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## Answering Reviewers

**Phylogenetic tree has low bootstrap values due to small fragment (400pb),**

**Difference in experimental study are not very evident. Is there any significant difference?**

**(1) Overall structure Overall the manuscript is completed. The conclusion is present in the last paragraph; nonetheless a specific topic "conclusion" is not included. Abstract does not contain the major achievements of the present work.**

The conclusion is added in the last part of the discussion (Line 293)

We added the main achievements from this work to the Abstract

**(2) Introduction section Authors suggest that two distinct lineages are co-circulating in Egypt. They provide a good experimental study to evaluate the. They also performed a partial sequencing of S1 protein, which has a limit result to conclude the two subgroups are different.**

We made partial sequencing in S1 gene targeting the hyper variable region 3 (HVR3) which considered one of the most targets for identification of virus pathogenicity according to several references (Abdel-Moneim et al., 2012 and Ganapathy, et al.,2015). However, full genome sequencing will provide much more accurate information about different subgroups and in further work we will provide these results.

**(3) Methods section. Samples and flock history: "showing mild to severe" not "sever"**

Done (line 109)

**How old were chickens when vaccination was performed??**

Vaccination was performed at one day old as stated in line 108

**Sentence needs to be rewritten: "birds were suffering from kidney damage… "**

This sentence was rewritten as "In addition, birds were suffering from kidney lesions such as enlargement, congestion, and uroletheasis." Line111

**Virus detection and isolation and Sequencing of the S1 gene and phylogenetic analysis Suppl table is not needed. Authors can only add the references for primers/probe. Sequencing of the S1 gene and phylogenetic analysis more representative sequences need to be added in the phylogenetic tree.**

Virus detection and isolation and Sequencing of the S1 gene tables were discarded and reference were added (Lines 120 and 129),

Phylogenetic analysis was updated by adding more representative sequences (n= 15) for observing different virus groups. Fig 1

**Some information of M&M is mixed up with results. For example: Pathogenicity subsection: The presence of IBV was checked in samples obtained from the inoculated groups at 14 days post-infection. The real-time rRT-PCR test was performed for the detection of virus concentration in the tissues.**

We removed these parts from M&M section

**(4) Results section. Samples obtained from sick flocks were screened by a described rRT-PCR assay. Positive samples were isolated and sequencing. One limitation was this study is the small fragment sequenced (up 400bp) of S1 protein. In consequence, the phylogenetic analysis has a low bootstrap (only 22%) defining branches. These values have to be higher. Please see the recent study Valastro et al 2016.**

The small fragment sequenced (up 400bp) of S1 protein was performed for rapid genotyping of the viruses and we include the new classification of Valastro et al 2016 in our results. 2 variant subgroups within the Egyptian viruses in addition to the earlier Israeli strain were indicated by high bootstrap values (over 90%).

**Table 3 and 4 can be fused. Some information is duplicated in both tables.**

Done, they are merged together (Table 4)

**Figure 2. It is not clear. "Histopathology illustration of the trachea and kidney from experimentally infected chickens." With which virus in figure A, B, C and D?**

This was explained for photos (Fig 2) in Lines 216-221.

**In experimental study, why authors did not quantify the virus in tissues as they performed a rRT-PCR?**

Real-time PCR in this study was used only for detection of virus not for quantification because the aim was to study virus tropism in different tissues not to measure virus shedding (line 155).

**(5) Discussion section Authors did a molecular and biological characterization of two variants and Mass variant. Based on pathogenicity study and phylogenetic study authors cannot prove that there are two distinct lineages co-circulating in Egypt. Are those differences (Mortality, gross scores).**

The two Egyptian variants beside the classical (vaccine –like) virus consititute 2 distinct groups, while inside variant group there are 2 subgroups based on partial HVR3. However there are minor differences between 2 variant subgroups the complete gene sequencing will provide clearer picture about this subgrouping (Valastro et al., 2016) (Lines 234-237).

**(6) Conclusion section. Authors claims presence of two variant groups co-circulating in Egypt with high mortality in SPF chicks. Nonetheless, it is not clear if there are two distinct lineages (Egy/Var-I and Egy/Var-II) as they had similar pathogenicity and amino acid identities. The only main difference was**

**virus detection in lung (present in Var-II but not in Var-I). Can authors explain this finding? Unfortunately, score of gross lesion in lung was not performed.**

This point was corrected in the Conclusion section as mentioned above

**(7) References Valastro et al Infect Genet Evol. 2016 Apr; 39:349-64. doi: 10.1016/j.meegid.2016.02.015 needs to be cited as they proposed a harmonize virus classification**

Done