Mapping the risk of spread of Highly Pathogenic Avian Influenza H5N1 in Indonesia using multicriteria decision modelling

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Background

The visual presentation of disease risk through risk maps can assist in the design of targeted disease surveillance and control activities. In circumstances in which data on disease occurrence is unavailable, estimates of risk can be produced using knowledge-driven models, such as multi-criteria decision modelling (MCDM). MCDM is an example of a static modelling approach in which knowledge of risk factors associated with the occurrence of disease are used to drive the model.

Highly pathogenic avian Influenza H5N1 (HPAI H5N1) is a serious constraint on poultry production in Indonesia. In order to assist surveillance activities, we used a MCDM methodology to map the predicted risk of spread of HPAI H5N1 in domestic poultry in Indonesia.

This study employed the following sequence of analytical steps:

1) Systematic literature review to identify risk factors for spread of HPAI H5N1 that were relevant to the situation in Indonesia and could be mapped
2) Sourcing digital maps of hypothesised risk factors
3) Conversion of digital maps to a standardised raster format
4) Defining the relative importance of each risk factor in the spread of HPAI H5N1 using expert opinion
5) Combining all risk factors to produce a final weighted estimate of risk for each location in the study area
6) Sensitivity analysis through alteration of the weighting of each factor in the model

Methodology

Results

A range of risk factors for the spread of HPAI H5N1 in Indonesia were identified (Table 1). Based on expert opinion, the presence of rice paddies was the most important risk factor for spread of disease. The importance of wild birds was considered to be low.

Table 1. Risk factors for the spread of HPAI H5N1 and the relative weight of each risk factor, determined through expert opinion and adjusted for assessor confidence

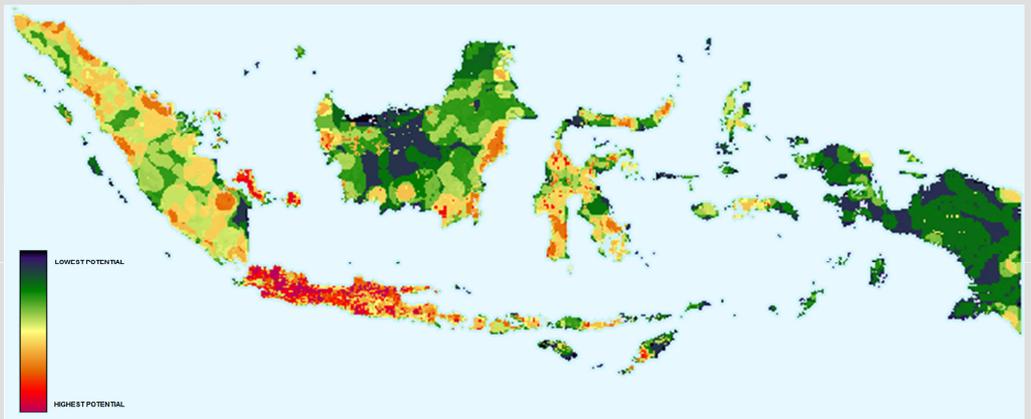| Risk factors for spread of HPAI H5N1	Weight
Rice Paddies	0.22
Poultry density	0.20
Main roads	0.14
Presence of poultry markets/cities	0.11
Sea ports	0.11
Wetlands and water bodies	0.09
Diversity of migratory bird populations	0.06
Density of cultivation production systems	0.06

Fig. 1. Risk map of the potential for spread of HPAI H5N1 in Indonesia, produced using multicriteria decision modelling. Quantitative risk estimates are derived from a 1-255 scale, 1 being extremely low potential for spread and 255 representing extremely high potential for spread

The risk of disease spread in Indonesia is heterogeneous, with large areas with low potential for the spread of disease (Papua, Kalimantan) interspersed with fewer areas with high to very high potential for spread (Java, Banka-Belitung) (Fig. 1). The frequency distribution of scores for the country is right skewed, indicating that in general, there is a low potential for the disease to spread (Fig 2).

Risk estimates were highly robust; altering parameter weights by 25% had a relatively minor average effect on the overall risk estimate (average change in risk score ranged from 0.46 to 4.19 on the 1 to 255 scale).
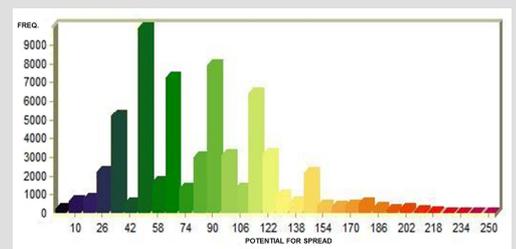

Fig. 2 Frequency distribution of numerical scores representing the potential for disease spread, derived for Indonesia using MCDM. Colour scale relates to that shown in Fig.1

Discussion

Although risk maps can be a useful tool to assist in disease control planning, several considerations must be taken into account when interpreting and using the outcome:
• 'Knowledge-based' models require a subjective assignment of weights which may create unquantifiable bias.
• Only risk factors that can be spatially represented are included in the model.
• Outcome is reliant on the accuracy of the model parameters; spatial data are often inaccurate or outdated.
• The model requires validation by comparison of risk estimates with quantitative data demonstrating HPAIV H5N1 spread. It is intended that prevalence data from studies currently underway in Indonesia will be used for this purpose.

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