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