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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

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1 Introduction

The results of an analysis of the spatial distribution of disease risk and its visual presentation through risk maps allow for the design of targeted and therefore more cost-effective animal disease surveillance strategies. There are various methods by which disease risk maps can be generated. One of these is multicriteria decision modelling (MCDM) which is a knowledge-driven approach to the production of risk maps.

As with all modelling work, it is important for the user of these outputs to be aware of the assumptions made in relation to the models and any potential sources of selection and information bias when interpreting the results of such analyses.

The objective of this study was to describe the spatial variation in the likelihood of (i) introduction and (ii) spread of highly pathogenic avian influenza virus (HPAIV) subtype H5N1 on a continental scale in Africa.

This report describes the methods used to produce likelihood maps illustrating the likelihood of introduction and subsequent spread of HPAIV H5N1 at both the continental and country level (Kenya, Nigeria, Ethiopia and Ghana; targeted countries of the DfID project), and highlights limitations associated with the maps.

2 Producing risk maps for Africa using multicriteria decision modelling (MCDM)

MCDM is an example of static knowledge-driven modelling that can be used to produce qualitative or quantitative estimates of risk ‘based on existing or hypothesized understanding of the causal relationships leading to disease occurrence’ (Pfeiffer et al., 2008). Knowledge of the risk factors associated with the occurrence of a disease and their interrelationships is used to drive the model.

In contrast to data-driven modelling, MCDM cannot generate estimates of absolute risk, but rather describes variation in absolute risk. This means a map produced using MCDM will allow for the identification of areas with relatively higher and lower risk of event occurrence without quantifying what the risk is, and but it will thereby still inform targeting of risk management activities. To reduce the chances of the map outputs being misinterpreted, the term ‘likelihood maps’ was used in this report instead of ‘risk maps’. However, it is acknowledged that both terms have a similar meaning.

MCDM involves the following sequence of analytical steps which were also used to structure this report:

1. Defining the objective(s)
2. Defining the factors
3. Defining the relationship between each factor and the risk
4. Sourcing digital maps of the factors and constraints
5. Standardising the maps so that they can be compared
6. Defining the relative importance of each factor in relation to the objective

7. Combining all factors and constraints to produce a final weighted estimate of risk for each location in the study area
8. Sensitivity analysis

Geographic data were visualised and manipulated using ArcGIS 9.2 (ESRI, Redlands, CA, USA) and IDRISI Andes (Clark Labs, Worcester, MA, USA). The multicriteria decision model was developed in IDRISI Andes.

2.1 Defining the objectives

The objectives of the likelihood mapping exercise were to identify factors associated separately with the (i) introduction or (ii) spread of HPAIV H5N1 in Africa, and to combine them using MCDM to produce maps separately showing the likelihood of introduction or spread HPAIV H5N1 in Africa. Note that no attempt was made to combine likelihood of introduction and spread, as it was felt that both processes will require different measures of risk mitigation. Furthermore, both results are subject to significant uncertainty which cannot be quantified when using MCDM, and combining the results may lead to propagation of bias that it would be difficult to consider when interpreting the results.

'Introduction' was defined as:

> '*The introduction of single or multiple instances of HPAIV H5N1 into an area through migratory birds or the legal or illegal movement of infected domestic poultry or poultry products'.*

'Spread' was defined as:

> '*The dissemination of HPAIV H5N1 within an area through the legal or illegal movement of infected domestic poultry or poultry products conditional on successful introduction*'.

2.2 Defining the factors associated with, and the relationship between each factor, and the likelihood of introduction and subsequent spread of HPAIV H5N1 in Africa

A systematic review of the published literature on the epidemiology of HPAIV H5N1 was used to identify risk factors associated with the introduction and subsequent spread of HPAIV H5N1, within an African context, and to define the relationship between each risk factor and the likelihood of introduction or spread. Searches for relevant literature were performed on two scientific databases assumed to represent the majority of the veterinary and medical journals; PubMed/Medline (a standard general medical database) and ISI Web of Knowledge (veterinary medicine and public health). A detailed description of the search algorithms and the complete list of risk factors identified can be found on pages 1-6 to 1-9 of the Initial Bird Flu Risk Maps Report (EDRS-AIA, 2009).

Risk factors were categorised according to their relevance for introduction or spread of the disease (Table 1 and 2). Two selection criteria were used to identify risk factors for inclusion in the MCDM:

- Relevance and importance of a risk factor to the epidemiology of HPAIV H5N1 in Africa
- Ability of the risk factor to be mapped (e.g. “owner lives off farm” [Kung, Morris et al. 2007] is a risk factor for spread that cannot be represented on a map whereas “water area” (Ducatez 2006) is a risk factor that can be spatially represented.

Tables 1 and 2 list the risk factors which meet both selection criteria for either introduction or spread of HPAI H5N1 in Africa, and were therefore incorporated into the model.

Table 1. Factors associated with the introduction of HPAIV H5N1 into Africa

Potential risk factors for the introduction of HPAIV H5N1	*Hypothesized relationship between potential risk factor and the introduction of HPAIV H5N1 in Africa*
Flyways	For the MCDM likelihood mapping, it was assumed that migratory birds constitute a risk for the introduction of HPAIV H5N1 into Africa. The migratory flyways covering areas in Africa represent areas expected to be at higher likelihood of introduction of bird flu. The role of migratory birds in long distance transmission of HPAI H5N1 has been considered in several studies, but still remains controversial due to many knowledge gaps. Wild birds (especially wild ducks) were identified as potential long distance vectors for the virus in various studies (Kilpatrick et al., 2006; Stallknecht, 2007; Gaidet et al., 2008b; Keawcharoen et al., 2008), while other authors considered it unlikely (Feare, 2007; Saad, 2007; Weber and Stilianakis, 2007). Different risk assessments of the introduction of HPAI H5N1 into different regions have concluded that the role of migratory birds was low but not negligible, with high uncertainty (Pfeiffer et al., 2006; Goutard et al., 2007; Sabirovic et al., 2007).
Surface water: wetlands and waterbodies	Increasing distance from surface water is expected to be associated with decreasing likelihood of introduction of the disease in Africa. Wetlands are considered to be aggregation sites for migratory and resident wild birds and therefore constitute potentially higher risk areas for introduction and transmission of HPAIV (Hlinak et al., 2006; Jourdain et al., 2007), as was suggested for Nigeria (Ducatez, 2006). Surveillance studies conducted in several major wetlands of Africa isolated AI viruses in Eurasian and Afro-tropical species of wild birds (Gaidet et al., 2007; Gaidet et al., 2008a). Distance to wetland areas containing migratory waterfowl species has also been hypothesised as a risk factor for the introduction of disease in Spain (Martinez et al., 2009).
Cross-border roads	For the MCDM likelihood mapping, it was hypothesized that international poultry trade occurs via roads, ports and airports, and that increasing density of ports, airports and roads is associated with a higher risk of introduction of HPAIV H5N1. Poultry trade has been identified as a risk factor for introduction of HPAIV (Ducatez, 2006; Kilpatrick et al., 2006). A study published in 2007 stressed the importance of formal and informal trade for the introduction of the disease in previously unaffected areas, as it seems was the case in Nigeria (Vannier, 2007). In addition, proximity to highways was found to be associated with the risk of HPAIV outbreak in China (Fang et al., 2008), and this is likely to be due to increased movements of poultry and poultry products for trade.
Ports	
Airports	

Table 2. Factors associated with the spread of HPAIV H5N1 in Africa given successful introduction

Potential risk factors for the spread of HPAIV H5N1 given successful introduction	***Hypothesized relationship between potential risk factor and the spread of HPAI H5N1 in Africa given successful introduction***
Roads	Increasing density of roads is expected to be associated with increasing movements of poultry and poultry products for trade, and thus higher risk of disease spread. Outbreak risk was associated with proximity to major roads in Romania (Ward et al., 2008) and China (Fang et al., 2008). This is likely to be due to transport of poultry for trade via road.
Navigable rivers	Increasing distance from navigable rivers is expected to be associated with decreasing risk of spread of the disease. There is no published evidence for the direct role of navigable rivers in the spread of HPAIV.,However, given the identification of roads as a risk factor (Fang et al., 2008; Ward et al., 2008) such a role can be hypothesized for important rivers in Africa known to be used for transport of consumption goods and livestock.
Poultry density	Increasing density of poultry is expected to be associated with a higher contact rate between susceptible and infected birds and therefore greater risk of spread. It was found that H5N1 persistence in Nigeria was correlated with backyard chicken and duck numbers (Cecchi et al., 2008). Proximity to an infected farm has been shown to be an important factor in the spread of low pathogenicity influenza viruses (Mannelli et al., 2006) as well as distance to the nearest case farm (Nishiguchi et al., 2007). Conversely, Fang et al., 2008 found no association between poultry density and the risk of HPAIV infection in China, arguing that this unexpected finding was due to a greater proportion of industrialised chicken production at higher poultry densities, with associated higher biosecurity standards and vaccination protocols. Henning et al. (2009) found that poultry density was a risk factor for HPAIV outbreaks in Vietnam, but only at medium population densities. High poultry density was postulated as a risk factor for HPAIV occurrence in Thailand (Tiensin et al., 2005) and in Hong Kong (Kung et al., 2007), although this has been shown to be associated more with duck density alone than total poultry density (Gilbert et al., 2006).
Presence of poultry markets/cities	Increasing density of cities is expected to be associated with increasing risk of spread of HPAI H5N1. Cities are associated with higher demand for poultry products and therefore the presence of trading areas providing live or freshly slaughtered birds. Low pathogenicity viruses have been isolated from poultry in live bird markets in the USA (Bulaga, 2003), China (Cheung et al., 2007) and Korea (Choi et al., 2005), and HPAI has been isolated from a live bird market in Vietnam (Nguyen et al., 2005). Sale of chicken at retail markets was also identified as a risk factor for HPAI infection of farms in Hong Kong (Kung et al., 2007). The risk of HPAI outbreak was found to be negatively associated with increasing distance from higher density human population areas (Pfeiffer et al., 2007), and this is likely to be due to increased intensity of production and trade of poultry in highly populated areas.
Natural wetlands and water bodies	Increasing distance from wetlands and waterbodies is expected to be associated with decreasing risk of spread of the disease. Proximity to wetlands has been shown to be a risk factor for the occurrence of HPAI in poultry in South-East Asia (Gilbert et al., 2006; Fang et al., 2008), as has proximity to rivers and wetlands in Romania (Ward et al., 2008; Ward et al., 2009). Distance to wetland areas containing migratory waterfowl species has been hypothesised as a risk factor for disease in Nigeria (Cecchi et al., 2008).
Irrigated areas	Proximity to irrigated areas is expected to be associated with increased risk of spread of HPAI H5N1. Rice crop production has been found to be associated with HPAI in Vietnam and Thailand (Gilbert, 2007; Pfeiffer et al., 2007), as has aquaculture (Pfeiffer et al., 2007).

2.3 Sourcing and standardization of maps

Geographic inputs for the model need to be in the form of raster maps. However, it seldom happens that the exact raster maps needed for the MCDM are readily available in the required format; they usually need to be derived from existing map layers of the risk factors. Sometimes all that is necessary is a simple conversion from vector to raster format, but at other times the first generation of risk factor maps require extensive manipulation to produce the raster maps that will be included in the modelling process.

Risk factor maps were manipulated as presented in Tables 3 and 4 to produce the raster maps needed for the multicriteria decision modelling. Where required the raster maps were then reclassified so that their scale was positively correlated with the outcome (likelihood of disease introduction or spread) and map scales were standardized by converting each one to a byte binary scale ranging from 0 to 255.

A more detailed description of the risk factor maps is available in the Initial Bird Flu Risk Map Report (EDRS-AIA, 2009).

Table 3: Manipulations required to convert risk factor map layers into risk factor raster maps (for risk of introduction of HPAIV into Africa)

Risk factor map	Manipulation	Raster map
Flyways for migratory birds (Vector map, FAO 2005)	Extraction of Black Sea flyway	Presence/absence of Black Sea flyway (Resolution 0.083 x 0.083 decimal degrees)
	Extraction of East Africa Flyway	Presence/absence of East Africa Flyway (Resolution 0.083 x 0.083 decimal degrees)
	Extraction of East Atlantic flyway	Presence/absence of East Atlantic flyway (Resolution 0.083 x 0.083 decimal degrees)
Location of surface water: Water bodies (Vector map, RWDB- USGS) Wetlands (Vector map, Lehner and Döll 2004) Irrigated areas (Vector map, Siebert *et al*. 2007)	Calculate and map distance from: (1) Lakes and impoundments, (2) irrigated areas, (3) swamps and marshes, (4) salty lakes, (5) lagoon, mangroves, and (6) salt pan	Distance from surface water (Resolution 0.083 x 0.083 decimal degrees)
Location of ports (Vector map, FAO)	Calculate and map density of ports per 1000 km^2	Density of ports (Resolution 0.285 x 0.285 decimal degrees)
Location of airports (Vector map, RWDB- USGS)	Calculate and map density of airports per 1000 km^2	Density of airports (Resolution 0.285 x 0.285 decimal degrees)
Location of roads (Vector map, CIESIN 2004)	Calculate and map linear density of roads per 100 km^2	Density of roads (Resolution 0.083 x 0.083 decimal degrees)

Table 4: Manipulations required to convert risk factor map layers into risk factor raster maps (for risk of spread of HPAIV in Africa given introduction)

Risk factor map	**Manipulation**	**Raster map**
Location of roads: (Vector map, CIESIN 2004)	Calculate and map linear density of roads per 100 km^2	Density of roads (Resolution 0.083 x 0.083 decimal degrees)
Location of rivers (Vector map, ESRI 2005)	Calculate distance (km) to navigable rivers	Distance to navigable rivers (Resolution 0.083 x 0.083 decimal degrees)
Location of cities (pop > 50000) (Vector map, GRUMP 2005)	Calculate and map density of cities per 100 km^2	Density of cities (Resolution 0.083 x 0.083 decimal degrees)
Location of surface water : Water bodies (Vector map, RWDB- USGS) Wetlands (Vector map, Lehner and Döll 2004) Irrigated areas (Vector map, Siebert *et al*. 2007)	Calculate and map distance (km) from: (1) Lakes and impoundments, (2) irrigated areas, (3) swamps and marshes, (4) salty lakes, (5) lagoon, mangroves, and (6) salt pan	Distance from surface water (Resolution 0.083 x 0.083 decimal degrees)
Poultry density (Raster map, Wint and Robinson 2007)	No manipulation required (Resolution 0.05 x 0.05 decimal degrees)	Poultry density (Resolution 0.05 x 0.05 decimal degrees)

2.4 Defining the relative importance of each factor in relation to the outcome (i.e introduction or spread of HPAIV)

Five members of the project team with experience in either avian influenza epidemiology or knowledge about the field situation in Africa weighted pairs of risk factors specifying firstly whether Factor A (for example) was more or less important than Factor B (for example) regarding the introduction or spread of HPAIV H5N1 in Africa and secondly, the degree of importance. Factor A could be (i) Equally, (ii) Moderately, (iii) Strongly or (iv) Very Strongly, more or less important than Factor B. These weightings were based on each team member’s expert opinion, and were performed for each pairwise combination of factors. The five sets of weightings were then compared and where three of the five team members had the same weighting, it was taken to be the agreed weighting. Where there were discrepancies between team members’ weightings for any pair of factors, the weighting was discussed and a final weighting agreed upon. The agreed weightings for each pairwise comparison of the risk factors for the introduction and spread of HPAIV H5N1 in Africa are presented in Tables 5 and 6. For the pairwise comparison risk factors in the rows are weighted relative to the risk factors in the columns. For example, reading from Table 5, the risk factor *density of airports* is considered to be *moderately more important* than *distance from waterbodies* for the introduction of HPAIV H5N1 into Africa. The agreed pairwise weightings were used to derive a weight for each risk factor by taking the principal eigenvector of the pairwise comparisons, and these weights were incorporated into the multicriteria decision model (Tables 7 and 8).

Table 5: Agreed weightings from the pairwise comparison of risk factors for the introduction of HPAIV H5N1 into Africa

	Black Sea flyway	East Africa flyway	East Atlantic flyway	Distance from waterbodies	Density of ports	Density of airports	Density of roads
Presence/absence of Black Sea flyway							
Presence/absence of East Africa flyway	Equal importance						
Presence/absence of East Atlantic flyway	Moderately less important	Moderately less important					
Distance from waterbodies	Moderately more important	Moderately more important	Strongly more important				
Density of ports	Strongly more important	Strongly more important	Strongly more important	Moderately more important			
Density of airports	Strongly more important	Strongly more important	Very strongly more imp.	Moderately more important	Equal importance		
Density of roads	Very strongly more imp.	Very strongly more imp.	Extremely more important	Strongly more important	Moderately more important	Moderately more important	

Table 6: Agreed weightings from the pairwise comparison of risk factors for the spread of HPAIV H5N1 in Africa (assuming introduction)

	Density of roads	Density of cities	Distance from waterbodies	Distance from irrigated areas	Poultry density	Distance to navigable rivers
Density of roads						
Density of cities	Equal importance					
Distance from waterbodies	Moderately less important	Moderately less important				
Distance from irrigated areas	Strongly less important	Strongly less important	Moderately less important			
Poultry density	Equal importance	Equal importance	Moderately more important	Strongly more important		
Distance to navigable rivers	Equal importance	Equal importance	Moderately more important	Strongly more important	Equal importance	

Table 7: Calculated weights of risk factors for the introduction of HPAIV H5N1 into Africa

Risk factor	**Weight**
Black Sea flyway	0.0341
East Africa flyway	0.0341
Atlantic flyway	0.0189
Distance from water	0.0686
Density of ports	0.1369
Density of airports	0.1369
Density of primary roads	0.2853
Density of secondary roads	0.2853

The data presented in Table 7 indicates that the experts felt that the likelihood of introduction is most strongly influenced by trade networks (total weight = 0.84) and much less by exposure to migrating wild birds (total weight = 0.16), and this assumption therefore strongly influences the likelihood scores generated by the MCDM for likelihood of introduction.

Table 8: Calculated weights of risk factors for the spread of HPAIV H5N1 in Africa given introduction

Risk factor	Weight
Density of primary roads	0.1527
Density of secondary roads	0.1527
Density of tertiary roads	0.1527
Density of cites	0.1527
Distance from water	0.0554
Distance from irrigated areas	0.0286
Poultry density	0.1525
Density of navigable rivers	0.1525

The data presented in Table 8 indicates that the experts felt that the likelihood of spread given introduction is most strongly influenced by road networks (total weight = 0.46), urbanisation (weight = 0.15) and poultry density (weight = 0.15) and much less by access to surface water (total weight = 0.08), and this assumption will therefore strongly influence the likelihood scores for spread generated by the MCDM.

2.5 Continental likelihood maps: Combining all factors to produce a final weighted estimate of likelihood of introduction and spread

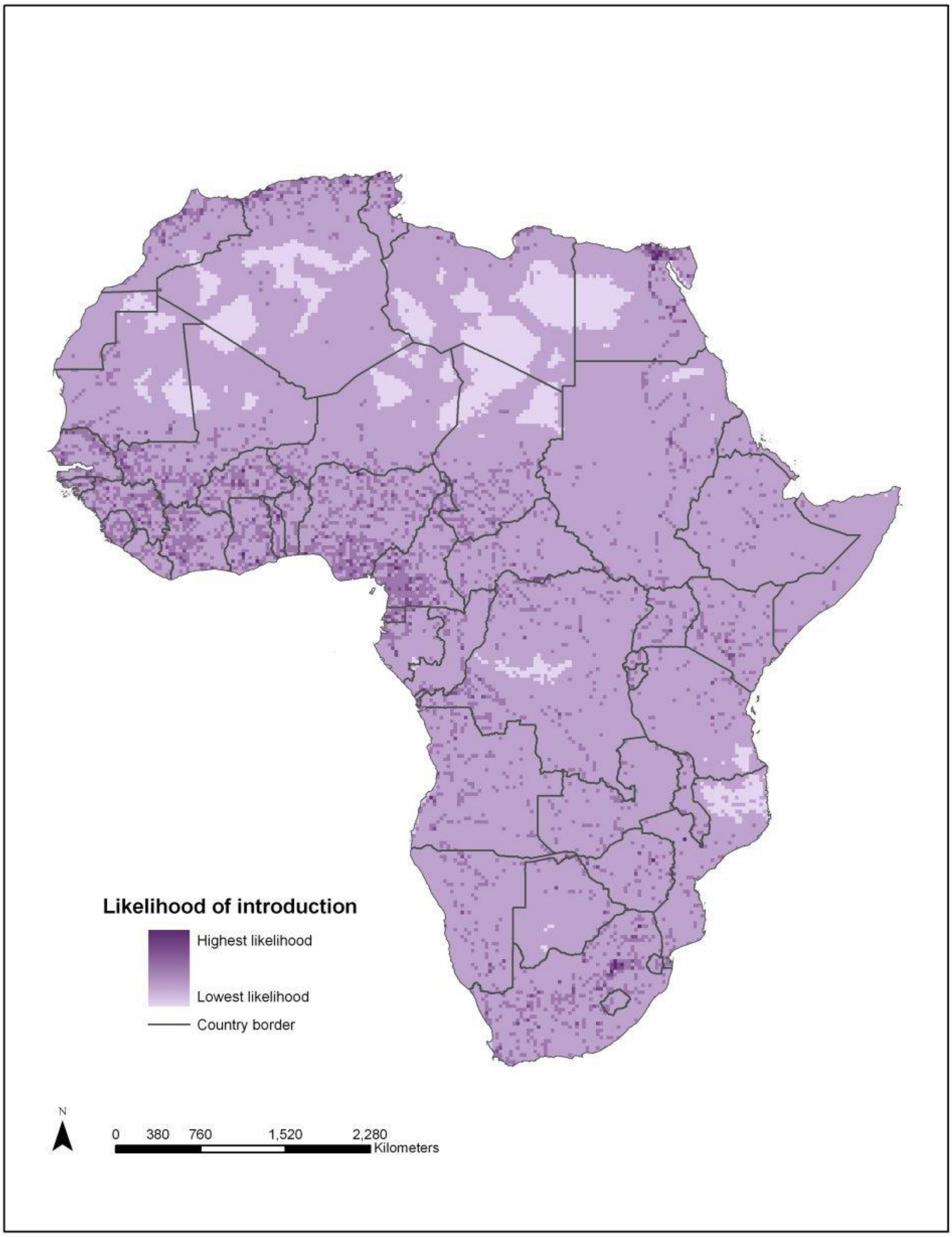
The risk factor maps and weights were combined using a method known as weighted linear combination (WLC) (Pfeiffer, Robinson et al 2008; Malczewski 1999) in which factors with a higher weight exert a greater influence on the final likelihood estimate. An explanation of the combination method can be found on pages 3-4 of the Initial Bird Flu Risk Map Report (EDRS-AIA, 2009). The combination method generated a numeric likelihood score on a scale of 0 (lower likelihood) to 255 (higher likelihood) for each pixel of the map. This score has a range from 0-255 to allow taking advantage of the colour range used by the Idrisi Andes software. The numerical value has no absolute likelihood interpretation but rather one of relative likelihood, i.e. allowing characterisation of locations with relatively lower or higher likelihood.

The resulting maps identify:

- Area(s) of the continent where HPAIV H5N1 is most likely to be introduced -based on the risk factors considered (Figure 1);
- Area(s) of the continent where an outbreak of HPAIV H5N1 has the greatest likelihood to spread given that it has been introduced - based on the risk factors considered (Figure 2).

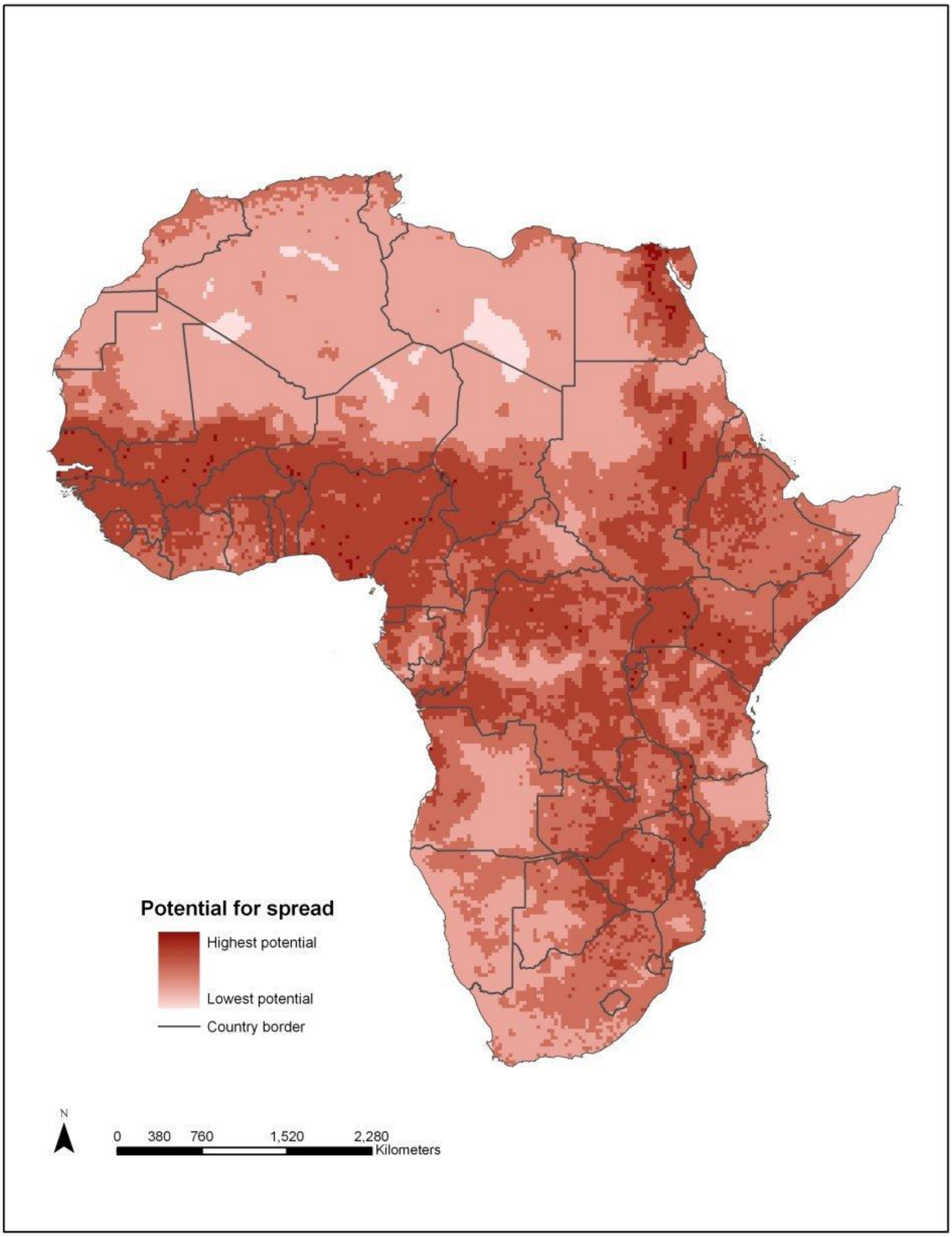
Areas identified as having the highest likelihood of introduction of HPAIV H5N1 include the Nile Delta, the coastline of Northern Africa, Western Africa, and parts of South Africa (Figure 1). Areas identified as having the lowest likelihood of introduction include Northern Africa, Somalia, Ethiopia and Botswana (Figure 1).

Most of sub-Saharan Africa was identified as having the highest likelihood for the spread of HPAIV 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 HPAIV H5N1. Regions with the lowest likelihood of spread include Northern Africa, Somalia, Angola, Namibia and the south-west parts of South Africa (Figure 2).



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

Figure 1: Map showing the likelihood of introduction of HPAIV H5N1 into Africa, produced using MCDM



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

Figure 2: Map showing the likelihood for spread of HPAIV H5N1 in Africa given that the disease has been introduced (generated using MCDM)

2.6 Sensitivity analysis

For each risk factor two new weights were calculated by (i) adding and (ii) subtracting 25% from the original weight. Each of the newly calculated weights was then individually incorporated into the multicriteria decision model, while holding all other factor weights constant, thereby generating 16 new likelihood maps. The likelihood estimate was measured at 10 000 randomly selected locations on each of the maps, and the average change in the likelihood estimate as a result of altering the different factor weights was calculated (Tables 7 and 8). The highest average change in the likelihood score was 3.91 ± 2.29 as a result of decreasing the weight assigned to tertiary road density in the spread of disease. In other words, changing the weight assigned to tertiary road density by 25% would be expected to change the final overall risk score for the spread of avian flu by only 2 to 6 points on a scale of 255.

Likelihood estimates for both disease introduction and spread were highly robust, showing little change as a result of the altered weights. But it needs to be noted that this does not provide information about the validity of the likelihood scores, but rather their stability given variation in the relative weighting of the risk factors used to generated the scores.

Table 7: Sensitivity analysis of the factors and weights used to estimate and map the likelihood of introduction of HPAIV H5N1 into Africa (average change in likelihood estimates was calculated from 10 000 randomly selected locations)

	Average change in likelihood estimate (± std. dev)	
Risk factor	**Factor weight increased by 25%**	**Factor weight decreased by 25%**
East Africa Flyway	0.10 ± 0.54	0.09 ± 0.56
East Atlantic Flyway	0.02 ± 0.52	0.02 ± 0.53
Black Sea Flyway	1.26 ± 0.67	1.29 ± 0.68
Airport density	1.05 ± 0.57	1.11 ± 0.59
Port density	1.09 ± 0.51	1.15 ± 0.53
Primary road density	2.05 ± 0.82	2.33 ± 0.89
Secondary road density	1.94 ± 0.85	2.21 ± 0.93
Tertiary road density	2.92 ± 1.26	3.03 ± 1.30

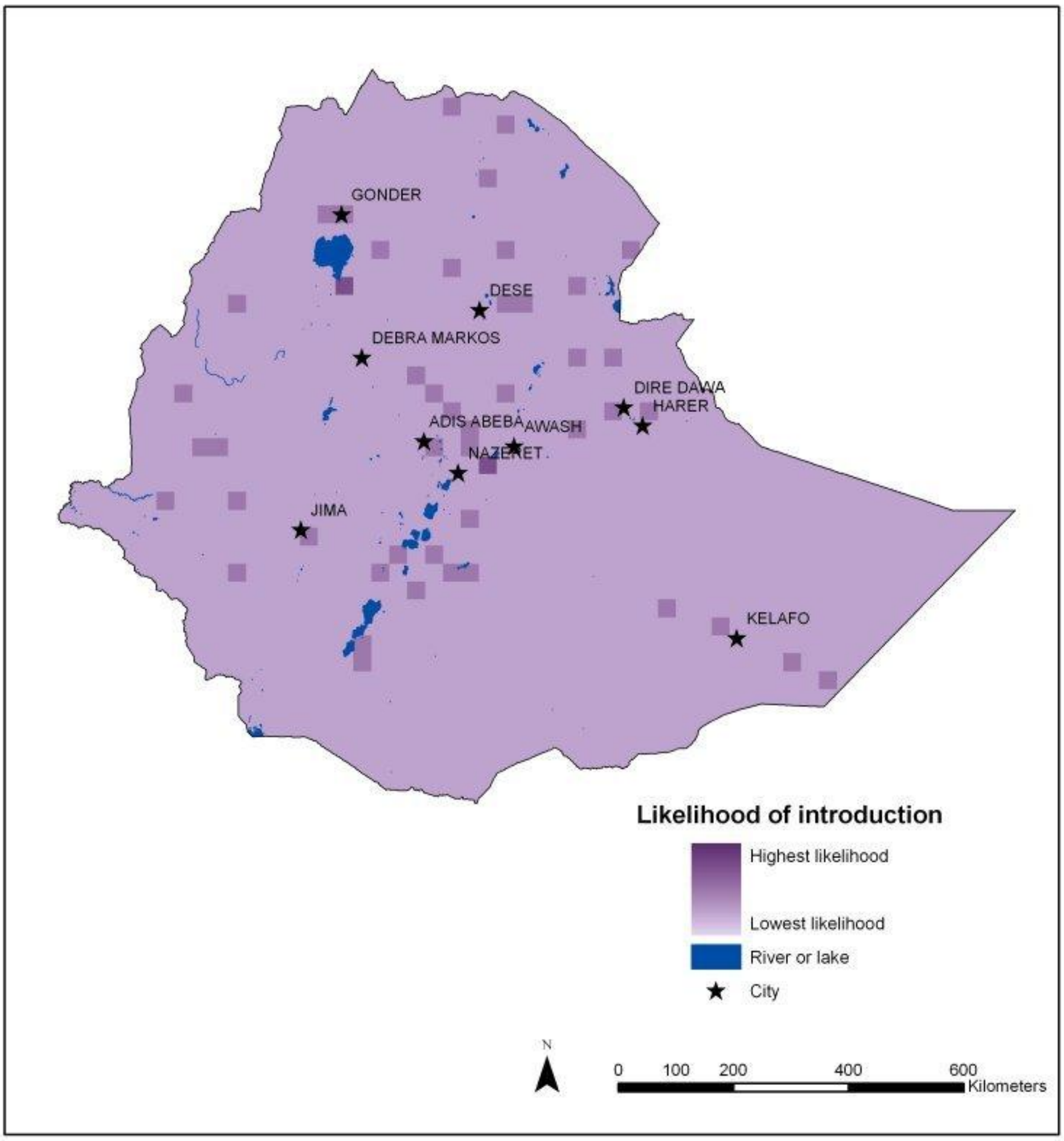
Table 8: Sensitivity analysis of the factors and weights used to estimate and map the likelihood of spread of HPAIV H5N1 in Africa given introduction (average change in risk estimates was calculated from 10 000 randomly selected locations)

	Average change in likelihood estimate (± std. dev)	
Risk factor	**Factor weight increased by 25%**	**Factor weight decreased by 25%**
Primary road density	3.46 ± 1.10	3.73 ± 1.18
Secondary road density	3.40 ± 1.11	3.66 ± 1.19
Tertiary road density	3.61 ± 2.13	3.91 ± 2.29
Density of cities	2.74 ± 2.03	2.96 ± 2.18
Distance to waterbodies	1.12 ± 0.89	1.15 ± 0.91
Distance to irrigated land	0.39 ± 0.64	0.40 ± 0.64
Distance to navigable rivers	2.51 ± 2.30	2.73 ± 2.48

3 Country maps

From the continental likelihood maps for introduction and spread (Figures 1 and 2), maps for four countries were extracted; Ethiopia, Nigeria, Kenya and Ghana. These country-level likelihood maps (Figures 3 to 10) are presented on the following pages. Note that the range of the colour scale used to present the variation in likelihood was based on the map for the whole continent.

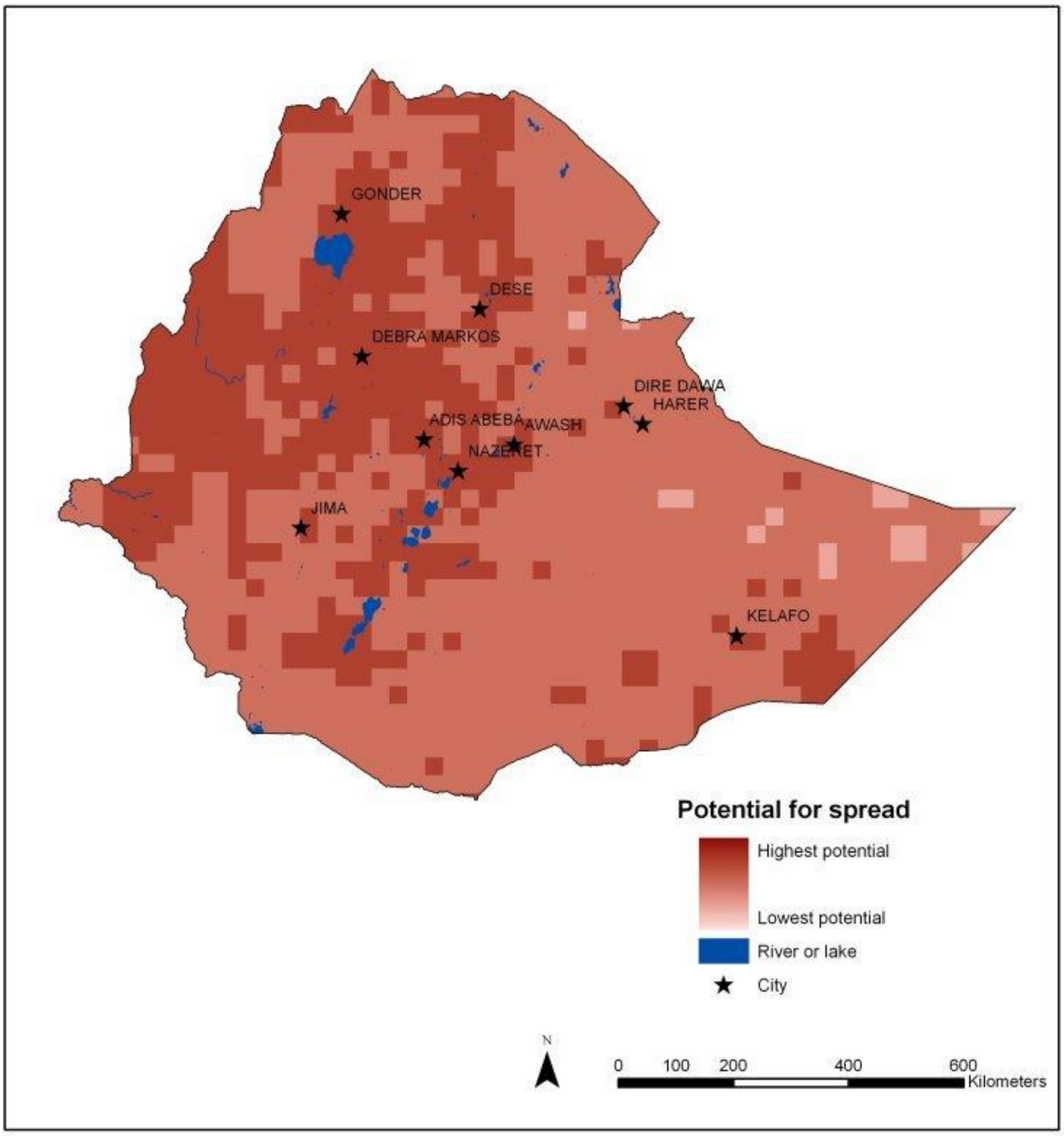
3.1 Ethiopia



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

Figure 3: Map showing the likelihood of introduction of HPAIV H5N1 into Ethiopia, produced using MCDM

The map presented in Figure 3 shows that the likelihood of introduction of HPAIV H5N1 is fairly homogeneous across Ethiopia. But there are some pockets of increased likelihood of introduction.

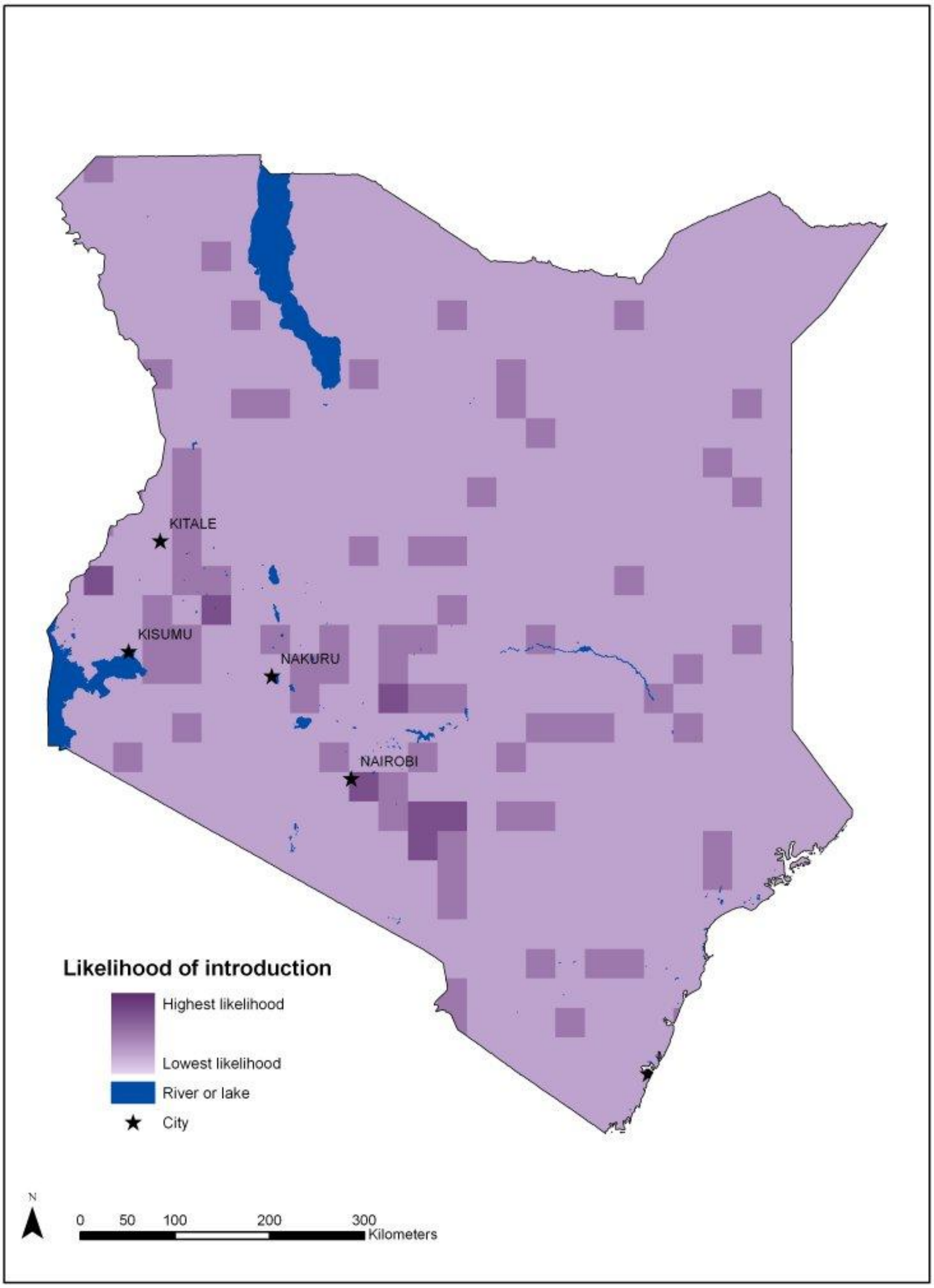


This map is the product of the EDRS-AIA project (2009)

Figure 4: Map showing the likelihood for spread of HPAIV H5N1 in Ethiopia assuming that the disease has been introduced (generated using MCDM)

The map presented in Figure 4 shows that the likelihood of spread of HPAIV H5N1 assuming that the virus has been successfully introduced into Ethiopia. It is apparent that the likelihood is higher towards the western half of the country, and lower in the eastern parts.

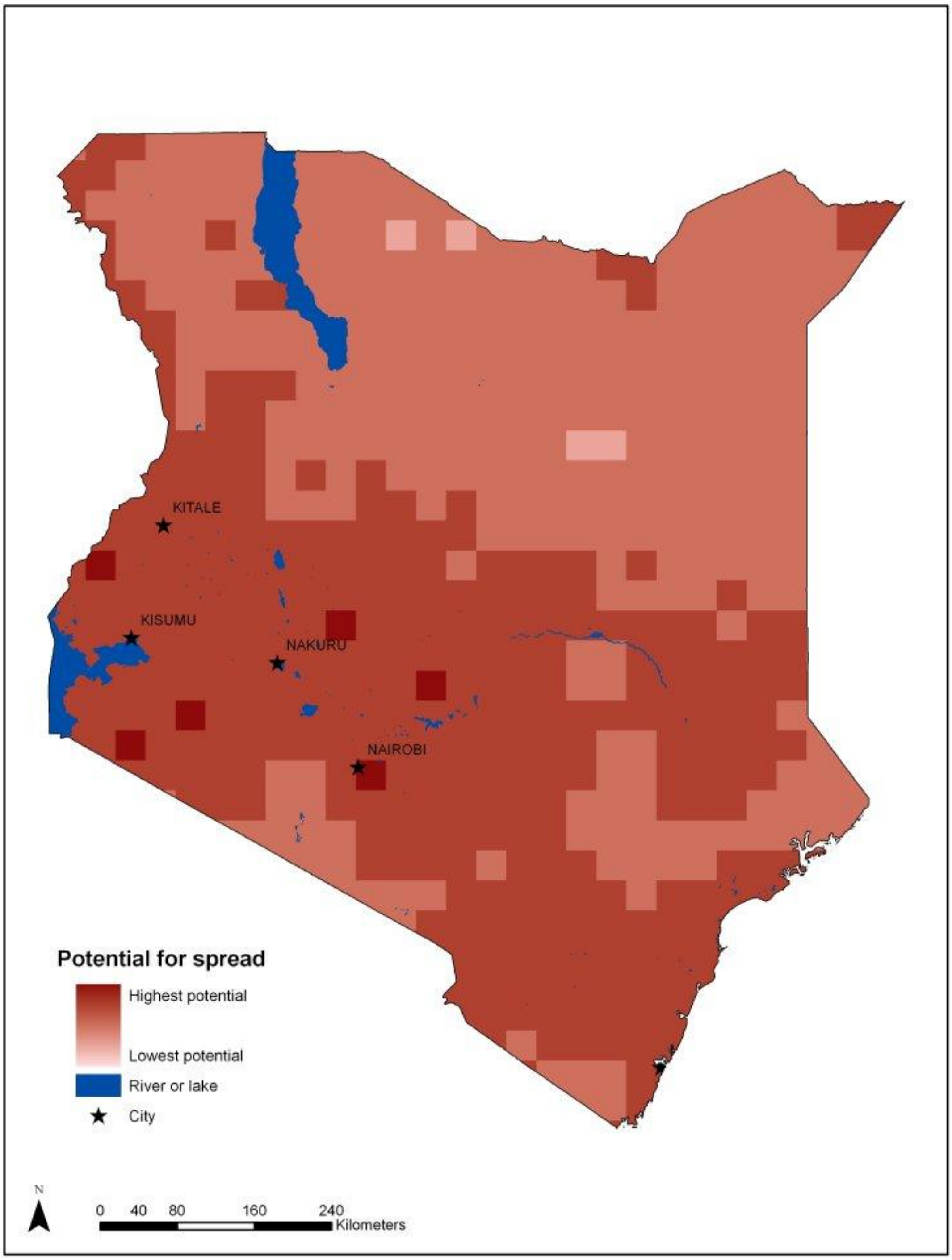
3.2 Kenya



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

Figure 5: Map showing the likelihood of introduction of HPAIV H5N1 into Kenya, produced using MCDM

The map presented in Figure 5 shows that the likelihood of introduction of HPAIV H5N1 is fairly homogeneous across Kenya. But there are some pockets of increased likelihood of introduction.

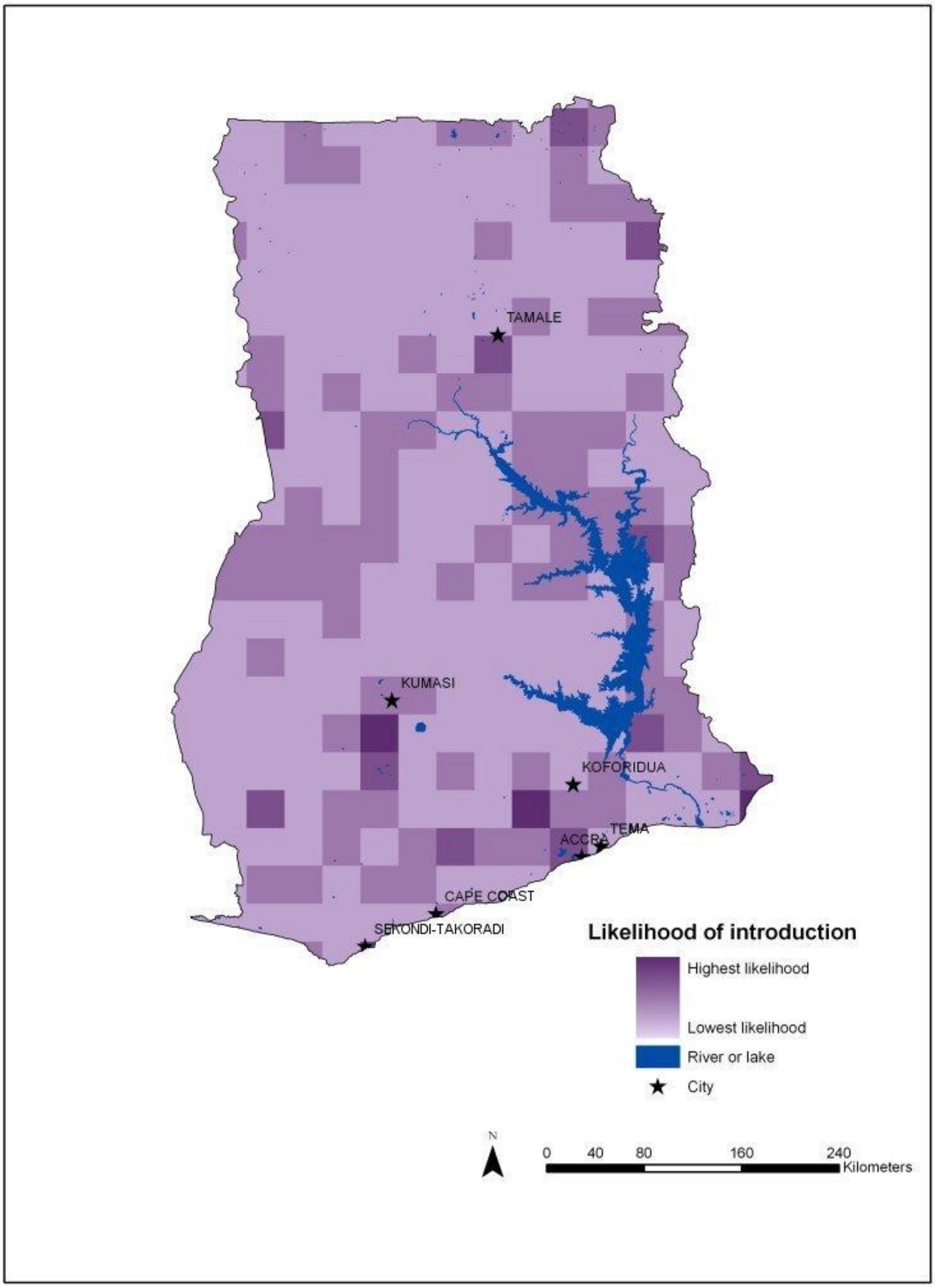


This map is the product of the EDRS-AIA project (2009)

Figure 6: Map showing the likelihood for spread of HPAIV H5N1 in Kenya assuming that the disease has been introduced (generated using MCDM)

The map presented in Figure 6 shows that the likelihood of spread of HPAIV H5N1 assuming that the virus has been successfully introduced into Kenya. It is apparent that the likelihood is higher towards the southern half of the country, and lower in the northern parts.

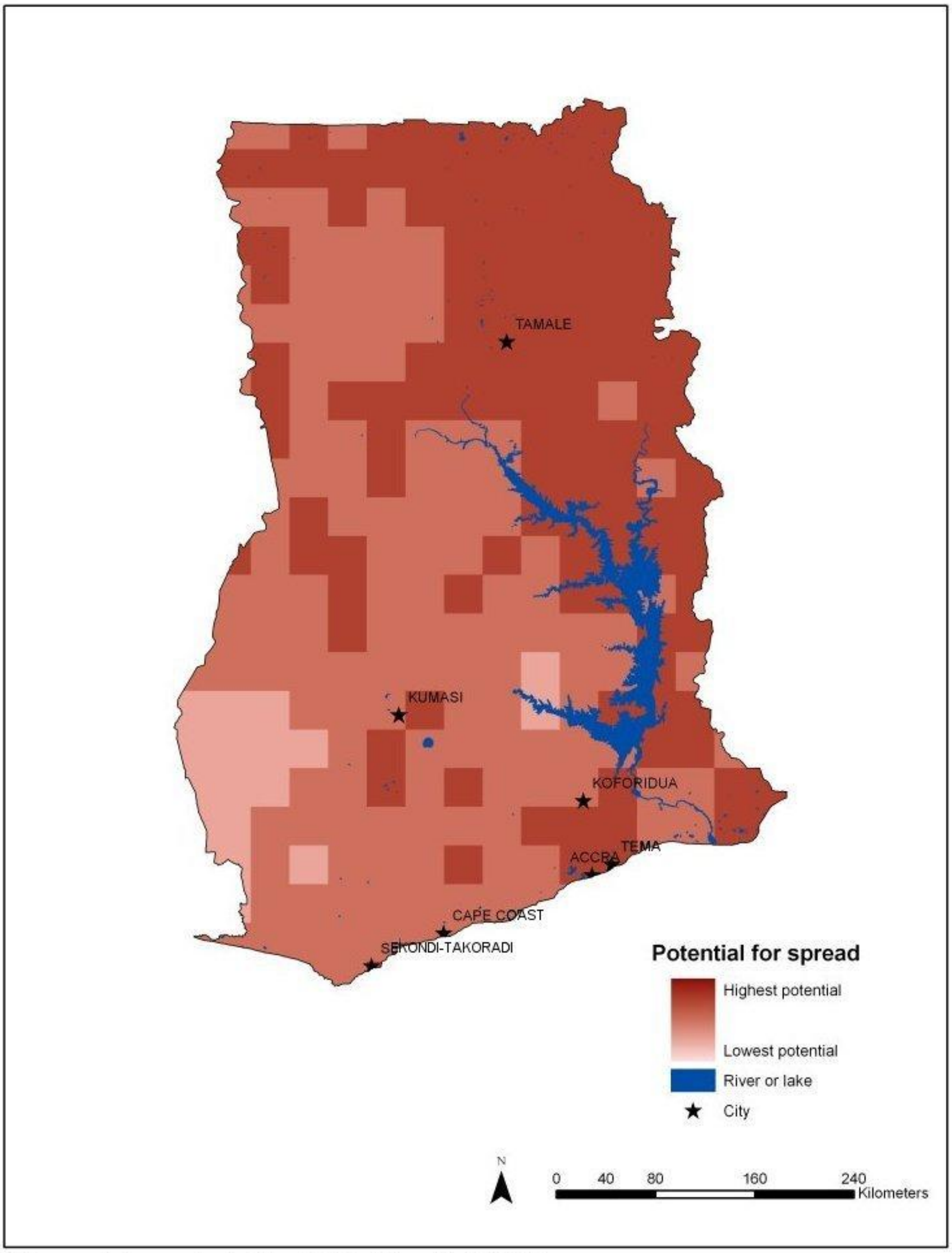
3.3 Ghana



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

Figure 7: Map showing the likelihood of introduction of HPAIV H5N1 into Ghana, produced using MCDM

The map presented in Figure 7 shows that the likelihood of introduction of HPAIV H5N1 varies across Ghana. But no clear pattern can be defined, apart from there being a small number of high likelihood locations.

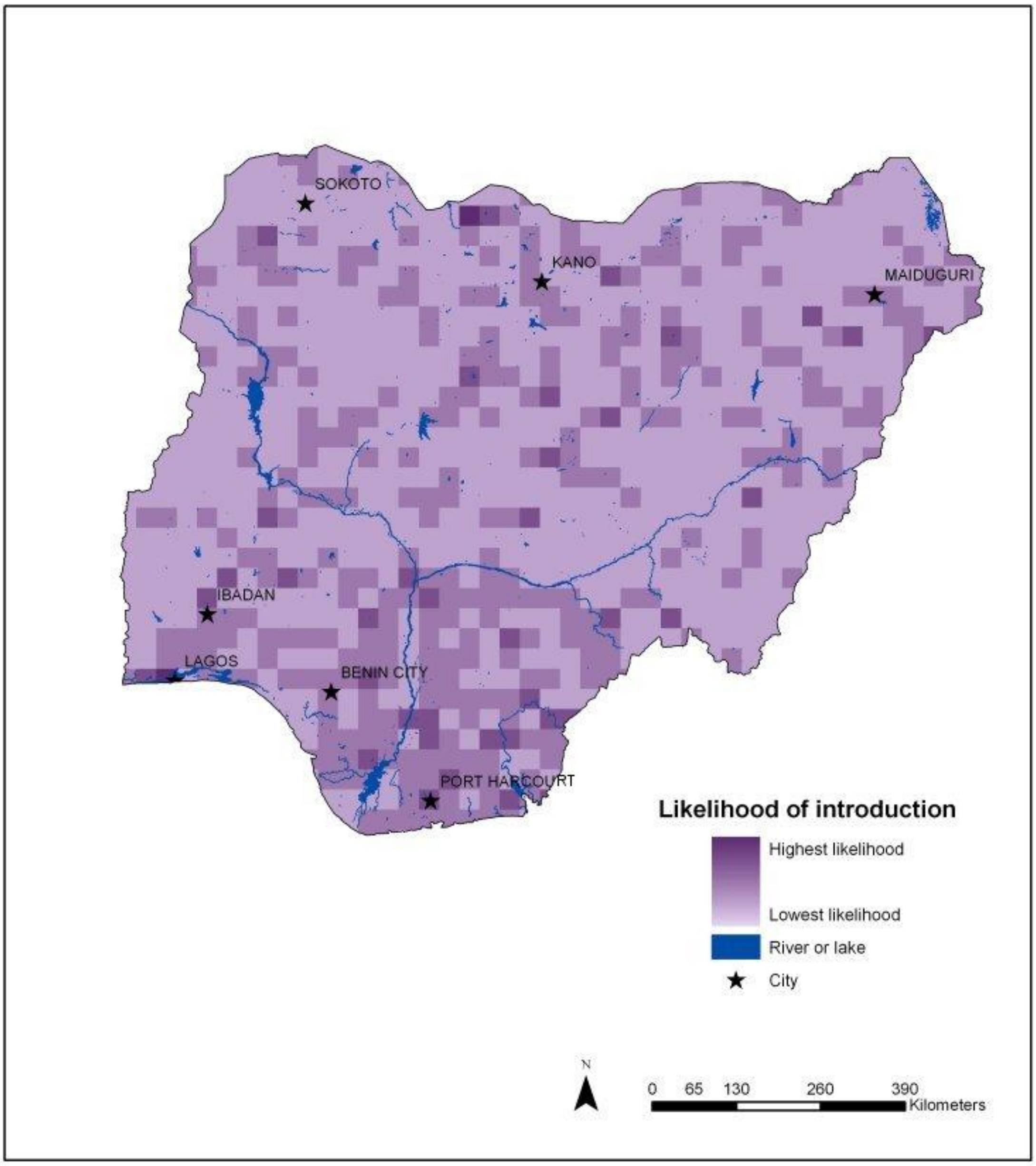


This map is the product of the EDRS-AIA project (2009)

Figure 8: Map showing the likelihood for spread of HPAIV H5N1 in Ghana once the disease has been introduced (generated using MCDM)

The map presented in Figure 8 shows that the likelihood of spread of HPAIV H5N1 assuming that the virus has been successfully introduced into Ghana. It is apparent that the likelihood is increases towards the eastern part of the country, and is lowest in the south-west.

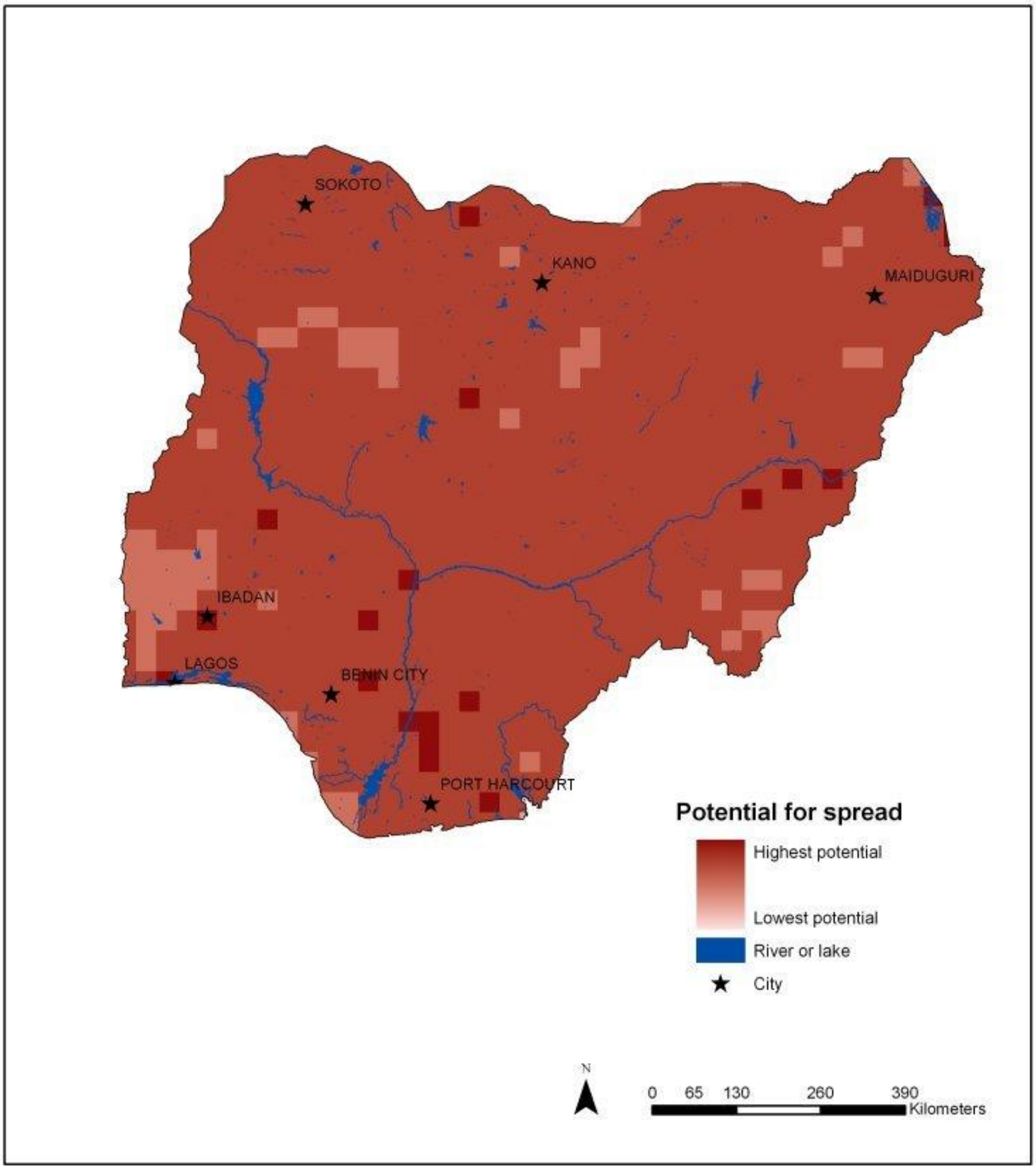
3.4 Nigeria



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

Figure 9: Map showing the likelihood of introduction of HPAIV H5N1 into Nigeria, produced using MCDM

The map presented in Figure 9 shows that the likelihood of introduction of HPAIV H5N1 varies across Nigeria. There a pockets of increased risk spread across the country, and the risk appears to be highest in the south.



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

Figure 10: Map showing the likelihood for spread of HPAIV H5N1 in Nigeria assuming that the disease has been introduced (generated using MCDM)

The map presented in Figure 10 shows that the likelihood of spread of HPAIV H5N1 assuming that the virus has been successfully introduced into Nigeria. It is apparent that the likelihood is relatively homogenous, but high across the country.

4 Interpretation and limitations of the likelihood or risk maps

One of the key findings of the continental analysis is that the likelihood of *introduction* is relatively homogenous across Africa with small pockets of increased likelihood spread out across Africa. This finding is most likely the result of giving ports and airports a relatively high weighting in the MCDM for likelihood of introduction. A high likelihood for *spread* assuming successful introduction of HPAIV H5N1 is geographically more widespread, mainly influenced by the assumption that continental transport networks (roads, navigable rivers and internal airports) have a key influence on spread once the virus has been introduced. However, these results should be interpreted with care, taking into account that they are based on assumptions made by the experts in relation to the selection of risk factors and their relative importance, the quality of the data used as well as the method used to weight the different risk factors.

4.1 Data considerations

Data quality: The quality of the data used as geographical inputs for the model varies. For example, we suspect that data pertaining to the number of ports and airports might be an underestimate of the current situation. In addition, the road map displayed only primary, secondary and tertiary roads; data on minor roads, which could play an important role in the illegal trade of poultry, were unavailable.

Proxies: When data for specific risk factors was unavailable, proxy data was used. For example, as there is no available data on the location of markets in Africa, cities with human populations of more than 50 000 were used as proxies for the location of markets. This may bias the results as even if the main markets would be located in the main cities, marketing activities in rural areas might play an important role in legal or illegal trade.

4.2 Weighting considerations

Influence: Weighting of the different risk factors was performed by only five people who have, of necessity, been involved in all aspects of the development of these risk maps from the outset. The participants may have therefore have influenced each other's opinion regarding weighting of the risk factors.

Lack of knowledge: There is a general lack of knowledge and uncertainty regarding the introduction and spread of HPAI H5N1, not only in Africa, but worldwide. However, our access to the most up-to-date scientific knowledge on the subject hopefully translates into a better assessment of the risk factors involved and their relative importance in the introduction and spread of HPAI H5N1 in Africa.

With data-driven models, outcome data and a set of risk factors are used to generate weights for the different risk factors so that the error in the outcome is minimised. With these methods, we are given an idea about lack of information through the amount of residual variance in the outcome. These models are affected by selection and information bias (misclassification of outcome and incorrect risk factor data) and by external validity issues. With a knowledge-driven model, we have no outcome data and therefore need to make subjective judgements to generate the weights for risk factors thereby creating a potentially substantial source of apparently unquantifiable bias, even with sensitivity analysis. This can be explored to some extent by using Dempster-Shafer theory (Dempster 1966; 1967). We also have no mechanism for knowing whether important information is missing, and although MCDA models will not be affected by misclassification bias of the outcome, they can still be affected by data errors in the risk factors. These considerations should be taken into account when interpreting and using the risk maps.

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