Reviewer's report

Title: Examining strain diversity and phylogeography in relation to an unusual epidemic pattern of respiratory syncytial virus (RSV) in a long-term refugee camp in Kenya

Version: 4  Date: 31 January 2014

Reviewer: rogier van doorn

Reviewer's report:

The authors describe the phylogeny of RSV viruses from a long-term refugee camp collected over a period of several years, to find an explanation for the unusual epidemiology of RSV in this camp that was described earlier in this journal.

Major compulsory revisions

The unusual epidemiology is already described in a previous paper. The authors find no clues in a 620bp fragment (HVR2 of G) of the viral genomes / phylogenetics to account for this, but do not look at anything else, specifically no information on the sampled patients is presented... how many ILI, how many SARI, were all patients typical RSV patients, i.e. young children (<2) with bronchiolitis? Were the patients' characteristics of all the different peaks all similar? The authors philosophize whether the population build up and increasing numbers of susceptibles in the camp could be a factor.

It would be informative if the authors could add additional information about known RSV seasonality in the region (in addition to the unpublished data from Kilifi)... are we seeing overlapping epidemiology of two different seasonal patterns?

In the absence of this, there is no need to focus on the epidemiological pattern in the manuscript and the authors should just present this as the phylogenetics of the HVR2 of the G gene of RSV collected in Dadaab over a 5 year period.

P8 (ii) Definition of clades and sub-clades: more information on definitions of RSV genotypes is needed here, how have clades and sub-clades been defined by other authors, what does ICTV say? Authors need to argue why it is acceptable to adopt similar strategies for RSV (an obligatory human virus) as for avian influenza (a rapidly evolving virus with multiple avian – and mammalian dead-end - hosts)

Discretionary revisions

P7 l8-9 (reverse transcriptase [RT]) – between parentheses, as adenovirus is a DNA virus

P7 l11-14 change to: only samples with a Ct value of 30 or lower were used.
P8 l1-9: specify primers used for sequencing reactions and whether sequencing was done bidirectional

P10 l7-8: delete “possibly due to low viral load as their CT values were close to 30”

P10 l14-25: can the authors add information on RSV seasonality among hospitalized children in Kenya / Somalia

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

Quality of written English: Acceptable

Statistical review: No, the manuscript does not need to be seen by a statistician.