

Location of the epicentre of avian bird flu might determine the rapidity of its spread in India

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In the recent outbreak of avian bird flu (H5N1) in West Bengal during January–February 2008, the Government responded promptly by distributing equipment for culling operations and Tamiflu¹, which resulted in effective control of the outbreak². The World Health Organization (WHO) rightly issued a warning notice that the outbreak in West Bengal was severe³ in comparison with the earlier outbreak in Manipur during July 2007. Coincidentally, there were reports that the emerging infectious diseases could be a potential public health threat to several countries^{4,5}. Five years after the first ever attack of H5N1 during 2003, scientists are still unable to predict the time and location of the next potential outbreak(s). Can the Indian Government take appropriate steps to prevent such an outbreak in future? Is it possible to predict the next location(s) of the outbreak in India or in any part of the world? Answers to these questions might not be easy or could be impossible. One of the reasons for the difficulty in predicting outbreaks is that migratory wild birds, not virus-infected humans, carry the H5N1 virus long distances⁶ (One cannot totally rule out the chance of humans carrying bird flu for long distances, as poultry staff could carry the virus through clothes and equipment).

A mathematical model developed for the recent Indian bird flu predicts that majority of the infection was in wild birds, market birds (includes backyard poultry birds taken to markets for selling) and farm birds, which play an important role in spreading the virus from the epicentre to the nearby centres in the region⁷. The model was developed by considering the transmission dynamics between migratory wild birds, domestic birds, poultry birds, market birds and poultry workers (poultry workers are not infected, but their clothes and equipment are assumed to carry H5N1). The virus was allowed to spread from the epicentre to other locations in the State by migrating infected birds, transportation of poultry and market birds. The model predicts the number of infected birds by type over

a period of time. Impact of intervention programmes on the spread of infected birds was predicted using the model⁷.

Such models are found to be efficient for predicting the spread of flu among birds after initial attack of H5N1, but they are not designed to predict accurately the location of the next outbreak. However, one important contribution of such modelling efforts is that they could predict the range of the infected bird populations depending upon the data and information available from the epicentre of the virus spread. Once the basic data (estimated number of infected birds, estimated susceptible bird population in the epicentre, bird population density, transmission related parameters, etc.) are available, mathematical models can help predict the course of the epidemic. In West Bengal the epicentres were the Birbhum and South Dinajpur districts⁷, where the estimated number of birds infected in ten days was 765,000. The actual number of infected birds might have been different had the epicentre of H5N1 attack been in a different geographical location. It could be less or more severe depending upon the density of poultry and the total susceptible bird population in that location. In Maharashtra, the estimated number of infected birds was one million and in Manipur¹ (where the poultry is less densely located) the estimated

number of infected birds was 150,000. The higher the density, higher is the rate of virus transmission between bird populations. Model-based results indicate that the infected bird numbers ranged between 327,000 and 1,795,000 with varying contact rates (which could be due to lower or higher density of poultry)⁷. Figure 1 explains how the densities of the poultry at the epicentre together with the other dependent parameters like bird population, transmission parameters, etc., determine the spread. In Figure 1, contact rates between birds are assumed to be proportional to the densities. Governments need to plan the culling and controlling operations proportional to the densities of the poultry. We need to generate a map of the poultry in the country and the distances between them.

A recent study indicates that small birds such as house sparrows are highly susceptible to the H5N1 virus⁸. Modelling the spread mechanisms in house-sparrow populations could be complex and obtaining transmission parameters could be difficult. Nonetheless, there is need for an expansion of the existing models by adding more bird populations as transmission variables. Statistical analysis conducted based on data from Thailand and Vietnam indicates free-grazing ducks and farmed ducks contribute more to high prevalence of H5N1 than poultry

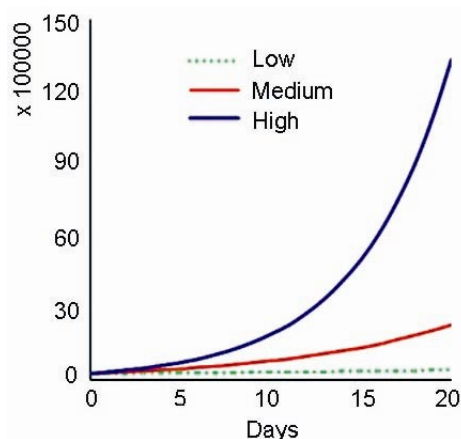


Figure 1. Spread of H5N1 by poultry density.

and domestic chicken in some parts^{9,10}. The H5N1 outbreak in Maharashtra and Manipur was reported predominantly in poultry birds and in West Bengal, it was reported in poultry birds and backyard birds. We do not have any evidence/studies which analyse the correlation between prevalence of H5N1 in bird populations and transmission dynamics through ducks. For India, direct computation of the basic reproductive rate, i.e. R_0 is not feasible due to non-availability of experimental data on H5N1 transmission. One way to compute R_0 is by assuming $R_0 = \beta c \delta$, where β is the H5N1 transmission probability, c the contact rate of infected birds with susceptible and δ the average infectious period of infected birds¹¹. R_0 computed for one geographic location may not be applicable to another geographic location, unless the bird population densities, bird populations and contact rates are comparable in both locations. There is need for cross-disciplinary collaborative experiments and data analysis projects for the preparation of avian influenza outbreaks surfacing in some parts of India at random intervals of time. We do not have evidence of seasonality with respect to H5N1 outbreak in India. There could be many more factors which evolve in computation of R_0 in case of availability of experimental data.

In India, the Government's new initiative on backyard poultry in collaboration with the Indian Council of Agricultural Research¹², could generate better data in the future. The Central Poultry Development Organizations (CPDOs) at Banga-

lore, Bhubaneswar, Chandigarh and Mumbai have been involved in quality chick production and other technological issues through State Agricultural Universities¹³. There is a need to strengthen the design of data collection and for advanced experimental facilities to understand the virus spread with respect to all seasons and food consumption patterns in India. The Government has responded promptly by announcing economic relief services after the avian influenza outbreak during 2006 in Maharashtra, Gujarat and Madhya Pradesh¹². Given the present situation, it is not easy for any government to predict accurately the timing and location of future avian influenza attacks; there is wide scope to strengthen the databanks and to train relief teams to minimize economic loss, if there is an outbreak. Already, there are useful initiatives on the genomic side of research activities in India^{14,15}. To complement these with the public health side of research activities, the Indian Government could consider launching large-scale experimental projects to estimate various rates of spread of H5N1 in different geographical regions, and to come up with a comprehensive approach for effective control of an outbreak.

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