalk had been completed? Thank you for pointing this out. The information required has been added to Table S1. The stalk deletion suggests a persistent circulation of the virus in poultry, as reported in the discussion section.

365 - Why do the authors exclude the east-west movements of (infected) wild birds here? - Wild birds were not sampled or analysed in this manuscript and it would be beyond this paper to dwell on a broader range for which we have no data

Comments on the Quality of English Language 247 - "have", not "has" modified accordingly

Thank you
Clement Meseko
(for authors)