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[Short Communication]

Initial Wave and Transmission Rate of the A (H1N1) Pandemic Influenza in Mongolia

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On October 12, 2009 Mongolia officially became one of the last countries with confirmed cases of pandemic influenza A virus of subtype H1N1, although this strain had been established in rest of the world since the initial diagnosis in North America in mid-April 2009. The virus was first diagnosed in Ulaanbaatar, the capital city with a population over a million people, starting from a Mongolian individual who came from Japan for a short visit to Mongolia. According to the Ministry of Health of Mongolia, the number of laboratory-confirmed cases is 955 as of November 11, 2009 after 30 days of initial infection: 737 of these cases are recorded in Ulaanbaatar and 218 in other parts of country (so far 18 out of 21 aimags (provinces) have at least one positive case). Although Mongolia's reaction to this infectious disease was immediate, there have been 12 death cases that were positively linked to the virus as of November 11, 2009 (MOH, 2009; http://www.moh.mn, accessed on November 11, 2009). The Government of Mongolia took immediate social-distancing measures, including suspension of domestic public transportation, suspension of kindergartens and schools (except for colleges and universities) and other public activities, and even shortening operating hours of some public services, including restaurants, night clubs and supermarkets etc. The initial outbreak of the virus overlapped with the onset of regular flu season in Mongolia and the public was warned to expect the worst in terms of infection and spread of the disease.

The dynamics of infectious diseases has become one of the hottest topics of modern ecology and its understanding has bearings in many of the fundamental and applied issues of ecology and evolutionary biology. Therefore, we ask the following questions. First, what is the dynamics of the H1N1 infections in Mongolia? Second, what was the transmission rate of this disease in the Mongolian population, as this parameter reveals some of the important characteristics of this pathogen (Nokes, 1992) and is a key determinant for success of containment? To answer these questions, we look at the initial wave and transmission rate of this infection by analyzing the data for the first 30 days of this novel virus in the country (for the period from October 12 to November 12, 2009). Spatially, most of the provinces in the country have at least one positive case and we will not concern with spatial aspect of the dynamics. However, Figure 1 shows that initial wave of infection may have already passed and the initial exponential growth of the number of infected individuals is approaching an asymptote as of November 11, 2009.

The first 13 days elapsed after the virus was positively diagnosed in Mongolia represent the phase of exponential growth in the number of infected individuals in the country during which time there had been no social-distancing activities in place. From the pure birth process of a single species population dynamics ($N_t = N_0 e^{rt}$), we can estimate an instantaneous growth rate (r) as the slope of regression line (b=0.453, SE=0.0442, 95% CL of 0.364 and 0.541) of the semi-log plot. The generation time (GT) is assumed to follow a gamma distribution with mean μ= 1.9 days and coefficient of variation v = 47% (Fraser *et al*., 2009, Nishiura *et al*., 2009). The basic reproductive number (R) of the virus is subsequently estimated using the estimator (Roberts & Heesterbeek, 2007):

$$R = (1 + rmv^2)^{\frac{1}{v^2}}$$

We should note that the uncertainties surrounding GT estimates are not addressed in this short note. However, from our intrinsic growth rate, we estimate that this strain of virus has the basic reproductive number of R=2.20 with 95% CL of 1.90 and 2.53 in Mongolia.

The basic reproductive number is a key measure of transmissibility and estimates the average number of secondary cases generated by a primary case. To make a few comparisons, Fraser *et al*. (2009) estimated the basic reproduction number

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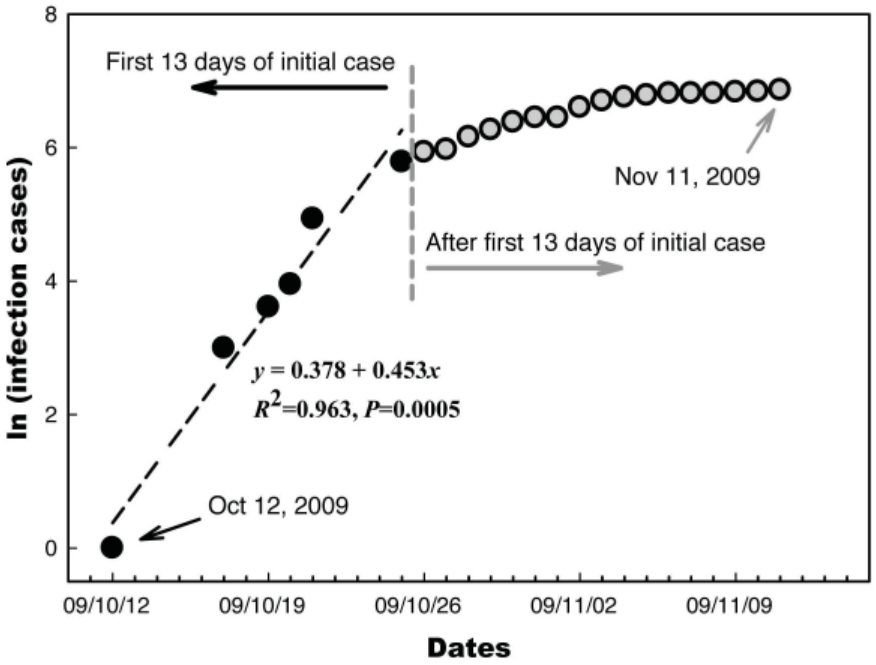

Figure 1. The time course for first 30 days of pandemic influenza A (H1N1) in Mongolia (note this is a semi-log plot). Solid circles represent the exponential growth phase of infection in the first 13 days after the virus was positively diagnosed. Slope of regression line (b=0.453, SE=0.0442, 95% CL of 0.364-0.541) represents the instantaneous transmission rate among human population in Mongolia (from the pure birth process of $N_t = N_0 e^{rt}$).

of the Mexican outbreak of influenza A (H1N1) to be in the range of 1.4-1.6. Their estimates are lower than the estimates in this note (R with 95% CL of 1.93-2.53). Moreover, Nishiura *et al*. (2009) estimated the reproduction number of A (H1N1) virus at 2.3 in Japan (with 95% CL of 2.0-2.6). These estimates are comparable to our estimates, as well as the lower estimates for the 1918 worldwide pandemic, where R ranged from 2.0-3.0 (Chowell *et al*., 2007; Mills *et al*. 2004).

Based on this admittedly simple survey of first 30 days of the infectious disease in Mongolia, we conclude that the measures to contain the initial wave of the infection were adequate. It can be seen from the time course that indicates an asymptoting number of infected individuals (Figure 1). It should be noted, however, any change in containment and management policy and interactions of confounding other factors such as harsh seasonal environment in Mongolia, will definitely affect the trajectory of the disease. Second, the basic reproductive number of A (H1N1) virus in the Mongolian population is estimated to be quite high, which is approximately the same as in Japan and higher than the original Mexican outbreak. This is comparable to lower estimates of basic reproductive number of the 1918 avian influenza pandemic, which caused an estimated death toll of 50 to 100 million people worldwide. Therefore, we caution that relaxation of any preventative measures against the disease spread and reduction in public vigilance may have adverse effects as we face the second wave of infection of A (H1N1). This is especially important because the second wave of the outbreak will be coupled with effects of regular flu season well underway in the country. Third, our estimates of R in this note could even be an underestimate given (*a*) we included first 13 days of data in estimating intrinsic growth rate, rather than the 8±2 days of exponential growth phase as suggested by Nishiura *et al*. (2009) for A (H1N1), and (*b*) uncertainties about generation time, which has not been addressed in this simple note. Finally, we urge the public health officials to start looking at the data as they are accumulated as the disease progresses and the specificity of the virus among different groups of the population should be addressed. These analyses should be done not only temporally, but also spatially. Rigorous analyses will be useful not only in formulating measures to prevent and combat the further spread of this disease, but also in case of any potential new diseases.

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