Static and Dynamic Factors for Predicting H7N9 Epidemics in China

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Background/Objective

Human infection with avian influenza (H7N9) virus continues to impact China since its first outbreak in early 2013.This rapid emerging, wide-spread, severe disease was considered to be highly correlated with exposure at live-poultry markets, while besides that, little is known about the relationship between spatial, temporal and environmental risk factors and onset of the cases.The objective of our study was to build a risk warning model of human infection with avian influenza H7N9. The model predicts the high risk region of new H7N9 outbreak and facilitates taking timely steps to regionally intervene in the spread of the disease and prevent pandemics.

Method

Newly assembled datasets of total cases in 24 months alongside related city-level environmental and climatic data (a total of 10 risk factors) over China were collected and applied in two statistical models respectively. We used spatial auto regression (SAR) model and generalized additive model (GAM) to estimate the static and dynamic risk factors for H7N9 epidemics. Afterwards, the risk map was created based on the combination of predicted values of both models.

Result

Highly spatial dependence and significant seasonality were confirmed in our study, we also provide evidence that live-poultry density, monthly average temperature, air pressure, relative humidity and wind speed may play an important role in H7N9 infection. The combined model we constructed accurately predicts the risk region in January 2015 in China. In particular, a precise predictive capacity was shown by 4 low risk cities which accurately predicted by our model.

Conclusion

The risk map based on our model showed accuracy and precision in terms of short-term prediction. Such modeling method may be adapted in real world avian influenza prediction practice and inspire better planning to control the spread.