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Commune-level Simulation Model of HPAI H5N1 Poultry Infection and Control in Viet Nam

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1. Summary

With the aim of contributing to evidence-based and equitable disease control strategies FAO's Pro-Poor Livestock Policy Initiative is promoting a systematic approach, referred to as *Strategic Pathogen Assessment for Domesticated Animals (SPADA)*, that combines rigorous epidemiological and economic analysis with risk management. In the case of HPAI, the epidemiological component focuses on development of stochastic simulation models of disease transmission to identify control policies that might be beneficial in the reduction of the transmission of HPAI virus at the local, sub-national and national level.

This report describes a farm-based disease transmission model that approximates the dynamics of HPAI H5N1 outbreaks in Vietnam poultry farms. During model experimentation the impact of varying different sets of epidemiological parameters on the number of infected farms, the force of infection and on the net reproductive number within a commune were simulated. The average net reproductive number (secondary cases arising from one infected farm in a vaccinated population), R_n , in the most lenient control scenario was 2.26. Current disease control measures are predicted to significantly reduce disease transmission but do not completely eliminate the possibility for circulation of residual infection ($R_n = 1.05$).

Future research foresees validation of the model with more complete data, economic assessment of the financial and economic implications of the different disease control scenarios, and field studies to assess incentive mechanisms for early disease reporting.

2. Background

Outbreaks of highly pathogenic avian influenza H5N1 (HPAI) viruses in poultry and their threatening zoonotic consequences emphasize the need for effective control measures (Ferguson et al. 2005). This becomes most significant in countries where poultry and human cases have reached relatively high incidences.

All four countries in the Mekong region have reported viral circulation in their poultry populations since late 2001 (Webster et al 2002). Incidence in poultry was specially high in Vietnam where outbreaks were reported seasonally from early 2003 to late 2005 with the highest incidence around the Tet-holiday festivities (Pfeiffer 2005). In addition to cases in poultry Viet Nam is the country with most HPAI H5N1-related human fatalities of all countries reported infected (OIE, 2006; WHO, 2006).

In Vietnam most outbreaks of HPAI H5N1 in poultry were observed in small commercial farms which rear chicken or ducks and in backyard flocks (Morris et al. 2005). These backyard flocks, subsistence (Sector 4) and market oriented (Sector 3), account for about two-thirds of poultry production and half of direct marketing in Vietnam. In rural areas, typically seven out of ten households, that is around eight million households, many of them living below the international poverty line, own chickens. If serious adverse impacts on these poor are to be avoided, it is essential to develop and implement control strategies that are adapted to initial conditions and local institutions.

Containment policies applied in Vietnam were irregular and different throughout the country for the three outbreak waves (Dung, pers. comm). These included movement control and a set of culling policies. Their differential efficacy and socio-economic impacts have not yet been quantified. Currently the country is not reporting outbreaks and is implementing a systematic vaccination campaign of their poultry flocks, which is regarded as a transitory policy (Dung, pers.comm).

Effective strategies for eradication of highly pathogenic avian influenza H5N1 infection in smallholder poultry flocks require an understanding of the dynamics of the infection process between flocks, as well as the factors influencing them. We model HPAI H5N1 transmission within a heterogeneous population of poultry farms at the commune level and quantify the differential effectiveness of different disease containment scenarios.

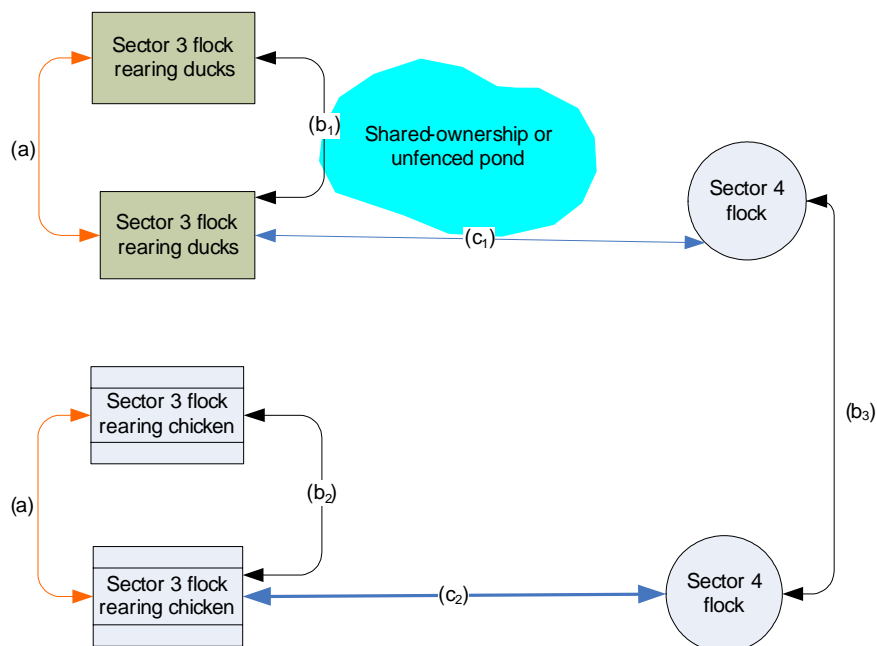
This report summarizes the current status of the epidemiological research component initiated by FAO's Pro-Poor Livestock Policy Initiative within the SPADA framework and sets the direction for future research.

3. Conceptual Setting

The risk of infection by a HPAI H5N1 strain has been found to differ in chicken and ducks (Gilbert et al. 2004). In order for the transmission model to take this biological feature into account, the small commercial farms of a commune were categorized according to their predominant poultry populations. This was achieved by disaggregating the Sector 3 farm population into two strata: Sector 3 farms rearing ducks only (D3) and Sector 3 farms rearing chicken only (C3). In our approximations we have considered Sector 4 farms (S4) as meta-populations of multiple species of poultry.

In our model we assume that virus is introduced and transmitted within and between Sector 3 and Sector 4 poultry farms by the movement of live poultry. Other risk pathways for virus introduction are not considered in our approximations. The conceptual structure describing live poultry movements between farms which can lead to the circulation of HPAI H5N1 infection in a commune is shown in Figure 1.

Figure 1 Schematic of the structure of contact between Sector 3 and Sector 4 poultry holdings. The arrows in orange represent the observed movement of poultry between Sector 3 holdings due to the seasonally-driven trade of unfinished birds. The arrows in blue represent the opportunity of direct contact between farms of different sectors due to the free ranging activity of individual birds. The arrows in black represent the opportunity of contact between farms of the same sector due to the free ranging activity of individual birds. (a) Trade of unfinished birds between sector 3 farms; (b₁) Direct contact between Sector 3 duck farms; (b₂) Direct contact between sector 3 chicken farms; (b₃) Direct contact between Sector 4 farms; (c₁) Direct contact between Sector 3 duck farms and Sector 4 farms; (c₂) Direct contact between sector 3 chicken farms and sector 4 farms.



These theoretical contact links form the basis of the epidemiological framework underlying the transmission model.

4. Data Sources

Outbreak data

Data regarding HPAI H5N1 infection at the commune level was obtained from the Department of Animal Health - Ministry of Agriculture and Rural Affairs for Viet Nam (DAH) for the three epidemic waves occurring between January 2003 and November 2005. These included time of reporting and estimated number of farms infected per commune.

Disease control data

Country level disease control data was obtained from the DAH to inform the parameters of the control model. This included information relating to the level of culling and the coverage of vaccination campaigns.

Commune farm structure data

The model used household census data from 2001 obtained from the General Statistics Office of Vietnam (GSO) and animal census data from 4 provinces (two within the Red River Delta and two in the Mekong River Delta) obtained during the pre-vaccination census in Viet Nam. Datasets were combined to obtain the number of farms per category of poultry subpopulation.

5. Preliminary Simulation Results

We have assessed the impact of four disease containment policies on the development of an HPAI H5N1 outbreak wave assuming an average commune structure in Viet Nam. The scenarios considered in these simulations are outlined in Table 1.

Table 1 Disease control interventions considered in different simulated scenarios

Scenario	Intervention(s)
I	Cull reported cases.
II	I + Pre-emptive cull (3 km radius) around reported cases.
III	II + Vaccination of all Sector 3 farms
IV	III + Vaccination of 25% of S4 farms

Scenarios I and II reflect disease containment measures used in the first and second waves (2003-2004; 2004-2005), respectively. Scenarios III and IV have taken into consideration the antiviral prophylaxis of poultry flocks which was initiated after the second outbreak wave. In Scenario IV a proportion (25%) of backyard flocks (S4) are also included in the vaccination campaign. The epidemiological impact of each control scenario is presented in Table 2.

When considering culling of infected farms only (Scenario I) the maximum R_n estimate obtained was 4.03. This means that a typical infected farm can infect up to 4 susceptible farms during its entire life expectancy (up to the moment it is culled). The variation of this maximum estimate was largely dependent on the time between infection and reporting (data not shown).

Table 2 Mean impact of disease control scenarios on HPAI H5N1 epidemiological parameters for all study communes. Simulations were run for a period of 10 years and each simulation was run over 1000 iterations.

Scenario	Disease Outcome		
	R_n^* (95%CI)	Cases (95%CI)	Force of infection** (95%CI)
I	2.26 (0.97-4.06)	6.88 (2.86-25.11)	3.43 (0.94-9.47)
II	2.24 (0.97-4.03)	6.19 (2.69-21.98)	3.09 (0.89-8.24)
III	1.05 (0.32-2.62)	3.6 (1.5-18.7)	1.24 (0.13-5.05)
IV	0.23 (0.07-0.58)	1.6 (1.4-1.9)	0.01 (0.003-0.04)

* farm; ** farm/day

However inclusion of a 3km pre-emptive culling ring (culling of all susceptible farms) around an index case (Scenario II) did not significantly reduce the commune reproductive number despite the force of infection being significantly reduced ($P=0.038$). This reduction however is not sufficient to contain disease spread as an average of 6 farms can still become infected per time step.

Inclusion of antiviral prophylaxis seems to produce the best disease containment results with all epidemiological parameters approaching threshold values. For $R_n < 1$ transmission is expected to

give rise to minor outbreaks while for $R_n > 1$ the outcome of transmission may be either minor or major outbreaks (Diekmann and Heesterbeek 2000). The results from simulations of Scenario III show that this policy may either lead to major or minor outbreaks. This finding is also supported by the estimates for the force of infection. This suggests that under the homogeneous population assumption vaccination of Sector 3 farms may not be sufficient to contain progression to major outbreak waves.

The inclusion of 25% vaccination coverage of backyard flocks seems to reduce disease transmission below threshold values. However from the resulting number of cases residual infection circulating amongst the poultry populations appears possible. The impact on commune outbreak status and progression of each scenario can be further understood by analyzing Figure 3.

Figure 3 Cumulative probability distributions of the values of R_n for different disease control scenarios at commune level. The R_n values plotted are the mean value per time-step (per day).

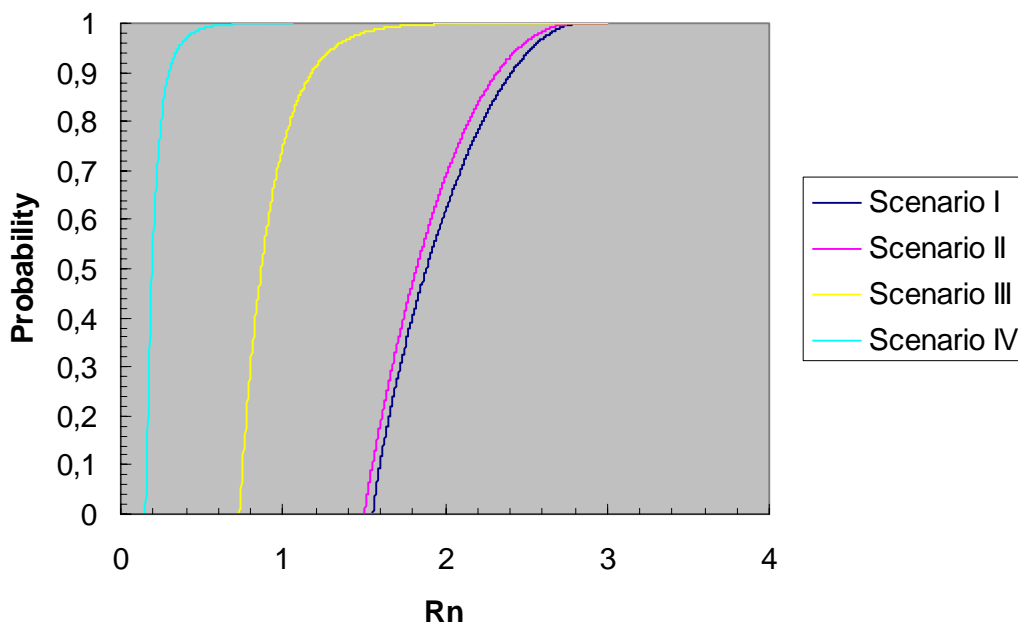


Figure 3 suggests that containment Scenarios I and II result in the highest probability of major outbreaks. Clearly Scenario IV is the one predicted to best control an active outbreak wave although there seems to be a probability for circulation of residual infection in the commune (95%CI: $0.07 < R_n < 0.58$).

6. Conclusions and Future Research Directions

Our model predicts that containment and elimination of a wave of HPAI H5N1 outbreaks at the commune level is feasible using a combination of vaccination and culling. An important conclusion, however, is the need for disease control policies that are adapted to local conditions, i.e. mixture of flock types, in order to achieve high levels of containment, with pre-emptive culling being particularly important in Northern communes.

We are in the process of validating model predictions with more complete data on the containment operations currently in progress such as the vaccination campaign and sero-surveillance results of the vaccinated flocks.

The financial and socio-economic burdens associated with the four disease control scenarios and the distribution of these burdens among different sectors will be subject to analysis by the economic component of the SPADA framework. Furthermore, we are designing field studies to test incentive schemes for disease reporting and for the assessment of traceability schemes that decrease surveillance costs.

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8. Disclaimer & Contacts

These Research Reports have not been subject to independent peer review and constitute views of the authors only. For comments and / or additional information, please contact:

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