Reviewer’s report

Title: Estimation of outbreak severity and transmissibility: Influenza A(H1N1)pdm09 in households

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Reviewer: Kathryn Glass

Reviewer’s report:

This paper estimates influenza transmission parameters in the context of a spectrum of health outcomes from uninfected, through subclinical, to lab-confirmed, and including other respiratory infections. This is a valuable approach that allows more detailed exploration of typical study data, and is clearly explained – I particularly like Figure 1 as a graphical representation of the underlying model. The authors also conduct a review of published estimates of influenza transmission parameters. I’d like to see this review connected more clearly to the main focus of the paper, and would appreciate some more detail and discussion of a few of the findings as outlined below.

Discretionary Revisions:

1) The authors have undertaken a thorough review of papers estimating household transmission parameters for influenza, but at present, this review seems disconnected from the main statistical analysis. It does not appear to be mentioned anywhere in the Methods or Results and Discussion sections, and is only alluded to briefly in the Conclusions. I think the paper can stand alone without this review, but if the authors see it as providing valuable context, then more effort should be made to integrate it into the main text.

2) To me, the most surprising finding of this analysis is the estimate for p, the proportion of swabs from H1N1 positive cases that were found to be negative by PCR. The authors estimate that 42% of cases of H1N1 did not return a positive swab. Although there are a number of rapid tests that show low sensitivity, RT-PCR is often taken as the gold standard in influenza testing. The authors discuss some data-related factors that could explain this low estimate – e.g. swabs taken too late, or in individuals with mild illness – but I think it is also important that they discuss any model assumptions that might lead to errors in this estimate. For example, does the model of other respiratory infections (estimated as the baseline prevalence, s) allow for these other infections to be transmitted within the household? Could the estimates of k include some infections other than influenza? I realise that a thorough testing of alternate models goes far beyond the scope of this paper, but some discussion of the possible impact of the underlying assumptions would be valuable here.

3) The relationship between household size and transmission rates is a complicated one that is not well understood. In their systematic review of pH1N1, Lim et al. (reference 24) found that "secondary infection risk was variously
observed to increase with household size or not to be associated with household size”. The one study they identified that showed a decline in secondary infection risk with household size was the Cauchemez study (reference 20), which Lim et al. noted has a “broader definition of household contact”. In this context, it would be helpful to know what definition was used for household contacts in the data analysed in this paper. The authors’ observation that they expect transmission probabilities to “decline swiftly as household size increases” seems a bit strong given this variability in findings.

Finally, I am very intrigued by the finding of heterogeneity in individual infectiousness. I hope the authors have an opportunity to explore this in further work – particularly in relation to the age of cases and contacts.

**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.