Reviewer's report

Title: Molecular typing of adenoviruses associated with respiratory infection in Egypt from 2003 to 2010

Version: 2 Date: 3 June 2013

Reviewer: Paola R Barrero

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Minor Essential Revisions

1- The authors had a clear objective: to characterize HAdV associated with influenza-like illness in the Nile region of Egypt from 2003-2010.

The work presented by Dr. Demian et al. is a sequel of previous work conducted by Metzgar et al., in 2005 that examined isolates in the NAMRU-3 collection from 1999 to 2002. It is relevant to continue the molecular surveillance as the prevalence of types seemed to change from the first report in 2005 to the present report. This switch in types between studies or years might be statistically assessed to strengthen the conclusions.

2- Methods are adequate. The trademark of the swabs is a good detail to add because there are many different forms and depending on that is the quantity of cells you recover. In that way, the quality of the sample might be assessed by PCR of a housekeeping gene, like RP, proposed in 2009 by the WHO and CDC (H1N1pdm protocol).

I'm concerned about cell culture: authors might be alert if they are disregarding the effect of selection due to the preference of cell line. It is known that adenovirus species B, C and E, even types from B1 subspecies have different receptors that can be absent or present in different proportions in different cell lines. In this context, the presence of co-infection might be underestimated and might be tested in the sample before cell culture to see if findings agree.

Sequence analysis is poor and phylogenetic analysis is absent, there is no tree to infer the relationships between the isolates, or the distance or the likelihood of the inferences. Nowadays, the sequencing of 600-620 bp in a big genome (~36 kb) is not novel. Authors might sequence the PCR products to see whether fragments obtained from early (PCR B-C-E), intermediate (PCR VA RNA) and late (hexon or fiber) blocks of the genome are in concordance. Authors might evaluate phylogeography and spatial-temporal distribution of types.

The total number of samples is confusing: the authors mention in the abstract 99 isolates, in methods they refer to 550 patients and in results they refer to 99/3106 FluA-negative specimens. It might be better to restrict the population to the 99 adenovirus isolates.

3- Data is sound only to those who are following adenovirus prevalence.

Figure 2 might be deleted as data is repeated in the text (results).
Figure 1 and Table 1 might be unified.
Patterns related to seasonality might be statistically proved by correlation tests.
Data related to age is referred to Figure 4 and has to be corrected in results and discussion (Results section "Distribution of HAdV species among different age groups", Discussion second paragraph).

4. The authors don't mention if they have performed negative controls, no template controls, heterolog (non HAdV) controls and cell culture controls.
Authors do not mention if they had submitted their sequence data to GenBank.

5-Discussion and conclusions are adequately supported by results.
6-Limitations of the work are stated: the type of sample is related to upper respiratory tract infections and other types might be present in lower respiratory tract infections.
Authors proposed to statistically test seasonality in a larger dataset.
Authors proposed to sequence fiber fragments, but they might consider to sequence different blocks of adenovirus genome (as proposed above) to assure types and discard recombinants.
I hope that the comments mentioned above will improve the manuscript and will give more power to the conclusions presented.

**Level of interest:** An article whose findings are important to those with closely related research interests

**Quality of written English:** Acceptable

**Statistical review:** Yes, and I have assessed the statistics in my report.

**Declaration of competing interests:**
I declare that I have no competing interests.