Author's reply: Estimation of the reproduction number for 2009 pandemic influenza A(H1N1) in the presence of imported cases

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To the editor: We thank Nishiura and Roberts for their interest in our paper [1]. They raise important issues concerning the accuracy of estimates of the reproduction number (R) and the need for early and comprehensive data to ensure such accuracy. We agree that this is one of the main points of our article and something that needs to be addressed further in the future.

Nishiura and Roberts draw particular attention to the need to adjust estimates of R early in an outbreak when the imported cases are external to the susceptible population. The key issue here, as noted by Nishiura and Roberts, is the need for early and accurate assessments of R to aid public health policy and planning. Clearly, as we noted in our article [1], quite different conclusions can be reached through overestimating R early in an epidemic, without adjustment for importations when imported cases are the predominant transmitters. In their calculation of the early estimation of R in New Zealand [2], the authors removed the imported cases from the dataset before estimating R , obtaining an estimate of 1.96. This is entirely consistent with our estimate of R when imported cases are removed, as seen by the upper curve in Figure 3 in our paper [1] – we estimated R to be between 1.82 and 1.94 over a similar time frame of 8–14 June 2009.

We agree that the issues highlighted by Nishiura and Roberts of not truncating the generation time for imported cases and using exponentially distributed generation time both lead to underestimates of R . Hence our estimates when allowing for imported cases in [1] are most likely underestimates of the true R . Tests that we have conducted with simulated data have shown that even moderate levels of imported cases can lead to a sizeable overestimation of R that is larger than the effect of the underlying generation time distribution used in standard methods (unpublished data). For the New Zealand data, the overestimate of R by removing the imported cases was approximately 25% whereas the underestimate due to using an

exponentially distributed generation time was approximately 5% when compared with a more realistic distribution such as the gamma distribution. Unfortunately, with current data collection it is rare to have accurate information that can be used to assess the truncation of the infectivity period of imported cases. This is clearly an area that needs addressing in the future.

Other issues may lead to overestimates of R early in an outbreak and these should also be considered when drawing conclusions from the calculations. For example, if the initial cases are in a subpopulation with an intrinsically higher R , for example children in Japan [3,4] or Pacific Peoples in New Zealand [1,2], then care must be taken when extrapolating R to whole population level.

Recent criticism of overzealous public health responses to the 2009 influenza A (H1N1) pandemic in New Zealand and elsewhere [5,6] highlights even further the need for responses that are modified to appropriately reflect the severity of newly emerged infectious diseases, including pandemic influenza [7]. A crucial element needed to allow appropriate policy decisions is accurate assessment of disease transmissibility and severity. Both of these rely on the rapid gathering, sharing and analysis of accurate and relevant data. Our method, with further refinements as suggested by Nishiura and Roberts, provides an important step forward in such early analysis of transmission dynamics. We recommend that this modelling approach, and data collection to support it, should be considered by those currently charged with revising pandemic plans in the light of events in 2009 and that our proposed methods should be tested in a variety of other settings to further demonstrate their validity.

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