Controlling Avian Flu and Protecting People's Livelihoods in Africa and Indonesia

Mapping the Likelihood of Introduction and Spread of Highly Pathogenic Avian Influenza Virus H5N1 in Africa and Indonesia using Multicriteria Decision Modelling

Kim Stevens, Will de Glanville, Solenne Costard, Raphaëlle Métras, Wachira Theuri, Russ Kruska, Tom Randolph, Delia Grace, Saskia Hendrickx, and Dirk Pfeiffer

Key Findings

- Areas most vulnerable to HPAI H5N1 introduction in Africa include densely populated roadways, ports, and airports.

- Most of sub-Saharan Africa has a potential for spread of HPAI H5N1, once the disease is introduced.

- In Indonesia, HPAI is more likely to spread in areas of rice production and in areas with high poultry, road, and port density.

Spatial analysis of the distribution of disease risk and its visual presentation through risk maps can be used to inform the design of animal disease surveillance resulting in more cost-effective strategies. It is suitable for application in the context of HPAI H5N1 in Africa and Indonesia where the disease has already been introduced and is endemic in some areas.

Two main approaches can be used to produce risk maps:

- A data-driven approach, which uses actual disease data to identify risk factors that allow the absolute risk of disease occurrence in an area to be determined;

- A knowledge-driven approach, which uses knowledge about the epidemiology of the disease to identify areas at higher or lower risk of disease occurrence relative to the surrounding areas.

Both approaches are based on available evidence. However, when empirical data about the distribution of the disease are not readily available or when data are only available on some aspects of the epidemiology of a multi-factorial disease, knowledge-driven approaches can be used to determine those areas in which a specific disease is most likely to occur using models such as multicriteria decision modelling (MCDM) (Clements et al. 2006, Pfeiffer et al. 2008).

In contrast to data-driven modelling, MCDM does not generate estimates of absolute risk. Instead, MCDM generates maps that identify areas with a higher or lower likelihood of an event of interest occurring relative to surrounding areas on the same map.

A study described in more detail in EDRS-AIA risk mapping documents (2009) was conducted using an MCDM approach to describe the spatial variation in the likelihood of:

- introduction and spread of highly pathogenic avian influenza virus HPAI H5N1 in Africa, and
- spread of HPAI H5N1 in Indonesia.

This brief summarizes the methodology used to produce the maps for continental Africa and Indonesia, and the findings. In addition to the three maps in this brief, maps for other African countries were produced and are presented in the report, *Mapping the Likelihood of Introduction and Spread of Highly Pathogenic Avian Influenza Virus H5N1 in Africa, Ghana, Ethiopia, Kenya and Nigeria using Multicriteria Decision Modelling* (Stevens et al. 2009); and maps for Indonesia can be found in *Mapping the Risk of Spread of Highly Pathogenic Avian Influenza H5N1 in Indonesia using Multicriteria Decision Modelling* (de Glanville et al. 2009). These reports also include a more detailed description of the methodology used to produce the maps.

Methodology

MCDM can be used to identify areas with a higher or lower likelihood of disease occurrence relative to other areas on the same map "based on existing or hypothesized understanding of the causal relationships leading to disease occurrence" (Pfeiffer et al. 2008). In this study, MCDM involved identifying risk factors associated with the introduction or spread of HPAI H5N1, defining the relative importance of each risk factor in relation to the introduction or spread of disease, and combining all risk factors to produce a weighted estimate of risk for each location in the study area.

Individual models were used to produce three likelihood maps: the likelihood of introduction of HPAI H5N1 to Africa, the likelihood of spread of HPAI H5N1 within Africa, and the likelihood of spread of HPAI H5N1 within Indonesia. Table 1 presents the risk factors hypothesized as being associated with each of the three situations based on a review of the literature.

Table 1. Risk factors included in the multicriteria decision models for the introduction and spread of HPAI H5N1 within Africa, and spread of the disease within Indonesia.

Africa		Indonesia
Introduction	Spread	Spread
Flyways	Poultry density	Poultry density
Distance to of surface water: waterbodies, wetlands, irrigated areas	Distance to surface water: waterbodies, wetlands, irrigated areas	Distance to surface water and wetlands
Density of airports	Density of cities (pop > 50,000)	Density of cities (pop > 50,000)
Density of ports	Density of navigable rivers	Density of sea and river ports
Density of roads	Density of roads	Density of roads
		Migratory bird species richness
		Location of rice paddies
		Percentage coverage of cultivated areas

To obtain the risk factor weightings, pairs of risk factors were compared based not only on their importance (whether Factor A was more or less important than Factor B in the introduction or spread of HPAI H5N1 in Africa or Indonesia) but also on the degree of importance (whether Factor A was (i) equally, (ii) moderately, (iii) strongly or (iv) very strongly, more or less important than Factor B in the introduction or spread of HPAI H5N1 in Africa or Indonesia).

The risk factors, and weights derived from the pair-wise comparison, were incorporated into the multicriteria decision model. The resulting maps in Figures 1-3 illustrate the likelihood of introduction or spread of HPAI H5N1 based on the risk factors and weights incorporated in the model.

Results – Africa

Density of roads, ports and airports were considered the most important factors for the introduction of HPAI in Africa. The map (Figure 1) indicating the relative likelihood of introduction in Africa was therefore predominantly influenced by the distribution of these factors, with lower influence from environmental factors such as distance to water bodies and migratory-bird flyways. The likelihood of introduction of HPAI H5N1 to Africa was higher in the Nile Delta, along the coastline of northern Africa, in western Africa, and parts of South Africa. Areas identified as having the lowest likelihood of introduction included northern Africa, Somalia, Ethiopia, and Botswana.

Regarding disease spread, density of roads was identified as the most important factor, followed closely by poultry density and density of navigable rivers. Most of sub-Saharan Africa was identified as having the highest likelihood for the spread of HPAI H5N1 (Figure 2). In other words, most areas of the continent are more vulnerable to spread once introduction has occurred, than to the initial introduction of the virus. Regions with the lowest likelihood of spread include northern Africa, Somalia, Angola, Namibia, and the southwest region of South Africa.

Figure 1. Map presenting the likelihood of introduction of highly pathogenic avian influenza H5N1 in Africa
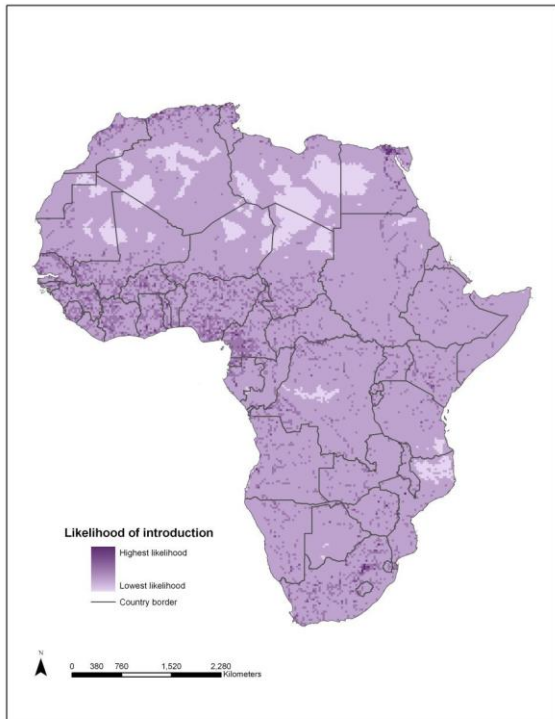

This map is the product of the EDRS-AIA project (2009)

Figure 2: Map presenting the likelihood of spread of highly pathogenic avian influenza H5N1 within Africa

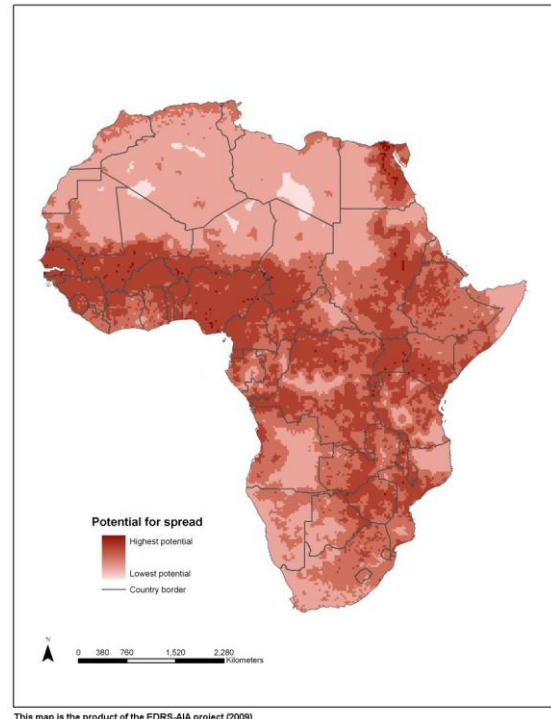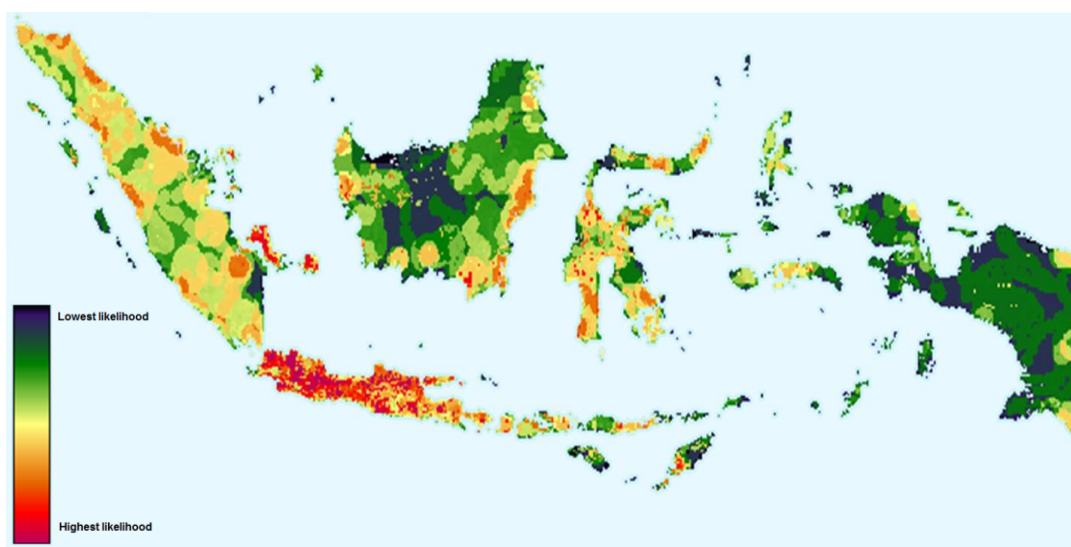This map is the product of the EDRS-AIA project (2009)

Figure 3. Map illustrating the likelihood of spread of highly pathogenic avian influenza H5N1 within Indonesia

Results – Indonesia

Areas of rice production, poultry density, and anthropogenic factors such as road and port density were considered to be most important for the spread of HPAI within Indonesia. The map (Figure 3) indicating the relative likelihood of spread in Indonesia is therefore predominantly influenced by the distribution of these factors, with lower influence from environmental factors such as distance to waterbodies and migratory bird species richness. Based on the results of the MCDM modelling, the likelihood of spread of HPAI in Indonesia is greatest on the island of Java, as well as some areas in the Banka-Belitung Islands and Sumatra. The relative likelihood of spread appears much lower in sparsely populated Papua and West Papua, as well as in a large area of the interior of Kalimantan.

Discussion

The likelihood maps produced should be interpreted bearing in mind the following points:

The accuracy of the maps depends on the quality of the data and current knowledge about the disease.

The quality of the data used as geographical inputs for the models varies. For example, some of the data used might be outdated. Additionally, not all risk factors for disease occurrence can be spatially represented. When data for specific risk factors were unavailable, proxy data were used. Weighting of the different risk factors was performed by only a small number of experts who have, of necessity, been involved in all aspects of the development of these risk maps from the outset. The experts may have therefore influenced each other's opinions. Also, there are gaps in our current knowledge, and therefore significant uncertainty, regarding the introduction and spread of HPAI H5N1, not only in Africa and Indonesia, but worldwide.

The data presented in the likelihood maps do not represent the absolute probability of disease introduction or spread.

The mapped values reflect the variation in the likelihood of introduction or spread of HPAI H5N1 relative to other grid cells on the same map, ranging from lowest to highest likelihood. In other words, the mapped values indicate where there is a lower or higher likelihood of introduction or spread of avian influenza for each grid cell with a given risk factor pattern in Africa for Figures 1 and 2, and in Indonesia for Figure 3.

It is not possible to compare findings from Africa and Indonesia.

Due to the absence of an absolute risk estimate, it is not appropriate to compare the highest (or lowest) relative likelihood of introduction or spread of avian influenza in Africa with the highest (or lowest) relative likelihood of introduction or spread in other regions or countries, such as Indonesia. The highest relative likelihood in Africa may in fact be equal to a "medium" or "low" likelihood elsewhere.

Variability and uncertainty are not accounted for in these likelihood maps.

The modelling approach applied here does not provide any indication of the uncertainty or degree of bias inherent in the output. Therefore, it is not possible to provide confidence intervals for the level of relative likelihood as they are a qualitative rather than quantitative measure (i.e. highest to lowest).

The likelihood maps do not necessarily reflect the actual distribution of avian influenza in Africa and Indonesia.

It is important to determine how closely the likelihood maps reflect the actual distribution of avian influenza outbreaks in Africa or Indonesia. However, the validation of the maps using outbreak data has not yet been carried out.

Despite these caveats, these likelihood maps can inform disease control strategies. Used critically and in conjunction with other tools such as risk assessment and local knowledge, risk maps can help policymakers target areas for strengthened surveillance and/or control activities.

References

Clements, A.C.A., D.U. Pfeiffer, V. Martin. 2006. Application of knowledge driven spatial modelling approaches and uncertainty management to a study of Rift Valley Fever in Africa. Int J Health Geogr 5 (57).

de Glanville W.A., K.B Stevens., S. Costard, R. Métras, D.U. Pfeiffer. 2009. Mapping the Risk of Spread of Highly Pathogenic Avian Influenza H5N1 in Indonesia using Multicriteria Decision Modelling. DFID funded project for Controlling Avian Flu and Protecting People's Livelihoods in Africa/Indonesia.

EDRS-AIA Early Detection, Reporting and Surveillance for Avian Influenza in Africa. 2009. Risk Mapping Products. http://www.ilri.org/research/Content.asp?CCID=11&SID=295.

Pfeiffer, D.U., T.P. Robinson et al. 2008. Spatial risk assessment and management of disease. In: *Spatial Analysis in Epidemiology*. Oxford University Press, Oxford, pp 113-117.

Stevens K.B., S.Costard, R.Métras, D.U Pfeiffer. 2009. Mapping the Likelihood of Introduction and Spread of Highly Pathogenic Avian Influenza Virus H5N1 in Africa, Ghana, Ethiopia, Kenya and Nigeria using Multicriteria Decision Modelling. DFID funded project for Controlling Avian Flu and Protecting People's Livelihoods in Africa/Indonesia.

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