Modeling of the HPAI H5N1 Spread through Traditional Poultry Trade Networks in Thailand: Implications for Disease Control

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Introduction

Thailand experienced two large epidemic waves of highly pathogenic avian influenza (HPAI) H5N1 in 2004 and 2005. Traditional poultry trade networks are believed to play an important role in the spread of HPAI H5N1 in backyard chicken populations in Southeast Asian countries. In Thailand, live bird markets are scarce and traditional networks revolve on small-scale traders, who roam around villages and move potentially contaminated vehicles, facilities, or live poultry from village to village.

The present study aimed to (i) model the spread of HPAI H5N1 between villages in Thailand via traditional backyard chicken trade networks and other local spread mechanisms and (ii) simulate different scenarios of control measures.

Materials and Methods

In the present study, the model was handled in three steps: (i) a compartmentalized stochastic dynamic model was developed to depict the flow of live chickens through the activities of traditional traders, (ii) a susceptible-infected (SI) model was constructed to include parameters related to the spread of HPAI H5N1 between villages and (iii) after calibration, different control measures were simulated including ban of chicken traders' movements, disinfection of traders' vehicles and facilities and disinfection of poultry areas in the villages.

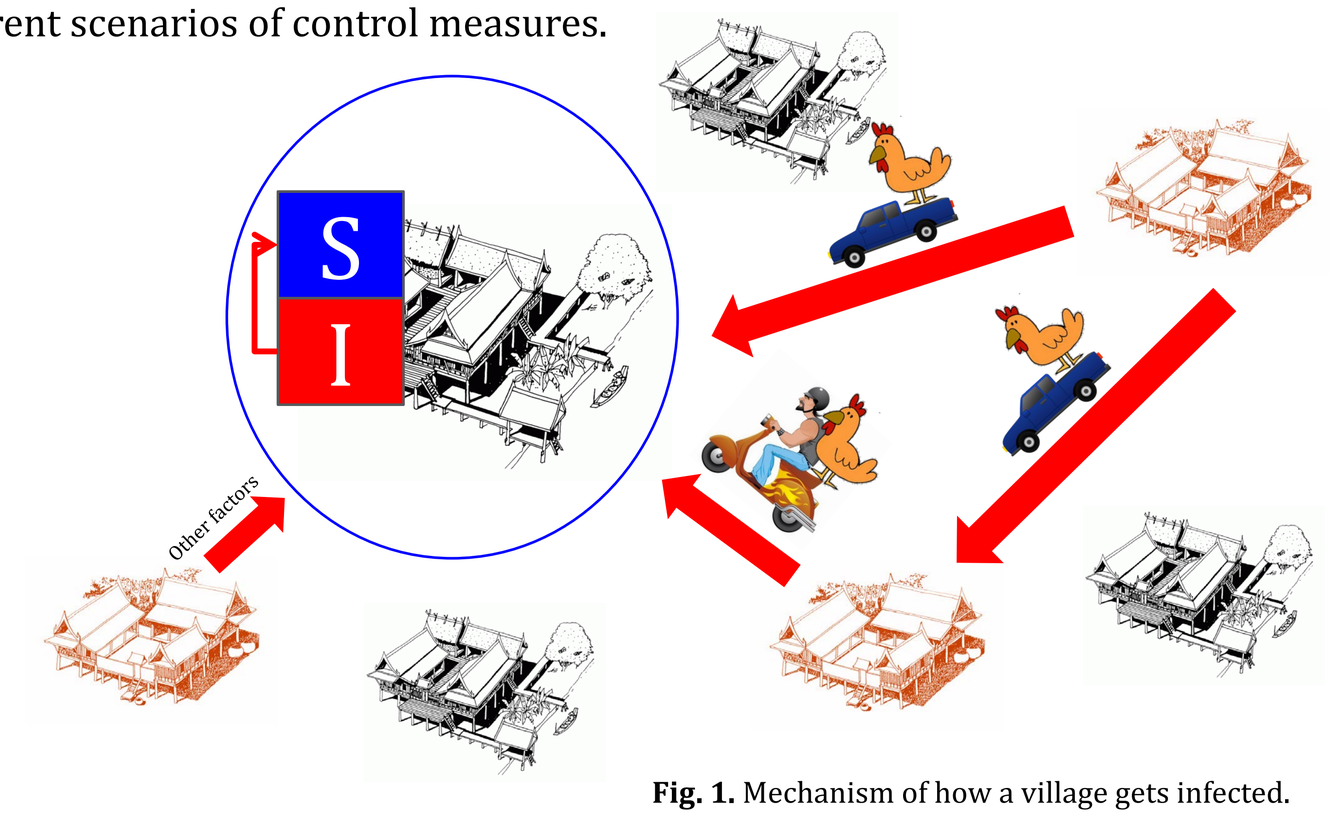

Fig. 1. Mechanism of how a village gets infected.

Results

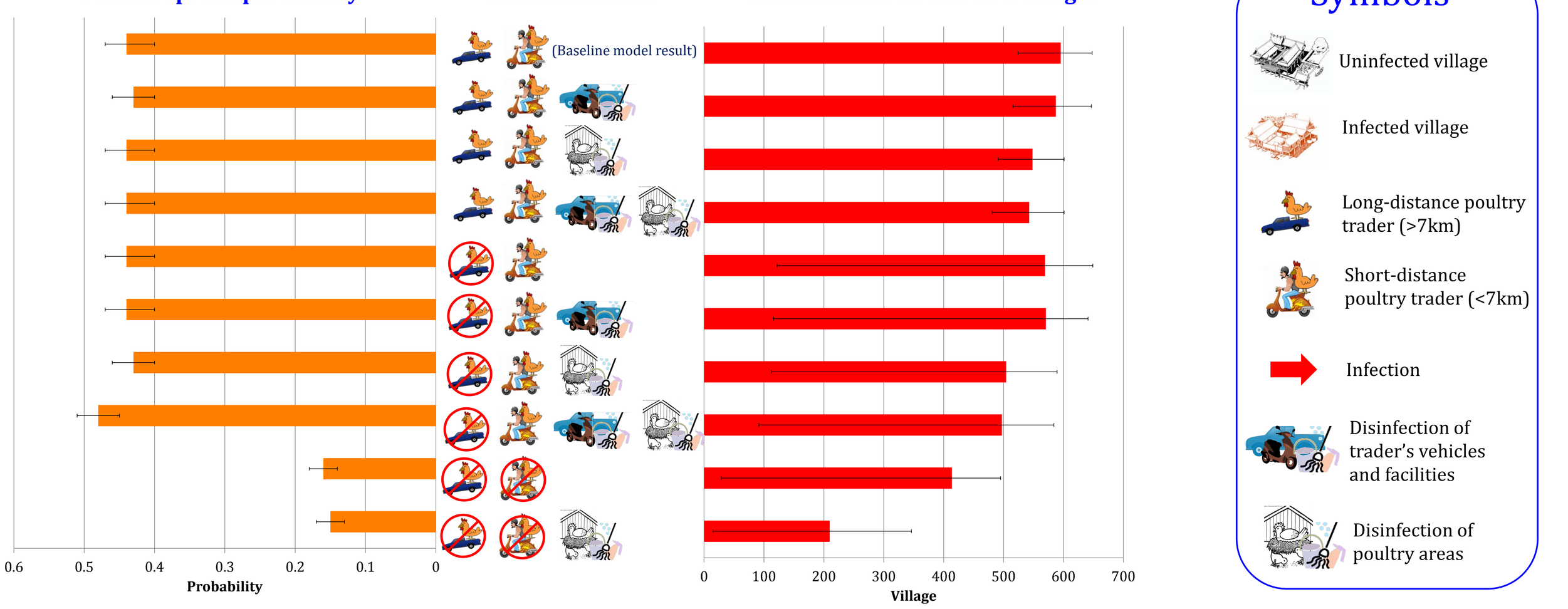

Fig. 2. Results of SI baseline model for HPAI H5N1 spread in traditional backyard chicken trade networks in Phitsanulok province, Thailand and related control measure simulations (1,000 simulations were used for statistics in each scenario).

Conclusion

Our results suggested that, once an outbreak occurs, all movements of poultry traders should be immediately banned regardless distances traveled to catch chickens and villagers should routinely disinfect poultry areas. Besides implications for HPAI H5N1 control, our results could be useful for designing response strategies to other emerging subtypes of Avian Influenza, including H7N9, which circulates throughout Southeast Asia.