Mapping of poverty and likely

zoonoses hotspots

Zoonoses Project 4

Report to Department for International Development, UK

ZSL
LIVING CONSERVATION

TRƯỜNG ĐẠI HỌC Y TẾ CÔNG CỘNG
HANOI SCHOOL OF PUBLIC HEALTH

The objective of this report is to present data and expert knowledge on poverty and zoonoses hotspots to inform prioritisation of study areas on the transmission of disease in emerging livestock systems in the developing world, where prevention of zoonotic disease might bring greatest benefit to poor people.

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Report sumbitted 18th June 2012

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Introduction

Mapping and measuring the burden of zoonoses, the density and number of poor livestock keepers and emerging markets for livestock products can help identify the ‘hotspots’ where zoonoses not only impose significant burdens but where zoonoses management is likely to be pro-poor (targeted at poor livestock keepers and poor consumers of livestock products) and have most impact on helping small farmers reach emerging markets.

All zoonoses are not equal and a first step of the study was to categorise zoonoses according to epidemiology and impact. We considered three groups of zoonoses:

- Endemic zoonoses are present in many places and affect many people and animals.
- Outbreak or epidemic zoonoses are sporadic in temporal and spatial distribution.
- Emerging zoonoses newly appear in a population or have existed previously but are rapidly increasing in incidence or geographical range. Many occur as outbreaks.

The first chapter reviews the substantial literature on prioritising disease and identifies prioritisation criteria relevant to this study, namely: burden of human disease; impacts on livestock production and productivity; amenability to agricultural intervention; and, concern because of emergence or severity. This allowed us to identify 24 zoonoses of high importance to poor people, 13 of which we investigated in depth. Our priorities were broadly similar to comparable exercises.

The next chapter reviews current evidence on poverty and livestock, on livestock systems and their dynamics, and on zoonoses and how they are currently mapped. We update the map of poor livestock keepers of Thornton et al. (2002) and present an additional map based on sub-national data. Maps of livestock systems that are changing most rapidly in response to emerging markets are taken from Herrero et al 2009 and Notenbaert et al 2009), and vulnerability to climate change from Ericksen et al 2011). The strengths and weaknesses of different maps are noted and quantitative examples provided on the massive under-reporting of zoonoses and animal diseases in poor countries.

The next chapter presents evidence from a systematic review of over 1,000 studies on the prevalence of the 13 priority zoonoses in people and animals. It focuses on the endemic zoonoses that impose greatest burden and a ‘top 20’ list is given of geographical hotspots. Data on zoonoses are also extracted from the WHO Global Burden of Disease and the ‘top 20’ countries identified. We include a case study that compares our systematic review with an ‘in-country review’ focusing on grey literature and literature in a language other than English. Finally, we discuss some of the challenges of the study and caution in interpreting the results. Maps are presented.

The next chapter updates the map of emerging disease events of Jones et al. (2008). For the first time, we map emerging zoonoses as distinct from other emerging disease events. A ‘top 20’ of geographical hotspots is given. Maps are presented. The last chapter provides maps of regional agro-ecosystems and summarises numbers of livestock, people and poor livestock keepers by system as well as the zoonoses context. It also draws some global conclusions from the study.

Annexes provide references for the papers in the systematic review of endemic zoonoses, the in-country review, and the systematic review of emerging zoonotic events. They provide information on the long list of zoonoses and the selection of the 13 most important to poor people in terms of burden and economic impacts.

Key points

There is a strong association between poverty, livestock keeping, and zoonoses
Strength of evidence: strong

Zoonotic disease has many aspects and existing disease reporting systems do not adequately capture the impact of zoonoses or identify investment opportunities. There is much unpublished information in grey literature of developing countries.
Strength of evidence: strong

Across a range of zoonoses burden, poverty burden, and reliance on livestock, the hotspots for poverty, emerging livestock systems and zoonoses are (in decreasing order of importance both by region and country; countries in red appear in multiple listings):

South Asia: India > Bangladesh > Pakistan
Is higher than: East and Central Africa: Ethiopia > Nigeria > Congo DR > Tanzania > Sudan
Is higher than: South East Asia: China > Indonesia > Myanmar > Vietnam
Is higher than: West Africa: Burkina Faso > Mali > Ghana

Strength of evidence: moderate

We updated maps of *poor livestock keepers* (table 0.1). Around 70% of the rural poor and 10% of the urban poor are dependent on livestock. The last decade has seen declines in density of poor livestock keepers in South America and South East Asia and lesser declines in parts of West Africa and South Asia. High density of poor livestock keepers is focal: around 6 hotspots and 14 countries bear the brunt. Four countries (India > Nigeria > Ethiopia > Bangladesh) have 44% of poor livestock keepers (table 0.1 and chapter 4.1).
Strength of evidence: moderate

Areas with both high livestock populations and strong rising demand for livestock products offer highest opportunities for livestock to be a pathway out of poverty. Demand is largely driven by urbanisation, demographic growth and increasing wealth. Monogastric (poultry and pig) production responds more to increased demand because of their high reproduction rates and ease of intensification. Hence total *number of monogastrics* and magnitude of *change in monogastric population* are proxies for identifying emerging livestock systems (table 0.1 and chapter 4.3). Countries with both high numbers and large change include: India > Myanmar > Pakistan > Bangladesh = China
Strength of evidence: moderate

The study distinguishes between three categories of zoonoses:

- Endemic zoonoses, present in many places and affecting many people and animals are responsible for the great majority of human cases of illness (we estimate 99.9%) and deaths (we estimate 96%) as well as the greatest reduction in livestock production. Examples are: brucellosis, leptospirosis, and salmonellosis. *Endemic zoonoses are of most concern where the objective is lowering the burden of human disease and increasing the productivity and profitability of livestock for poor people*.
- Outbreak or epidemic zoonoses are zoonoses that typically occur as outbreaks. Examples are anthrax, rabies, Rift Valley fever, and leishmaniasis. They are much more sporadic in temporal and spatial distribution than endemic zoonoses but may be more feared because of their unpredictability and in some cases, severity. They are often present in neglected populations with poor health services and infrastructure. *Outbreak zoonoses are of concern when there is an objective of reducing vulnerability of neglected populations*.

- Emerging zoonoses newly appear in a population or have existed previously but are rapidly increasing in incidence or geographical range. Many occur as outbreaks. They are relatively rare, around 300 events in the last 70 years. Most are of minimal impact, but historically, emerging diseases have been responsible for massive impacts (e.g. HIV AIDS). *Emerging zoonoses are of concern when the object is foresight, and understanding disease emergence in order to try and avert pandemics of major impact.*

Strength of evidence: strong

The study assessed 56 zoonoses, together responsible for around 2.5 billion cases of human illness and 2.7 million human deaths a year. We identified the 13 zoonoses most important to poor livestock keepers because of their impacts on human health, livestock sector, amenability to agriculture-based control, and other criteria (chapter 2). These were, in descending order: zoonotic gastrointestinal disease; leptospirosis; cysticercosis; zoonotic tuberculosis; rabies; leishmaniasis; brucellosis; echinococcosis; toxoplasmosis; Q fever; zoonotic trypanosomosis, hepatitis E; and anthrax.
Strength of evidence: moderate

The study searched for papers on *zoonotic disease emergence events* since 2004. Out of 43 new or newly identified events, most are viral and zoonotic from wild animal hosts. Although the mappable zoonotic new events (n = 30) are globally spread across every continent, there may be clusters in northeast US, South America, Europe and South East Asia. These trends may reflect surveillance differences and the possible trend to more events in developing countries may reflect increased attention over this period. Combined with existing data on zoonotic EID events from 1940-2004 (n = 202), the clearest potential hotspots are USA and Western Europe, (this may also reflect historical surveillance differences). Countries with most events are USA, UK, Australia, and France (table 0.1).
Strength of evidence: weak-moderate

Massive under-reporting constrains our ability to understand and prevent disease. In sub Saharan Africa, 99.97% of livestock losses do not appear in official reports. At least 50% of these losses are probably due to notifiable diseases as farmers and experts rank many notifiable diseases as major causes of mortality (Newcastle disease, African swine fever, classical swine fever, trypanosomosis, East Coast fever, peste de petits ruminants most notably).
Strength of evidence: moderate to strong

The study accessed information around 1000 surveys on *prevalence of endemic zoonoses*, covering over 16 million subjects. A qualitative and semi-quantitative analysis suggests a strongly spatial distribution, with a few countries bearing most of the human and animal disease burden (chapter 3). The study also assessed the burden of zoonoses in the *Global Burden of Disease* (GBD) extracting data on 7 important zoonoses. This also shows a highly skewed distribution of human disease burden: 19 countries are responsible for 75% of the total burden. Hotspots are: Nigeria, Ethiopia, Tanzania, Togo, and India.
Strength of evidence: moderate

Countries appearing multiple times at the top of multiple metrics are (in descending order of importance): India, China, Bangladesh, Ethiopia, Nigeria, Pakistan, Congo DR, Indonesia, Myanmar, and Tanzania[1].

[11] However, this analysis does not consider trends in reducing the burden of zoonoses and the numbers of poor livestock keepers. If this were to be factored in, then China, Brazil and perhaps Indonesia would have a lower rank.

Table 0.1: The top 20 countries at the interface of poverty, emerging livestock systems and zoonoses according to different metrics (in descending order of importance)

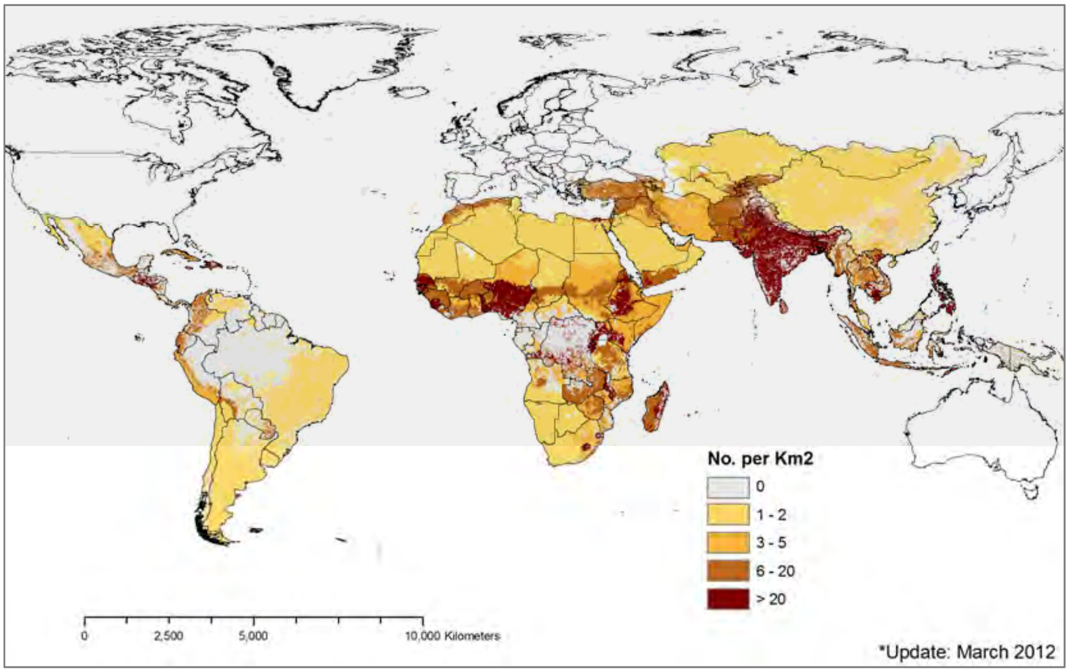
POVERTY INTERFACE		EMERGING MARKET INTERFACE		ZOONOSES INTERFACE		
Poor livestock keepers	**Protein energy malnutrition^**	**Monogastrics (TLU) 2010**	**Rapid change monogastrics 2010-2030**	**Zoonoses burden GBD**	**Endemic zoonoses prevalence***	**Emerging zoonoses events***
India	India	China	Myanmar	India	Nigeria	USA
Nigeria	Ethiopia	Brazil	Burkina Faso	Nigeria	Ethiopia	UK
Ethiopia	Nigeria	Indonesia	India	Congo DR	Tanzania	Australia
Bangladesh	China	India	Pakistan	China	Togo	France
Congo DR	Congo DR	Viet Nam	Ghana	Ethiopia	India	Brazil
Pakistan	Bangladesh	Iran	Afghanistan	Bangladesh	Mali	Canada
Kenya	Pakistan	Philippines	Bangladesh	Pakistan	Vietnam	Germany
Sudan	Indonesia	Thailand	Liberia	Afghanistan	Sudan	Japan
China	Angola	Nigeria	Central African Republic	Angola	Bangladesh	China
Tanzania	Afghanistan	Ukraine	Chad	Brazil	Burkina	Sweden
Indonesia	Tanzania	Pakistan	Cambodia	Indonesia	Cameroon	Italy
Madagascar	Brazil	Myanmar	Benin	Niger	Chad	Malaysia
Niger	Philippines	Bangladesh	Laos	Tanzania	Rwanda	Switzerland
Uganda	Uganda	Peru	Thailand	Kenya	Ghana	Congo DR
Turkey	Mali	Colombia	Zimbabwe	Côte d'Ivoire	Mozambique	Sudan
Philippines	Sudan	Ecuador	Ethiopia	Uganda	South Africa	Argentina
Afghanistan	Mozambique	Morocco	Guinea	Sudan	Congo DR	India
Egypt	Malawi	South Africa	Guinea-Bissau	Burkina	Egypt	Israel
Mozambique	South Africa	Bolivia	China	Mali	Gambia	Peru
Burkina	Viet Nam	Egypt	Mali	Iraq	Ivory Coast	Trinidad & Tobago
					Pakistan	Uganda
					Zimbabwe	Vietnam

^ Protein-energy malnutrition is the term used in the WHO GBD. WHO defines it as a nutritional deficiency resulting from either inadequate energy (caloric) or protein intake and manifesting in either marasmus or kwashiorkor.
*More than 20 countries because of tied ranks

Data sources for table 0.1. Poor livestock keepers, this study; Protein energy malnutrition: extracted from WHO GBD, 2009; Monogastrics, number of poultry and pigs in developing countries converted to tropical livestock units (TLU), FAOSTAT, 2012; Rapid change monogastrics: % increase in pigs and poultry in developing countries from 2000 to 2030, this study (based on IMPACT model); Zoonoses burden GBD: Burden of zoonoses extracted from WHO GBD, 2004 using the assumptions set out in chapter 3; Endemic zoonoses prevalence, this study; Emerging zoonoses events, this study,

Key maps

Density of poor livestock keepers (update of Thornton et al., 2002 by Kruska, this study)



This map shows the density of poor livestock keepers (number of poor livestock keepers per km square). Countries with most poor livestock keepers are ranked in table 0.1 and estimates of the absolute number of poor livestock and density of livestock keepers per country are given in chapter 4.

Hotspots for poverty & livestock keeping

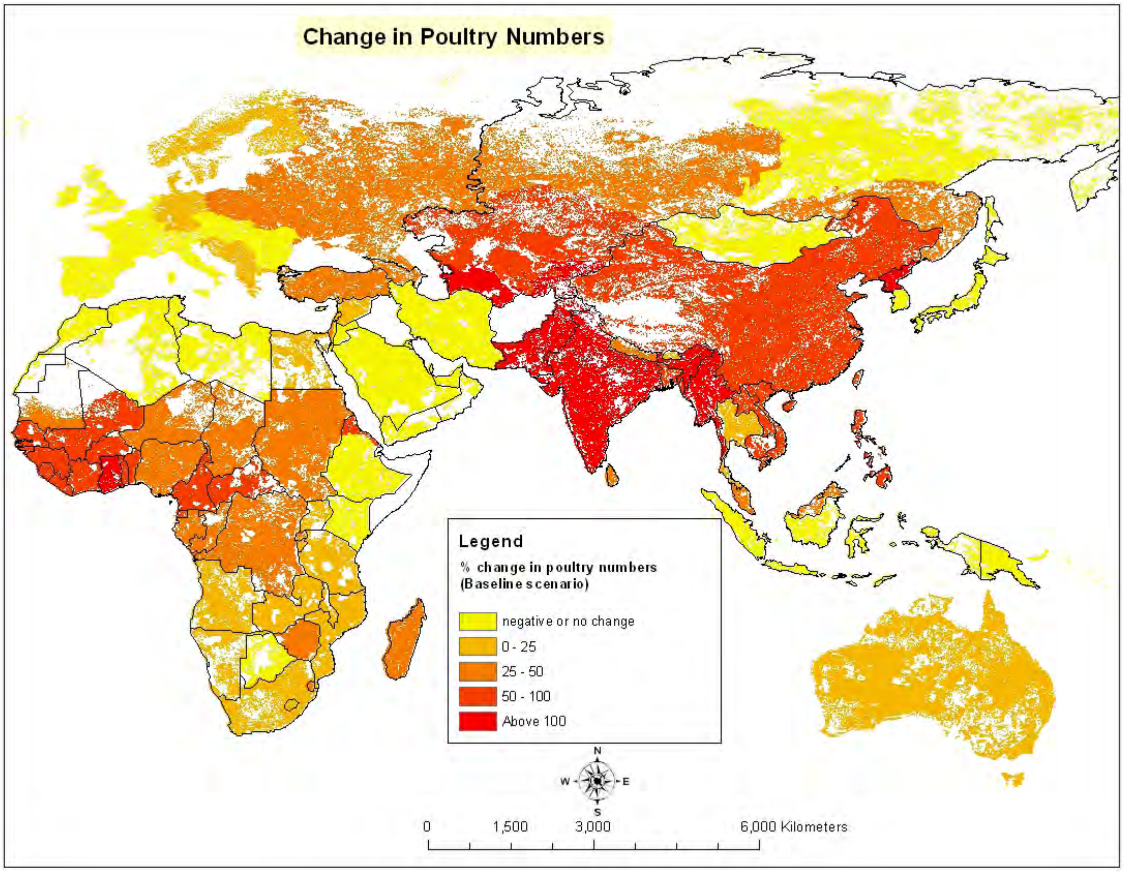
- Absolute numbers: India > Nigeria > Bangladesh > Congo > Pakistan > Kenya > Sudan
- High density: South Asia, East Africa highlands, great lakes, Nigeria, west Africa, littoral South-East Asia

Key points

- Around 1 billion poor people (<$2 a day) depend on livestock
- Around two thirds of the rural poor and one third of the urban poor depend on livestock
- Livestock provide one fifth to one half of household income for the poor
- In poor countries, livestock provide from 6 to 36% of protein intake

More details on poor livestock keepers are provided in chapter 2.

Change in poultry numbers from 2000 to 2030 – a proxy for emerging markets (Herrero et al., 2009)



This map shows the percentage change in poultry numbers from 2000 to 2030 based on projections by Herrero et al (2009) using the International Model for Policy Analysis of Agricultural Commodities and Trade (IMPACT) model for the 'business as usual' scenario used in the International Assessment of Agriculture Science and technology for Development (IAASTD). Increase in poultry production is one possible proxy for the demand-driven increase in livestock production called the 'livestock revolution'. According to that study:

Hotspots for livestock sector growth in developing countries are:

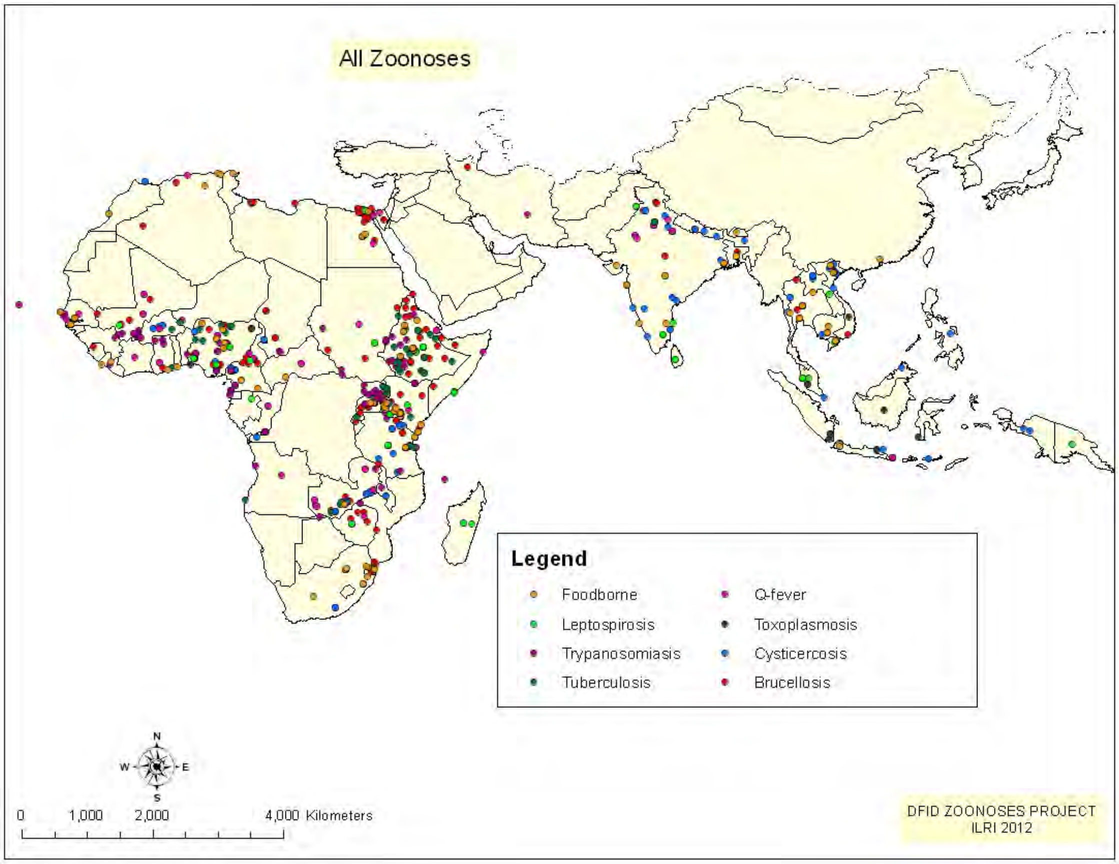
- Poultry in South and East Asia > bovines in South and East Asia > poultry in sub Saharan Africa = pigs in sub Saharan Africa

Key points

- Livestock production is increasing rapidly in response to growth in population, growth in income, urbanisation and changing diets: the so-called livestock revolution
- Herrero et al (2009), projects that, over the next 40 years, absolute growth in consumption will be greatest in South Asia and South East Asia and relative growth greatest in sub-Saharan Africa
- On the supply side, growth will be greatest in the poultry sector followed by bovine then small ruminants then pigs
- Emerging livestock systems offer opportunities for smallholders if they can access the inputs needed to reach emerging markets

More details on poor livestock keepers are provided in chapter 2.

Map of endemic zoonoses surveys – the burden of zoonoses (Grace et al., this study)



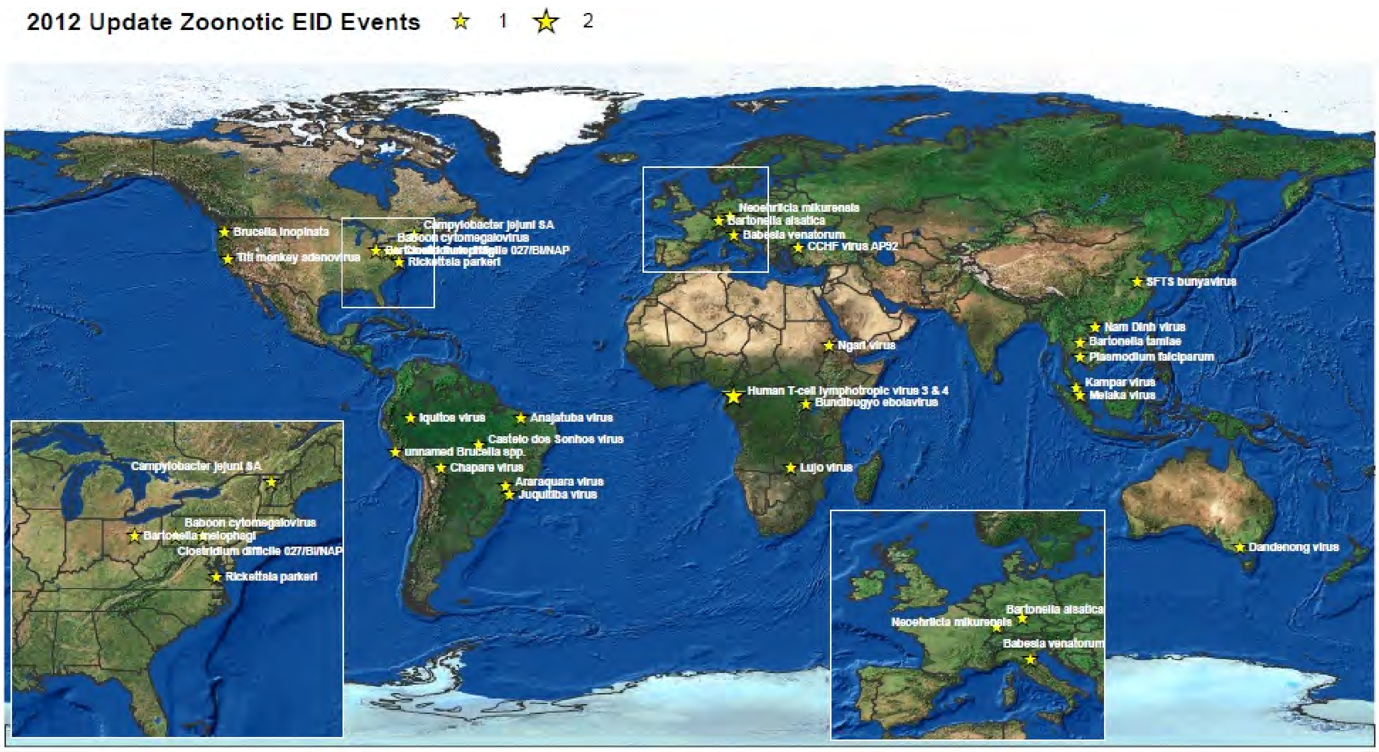
This map shows the surveys on endemic zoonoses reviewed in this report. Over 1,000 surveys were accessed covering over 14 million animals, humans and livestock products.

Hotspots for high prevalence of endemic disease confirmed by multiple surveys
Nigeria, Ethiopia, Tanzania, Togo, India, Mali, Vietnam, Sudan, Bangladesh

Key points
In poor countries as a whole:

- 12% of animals have recent or current infections with brucellosis, reducing production by 8%
- 10% of livestock in Africa are infected with trypanosomosis, reducing their production by 15%
- 7% of livestock are currently infection with tuberculosis (TB), reducing their production by 6% and from 3-10% of human TB cases may be caused by zoonotic TB
- 17% of smallholder pigs show signs of current infection with cysticercosis, reducing their value and creating the enormous burden of human cysticercosis
- 27% of livestock show signs of current or past infection with bacterial food-borne disease, a major source of food contamination and illness in people
- 26% of livestock show signs of current or past infection with leptospirosis reducing production and acting as a reservoir for infection
- 25% of livestock show signs of current or past infection with Q fever, and are a major source of infection of farmers and consumers

Map of emerging zoonotic disease events from 2004 to 2011 (Jones et al., this study)



This map shows locations of zoonotic emerging disease events between 2004 and 2011.

Geographical hotspots

Combined with existing data on zoonotic EID events from 1940-2004 (n = 202), the clearest potential hotspots are USA, South America, South East Asia and Western Europe, which may reflect historical surveillance differences.

Chapter 1: Zoonoses of most relevance to poor people in emerging livestock systems

Summary

This chapter identifies three categories of zoonoses important for different reasons: endemic zoonoses, outbreak zoonoses, emerging zoonoses, and, old zoonoses. We discuss previous work to prioritise zoonoses and some of the challenges in identifying zoonoses of importance to the poor. We identified 56 zoonoses that appeared in multiple listings and selected criteria to prioritise them. Together, the 56 zoonoses are responsible for an estimated 2.7 human million deaths and around 2.5 billion cases of human illness a year. For the top 13 zoonoses, the figures were 2.2 million human deaths and 2.4 billion cases of illness. Our prioritisation is broadly compatible with other exercises.

1.1 Introduction

Zoonoses are diseases transmissible between animals (domestic and wildlife) and humans. Around 60% of all human diseases and around 75% of emerging infectious diseases are zoonotic (Taylor et al., 2001; Woolhouse et al., 2005). In aggregate, they have high impacts on human health, livelihoods, animals and ecosystems. In the first global syntheses of the impact (partial) of zoonotic diseases, Grace et al. (2011a) estimated that, in least developed countries, 20% of human sickness and death was due to zoonoses or diseases recently jumped species from animals to people.

1.2 The rationale for prioritising zoonoses

What cannot be measured cannot be managed and the first recommendation of a high-level WHO-convened group was to assess the societal burden of disease attributable to zoonoses (Molyneux et al., 2011). Assessing, including mapping, of zoonoses is key to guide decision-makers and implementers.

Zoonoses can threaten human health in different ways:

- Endemic zoonoses are typically present to a greater or lesser degree in certain populations. Examples are cysticercosis, brucellosis, bovine tuberculosis, leptospirosis and food-borne zoonoses[2]. They are common in poor populations and are responsible around a billion illnesses and millions of deaths every year (table 2.1). However, endemic zoonoses have been neglected by the international donor, standard setting, and research communities. Maps exist for human health burden of individual zoonoses, usually at country level but there are no available maps of endemic zoonoses as a group, and few maps for the impact of zoonoses on livestock.
- Outbreak or epidemic zoonoses typically occur as outbreaks. Examples are anthrax, rabies, Rift Valley fever, and leishmaniasis. Endemic zoonoses may occur as outbreaks in naïve populations or when triggered (e.g. sleeping sickness, leptospirosis). Outbreaks may be triggered by climate changes, flooding, and epidemiological phenomena such as waning immunity or other drivers. They typically have high temporal and spatial variability. Their overall impact in terms of morbidity, mortality and production loss is much less than endemic zoonoses but because they can ‘shock’ systems they are often of high priority to farmers and decision makers. They can also cause important economic losses, which are often related to reaction to the disease rather than the disease itself (Butler and Grace, forthcoming).
- Emerging zoonoses newly appear in a population or have existed previously but are rapidly increasing in incidence or geographical range. They are relatively rare, around 300 events in

[2] Some of these also occur as outbreaks but are differentiated from the outbreak zoonoses in that community surveys will generally show that the disease is present in communities, although it may only get attention when there is an outbreak involving multiple cases.

the last 70 years (Jones et al., 2008). Most are of minimal impact. Many are endemic in other places and burdens are not necessarily linked to site of emergence, so mapping the point of emergence may not correlate to impact on poor people at that point. Donors and decision-makers are often concerned about emerging diseases, whose impacts on poor farmers are orders of magnitude less than the impacts of endemic zoonoses. However, the potential impact (e.g. a new HIV AIDS) is at least of similar magnitude to endemic zoonoses. Good maps exist but may not be useful for informing research aimed at identifying poor at risk from zoonoses.

- 'Old zoonoses' were originally zoonotic but are now spread mainly or entirely by human-to-human transmission (some with zoonotic reservoirs) (Grace and McDermott, 2011). These include HIV-AIDs, influenza, malaria, measles and dengue. These diseases can emerge anywhere in the world and their burden is not linked to site of emergence. Their current order of magnitude is about similar to that of the endemic zoonoses (almost all due to HIV-AIDs). The ability of the livestock sector to predict, prevent and control these diseases is small and maps not likely to be useful for directing research activities so these will not be further discussed.

1.3 Review of zoonoses prioritisation exercises

In order to map zoonoses and poverty, information is needed on which zoonoses pose risk to the poor. One of the earliest attempts to prioritise zoonoses was conducted by ILRI (Perry et al., 2002) with support from DfID. Recent years have seen several other prioritisation exercises for zoonoses and animal health. These have been reviewed by the ENHanCE group (http://www.liv.ac.uk/enhance/) (Enhance, undated). Most use experts, criteria setting, and weighting to come up with lists. However, when evidence is both highly scarce and highly scattered (as is the case for zoonoses) then expert opinion is less useful; this is illustrated by major discrepancies between different systems of prioritising (Perry et al., 2009).

Prioritisation exercises use various criteria including: livestock pathogens with a high actual human disease burden; rare zoonotic pathogens with severe disease manifestations in people; arthropod-borne and wildlife associated pathogens which may pose a severe risk in future (Havelaar et al., 2010; health consequences in animals, economic consequences in animals (Dufour et al., 2006); public health (severity and occurrence in humans), animal health (severity of disease coupled with economic consequences and occurrence in animals), and food (occurrence in food) (Cardoen et al., 2009).

Most of these prioritisation exercises were done in rich countries and additional challenges in identifying the zoonoses that matter most to the poor include:

- Capturing multiple impacts: Many endemic zoonoses and some emerging zoonoses have impacts on livestock causing death and reduced productivity as well as costs for control.
- Lack of evidence on the adverse impacts caused by disease: Many zoonoses are not notifiable so are not recorded in official statistics. Even for notifiable diseases, many national reports are highly unreliable. As described in the previous chapter, under-reporting is a serious problem both in animal and human populations.
- Variability: zoonoses are often focal and some vary from year to year (predictably or not). For example, Rift Valley fever may be absent for decades before causing severe problems. Human trypanosomosis currently affects only thousands of people, but historically there have been major epidemics affecting millions of people.

1.4 Selection of zoonoses for prioritisation

In order to select 'important' zoonoses for further study, we used information from five listings of priority zoonoses or priority diseases that included zoonoses and were relevant to developing countries:

1) The World Health Organisation Global Burden of Disease
2) The World Animal Health Organisation list of notifiable zoonoses
3) Zoonoses important to poor people identified by expert consultation (Perry et al., 2002)
4) The Rosetta listing of infectious causes of death
5) A systematic review of zoonoses commissioned by DFID, which identified 373 zoonoses as important (Grace et al., 2011).

Zoonoses that appeared in more than one list were considered (n=56). We ranked these 56 zoonoses according to criteria considered important by the authors of this study. We selected the following criteria (Table 2.1):

- Human mortality (>1,000 deaths per year
- Human morbidity (>1 million people affected
- High impact on livestock sector
- Amenability to agriculture-based control
- Emergence or severity of disease in people

The major difference between our criteria and criteria used in previous studies was the inclusion of ‘amenability to agricultural intervention’. The rationale was that the ability to do something about a problem was an important criterion for prioritisation. The complete table and weighting used is given in annex 1. By these criteria, 13 zoonoses were defined as most important (Table 1.3). These 13 were selected for in-depth systematic literature review and mapping.

Together, the 56 zoonoses are responsible for an estimated 2.7 human million deaths and around 2.5 billion cases of human illness a year. For the top 13 zoonoses, the figures were 2.2 million human deaths and 2.4 billion cases of illness. Nine of the top-ranked zoonoses were considered to have high impact on livestock and all of the top-ranked zoonoses are amenable to agriculture-based interventions.

Table 2.1 The most important zoonoses in terms of human health impact, livestock impact, amenability to agricultural interventions, severity of disease and emergence (data from WHO and authoritative literature: when several authoritative estimates the mid point is given)

Disease	**Wildlife interface**	Deaths human annual	Affected humans annual	Death >1000 people	Affected> 1 million people	Animal impacts high	Farm intervention	Other (score =1)	**Total score**
Gastrointestinal (zoonotic)	Important	1,000,000	800,000,000	2	1	1	1	0	**5**
Leptospirosis	Very important	123,000	1,700,000	2	1	1	1	0	**5**
Cysticercosis	Sometimes	50,000	50,000,000	2	1	1	1	0	**5**
Tuberculosis (zoonotic)	Sometimes	100,000	554,500	2	0	1	1	0	*4*
Rabies	Important	70,000	70,000	2	0	0	1	Severe	*4*
Leishmaniasis	Important	47,000	2,000,000	2	1	0	1	0	*4*
Brucellosis	Sometimes	25,000	500,000	2	0	1	1	0	*4*
Echinococcosis	Not important	18,000	300,000	2	0	1	1	0	*4*
Toxoplasmosis	Important	10,000	2,000,000	1	1	1	1	0	*4*
Q fever	Important	3,000	3,500,000	2	1	0	1	0	*4*
Trypanosomosis (zoonotic)	Important	2,500	15,000	2	0	1	1	0	*4*
Anthrax	Sometimes	1,250	11,000	2	0	1	1	0	*4*
Hepatitis E *	Sometimes	300,000	14,000,000	2	1	0	1	0	*4*
Chagas	Important	10,000	8,000,000	2	1	0	0	0	3
Chickungunya	Very important	12,500	500,000	2	0	0	0	Emerge	3
Clostridium difficile disease	Possible	3,000	300000	2	0	0	0	Emerge	3
Dengue fever	Minor	20,000	50,000,000	2	1	0	0	0	3
Ebola	Very important	500	800	2	0	0	0	Severe	3
Hanta disease	Very important	1,750	175,000	2	0	0	0	Emerge	3
Avian influenza	Important	77	145	0	0	1	1	Emerge	3
*Bov. Spongiform Encephalopathy^*	Sometimes	182	188	0	0	1	1	Severe	3
Psittacosis	Important	2,250	22,000	2	0	0	1	0	3
Japanese encephalitis	Possibly bats	11,000	40,000	2	0	0	1	0	3
Buffalo pox	Not important	Negligible	Common	0	1	1	1	0	3
Rift Valley fever	Important	45	150	0	0	1	1	Emerge	3

Note: high human mortality gets a double weight of as the most important criterion for many stakeholders. Total score = (human death x 2) + (humans affected) + (high livestock impacts) + (farm intervention possible) + (other concerns: severe or emerging disease). The maximum possible score is therefore 6 and the minimum 0.

* Importance of zoonotic transmission not fully known ^ Not a problem in poor countries

1.6 Comparing with other assessments

ENhanCE (undated) reviewed 12 methods of disease prioritisation. Two were global (FAO/OIE and WHO), one focused on Rajasthan in India, while the rest focused on developed countries. A variety of methods were used: risk assessment approach, multi-criteria decision tools, and qualitative methods. Together the studies reviewed covered animal diseases, human diseases, and zoonoses. Of the 99 diseases appearing in the ranking, 33 were zoonoses.

Zoonoses appearing in multiple listings according to the ENhanCE review, in declining order of number of appearances, were:

- Salmonellosis
- Leptospirosis = rabies
- Campylobacteriosis = tuberculosis = West Nile virus = toxoplasmosis
- Listeriosis = anthrax = echinococcosis = *E. coli* infection = BSE = botulism
- Cryptosporidiosis = Japanese encephalitis = Q fever = Rift Valley fever = tetanus

Out of the top 18 ranked zoonoses across the 12 studies, 17 appeared in our top 25 listing. The exception was West Nile, which has been most problematic in the Americas. Of the 33 zoonoses, 24 appeared in our list of top 25 zoonoses, suggesting reasonable similarity given the different criteria and focus.

A notable characteristic of these prioritisations is the high ranking given to common, food-borne diseases (salmonellosis, campylobacteriosis, toxoplasmosis, listeriosis, toxigenic *E. coli*, and cryptosporidiosis). Decision makers and implementers using unstructured prioritisation often focus on classical zoonoses or emerging diseases rather than food-borne zoonoses (Grace et al., 2010).

1.7 Mapping zoonoses: strengths and weaknesses

There are three types of existing zoonoses maps: emerging disease event maps, disease report maps and research-derived prevalence maps. A summary along with strengths and weaknesses are presented in table 1.2.

1. Emerging disease event maps. Jones et al. (2008) have identified emerging disease events as *"the first temporal emergence of a pathogen in a human population which was related to the increase in distribution, increase in incidence or increase in virulence or other factor which led to that pathogen being classed as an emerging disease*". They identified 335 events between 1940 and 2004: 60% of which are zoonotic. An updated map showing only zoonotic emerging disease events is presented in Chapter 4.

2. Disease report maps. There are several systems for reporting disease outbreaks: these are summarised in table 1.2. The most authoritative is the World Animal Health Organisation (OIE) World Animal Health Information Database (WAHID) maps. HealthMap (www.healthmap.org) aggregates all the major disease reporting systems and information sources. Members of the OIE (currently 178 countries) have a legal obligation to report certain diseases (currently 115). Maps are generated from the information provided.

3. Prevalence maps. These are based on studies assessing the prevalence of zoonoses in livestock, livestock products and people. Global prevalence maps exist for some individual zoonoses but data is often at country level. Some zoonoses have been mapped using geo-spatial data – notably trypanosomosis. The World Health Organsiation (WHO) Global Burden of Disease (GBD) has also been mapped at country level.

Table 1.2 Zoonoses disease and disease outbreak reporting systems

	Zoonoses included	Source of data	Strengths	Weaknesses
World Animal Health Information Database (WAHID) Interface	33	Reports from state veterinary services	Notifiable so all 172 OIE member states obliged to report	Little reporting of endemic disease by developing countries
Transboundary Animal Diseases Information System (TADinfo)	2 (EMPRES)	Reports from state veterinary services	Supported by FAO. Resolution to village level possible	Not widely used. Access to data limited to users
ProMED mail	All animal & human diseases		All reports verified by qualified moderators	Quality, comprehensiveness and timeliness dependent on quality of surveillance
Global Public Health Intelligence Network (GPHIN)	Preliminary reports of public health significance	Media sources and then verified by GPHIN officials	Real time reports in 7 languages	Developing countries under-reported. Not universally accessible and costs with use
Global Early Warning and Response System (GLEWS)	19 zoonoses	Combines alert mechanisms of OIE, FAO, WHO	Official reports	Developing countries under-reported
HealthMap	Human, animal and plant diseases	Aggregates data from many sources	Real time, most comprehensive	

1.7 Challenges in reporting systems for zoonoses in developing countries

The challenges of mapping the multiple burdens of zoonoses include:

- Reporting systems cover only few of the important zoonoses. There are over 600 zoonoses and around 100 of these are of some importance (Grace et al., 2011). However, WHO GBD and OIE only cover 11 and 33 zoonoses respectively.
- The GBD does not distinguish between zoonotic and non-zoonotic causes of disease (for several diseases tuberculosis, schistosomiasis, gastro-intestinal disease the proportion of disease attributable to zoonoses is not known).
- Zoonoses are often confused with other diseases (e.g. malaria and typhoid) and this misdiagnosis leads to systematic under-reported in the human health system.
- OIE reporting grossly underestimates the importance of endemic zoonoses – see next section.
- Emerging disease databases give little information on actual burden on poor people or which diseases are likely to be problematic.
- Meta-disease reporting systems (summarised in HealthMap) are only as good as the data they aggregate.

An important conclusion of our study is that massive under-reporting of zoonotic (and other diseases) in developing countries is a major impediment to understanding prevalence and impacts of disease and developing appropriate control. We illustrate this with the examples of brucellosis in poor countries and Q fever in Africa and also compare official reports of notifiable diseases with probable mortality of livestock in Africa.

a) The case of brucellosis – a well-known, widespread, notifiable zoonosis

Brucellosis is an important disease of cattle, sheep, goats and pigs. It is also important zoonosis and is notifiable to the OIE. In cattle, it can be suspected on clinical signs, as it causes late abortion with characteristic lesions on the placenta. It also causes carpal hygromas, a very specific indicator of brucellosis. Diagnostic tests are widely available and relatively inexpensive.

Commonly used tests for brucellosis detect antibodies produced in response to infection. Antibodies tested for persist for several months (IgG) or several years (IgM). Positive tests (to both antibodies) indicate the animal is currently sick, is chronically infected or has been infected in the last year or so. Hence positive tests are roughly equivalent to annual cases.

Our review captured information from 241 community surveys (that is, surveys from the general livestock community and not targeting high risk animals) of bovine, sheep and goat populations, representing 475,968 samples. The prevalence for different regions is shown in Table 1.2. From the number of ruminants, the prevalence of seropositive cases, and the relation between sero-positivity and disease we can predict the number of cases of brucellosis a year. The discrepancy between the number reported and the number predicted is several orders of magnitude. For example, for every 1 million cases in East Africa less than one case is reported to OIE. The situation is similar for other diseases reported to OIE. When there are 999,999 missed reports for every one report, surveillance is not fulfilling its purpose.

Table 1.3 Predicting the number of annual cases of brucellosis based on sero-prevalence and comparing to the numbers reported to the World Animal Health Organisation

	Livestock prevalence %	Number ruminants	Predicted cases a year	Cases reported 2010
East Africa	8.2	257,377,760	21,104,976	12
West Africa	15.5	197,716,517	30,646,060	37
South Africa	14.2	59,806,724	8,492,555	6305
North Africa	13.8	57,629,367	7,952,853	1073
South Asia	16.0	683,181,040	109,308,966	156
South East Asia	2.9	21,247,586	616,180	164

b) The case of Q fever – a less well-known, difficult to diagnose, notifiable zoonosis

Q fever is an infectious disease of animals and humans caused by a species of bacteria (Coxiella burnetii). The main reservoirs are sheep, goats and cattle. It is highly contagious to humans and typically causes influenza-like illness, although some infections are asymptomatic and in rare cases fatal complications can ensue.

Q fever is a notifiable disease and appeared in the top 13 zoonoses in terms of impact on human health, livestock sector and other criteria in our listing (table 2.1).

Most tests for Q fever detect antibodies. Antibodies may persist for several years. Most of the surveys in our review were community based. For these, a positive result indicates current infection, chronic infection or infection in the last few years.

In our review the average sero-prevalence from community surveys in Africa was 26% suggesting half a billion animals infected each year.

We reviewed cases of Q fever reported to OIE between 2006 and 2010, retrieving 742 reports from 54 African countries. Only one report had numbers of animals affected, no report had population at risk. The reports were:

- Disease outbreak report — 1 report, 8 animals affected, 1 death
- Confirmed infection without clinical signs — 10 reports
- Disease present but without quantitative data — 16 reports
- Diseases suspected but not confirmed — 10 reports
- Disease absent — 226 reports
- No information available — 479 reports

Given that surveys carried out in the field suggests millions of cases occur in livestock in Africa each year, and that all surveys conducted in Africa found evidence of sero-positive animals indicating infection is present. It is obvious that official reporting seriously under-estimates the occurrence of this important notifiable zoonosis.

c) Comparing probable livestock mortality with notifiable disease reports

The World Bank and OIE produced a very useful atlas summarising animal disease reports between 2006 and 2009 (World Bank, 2011). This also allows us to assess under-reporting for developing countries. We do this by estimating number of livestock in Africa from FAOSTAT, annual mortality from systematic reviews, proportion of mortality likely to be due to notifiable diseases from expert opinion, and we compare these with official reports to OIE.

Number of livestock in Africa

FAO estimate that globally there are 24 billion livestock in 2010 (FAOSTAT, 2012), corresponding to 2.4 billion livestock standard units (using the OIE definition given in the aforementioned Atlas) (World Bank, 2011). Sub-Saharan Africa has two billion livestock corresponding to 253 million standard livestock units.

Number lost each year

Numerous studies on African livestock indicate annual mortality is high. Otte and Chilona (2002) reviewed production parameters of ruminants in traditional and non-traditional production systems reported in published and grey literature between 1973 and 2000 (table 1.3). Depending on species and age category, mortality ranged from 6-28% with three quarters of the species-age categories having a mortality of 10% or more.

Table 1.4 Annual mortality (%) in traditional ruminant systems

	Young	Growing female	Growing male	Adult female
Cattle	22%	7%	9%	6%
Sheep	27	10	11	11
Goats	28	13	14	12

From Otte & Chilona, 2002

Otte and Chilona did not include poultry in the review but production parameters and characteristics of family poultry production have been compiled and published for eleven African countries (IAEA 2002). These give a range of mortalities from around 30% to 80% depending on the age category and country. Rege and Gibson (2009) estimate mortality in backyard poultry in Africa at 70%. There is little comprehensive information on mortality among smallholder pigs, but mortality is often high among pre-weaned piglets in smallholder systems (around one fifth) and very high losses occur during outbreaks of African swine fever and other epidemics (Wabacha et al., 2004).

Proportion of losses due to notifiable disease

Some of the annual livestock losses are due to non-infectious causes (mainly accidents, poisoning, predation and malnutrition). Other losses will be due to non-notifiable diseases (such as endoparasites) but farmers and experts agree that the 87 notifiable diseases are among the most important causes of mortality for livestock in Africa (e.g. Newcastle disease, trypanosomosis, classical swine fever, East coast fever, contagious bovine pleuropneumonia, and peste des petits ruminants) in sub Saharan Africa. The authors of the report consider at least 50% of mortality is due to notifiable diseases

Combining these assumptions indicate a major discrepancy between the probable losses from notifiable disease (around 10 million) and the losses reported to the OIE (around 100,000) can only be explained by under-reporting of several orders of magnitude. The following worked example makes this clear:

- Livestock in Africa = 253 million standard livestock units (FAOSTAT, 2011)
- Livestock death, slaughter, or destruction reported to OIE = 82,319 units (World Bank, 2011)
- Livestock annual estimated losses = 25,300,000 TLUs (literature: 10% as a conservative estimate[3])
- Estimated losses due to notifiable diseases = 12, 800,000 TLUs (expert opinion: 50%)
- Losses (notifiable) reported to OIE = 0.2% (less than one fifth of one percent)
- Losses (notifiable) probably not reported to OIE = 99.8% of losses

[3] Mortality is lowest in cattle which contribute the most to tropical livestock units so we chose a low estimate of mortality

Chapter 2: Mapping of poverty, livestock, zoonoses and vulnerability to climate change

Summary

Information of reasonable quality is available on number of people in poverty by country and the number of livestock by country and by farming system. Literature provides estimates on the number and proportion of poor people keeping livestock. Emerging zoonotic disease events have been mapped, but because of the nature of the data, maps may not be informative about the impacts on poor people. The World Health Organisation information on the Global Burden of Disease provides information by country on the human health impact of around 11 important zoonoses and also on protein-energy malnutrition which is indirectly linked to livestock product availability and hence zoonoses. The World Animal Health Organisation collates information on 33 zoonoses but data from developing countries is prone to under-reporting.

2.1 Poverty

Poverty can be defined as a pronounced deprivation in wellbeing. No single indicator exists to measure all dimensions of poverty simultaneously, however, internationally comparable metrics, such as the US 1$ a day ($1.25), are useful for spatial and temporal comparisons. Estimates of poverty are probably reasonably accurate. The proportion of people living in poverty (<$1.25 per day[4]) dropped by half between 1990 and 2010, but 1.3 billion people still live on less than $1.25 a day and around 2.5 billion on less than two dollars a day (World Bank, 2012).

In the past 3 decades, dramatic drops in poverty are mainly due to development in China: in Africa and South Asia numbers of people in poverty or stable or increasing. In terms of numbers, more than 75% of the people living in poverty live in 9 countries and 80% of poor people in 12 countries. In terms of intensity of poverty, 17 countries have more than 50% of the population living on less than $1.25 per day. Whereas in 1990, nine tenths of the poor lived in poor countries, presently three quarters live in middle-income countries (mainly India, China and Brazil).

2.2 Livestock

How many livestock are kept and where are they?

In 2012, the human population reached 7 billion and the production animal population around 24 billion (FAOSTAT, 2012). Global livestock systems have been recently re-mapped (Robinson et al., 2011). Poultry and pigs increasingly dominate in terms of number of animals kept (although in terms of tropical livestock units ruminants are more important): 85% of all domestic animals alive are now pigs or poultry. As disease transmission is dependent on numbers and contact rates, and monogastrics are kept in higher numbers and more intensive systems, monogastrics may become more important in disease emergence.

Livestock density maps

Livestock density reflects the number of livestock and the level of intensification. Human population density is a major determinant of livestock density. High density is also an important factor in the transmission of disease through increasing the probability and number of contacts. However, density may also be associated with better biosecurity and control systems which reduce risk. High livestock density, especially of monogastrics, often reflects intensification and tends to be inversely correlated with poverty. In our study, livestock density seems more correlated with zoonotic disease event emergence than burden of zoonotic disease. Figures 1.1 to 1.3 show global cattle density from the FAO gridded livestock maps (FAO, 2007).

[4] 2005 international prices

Figure 2.1 Global poultry density (Robinson et al., 2011)

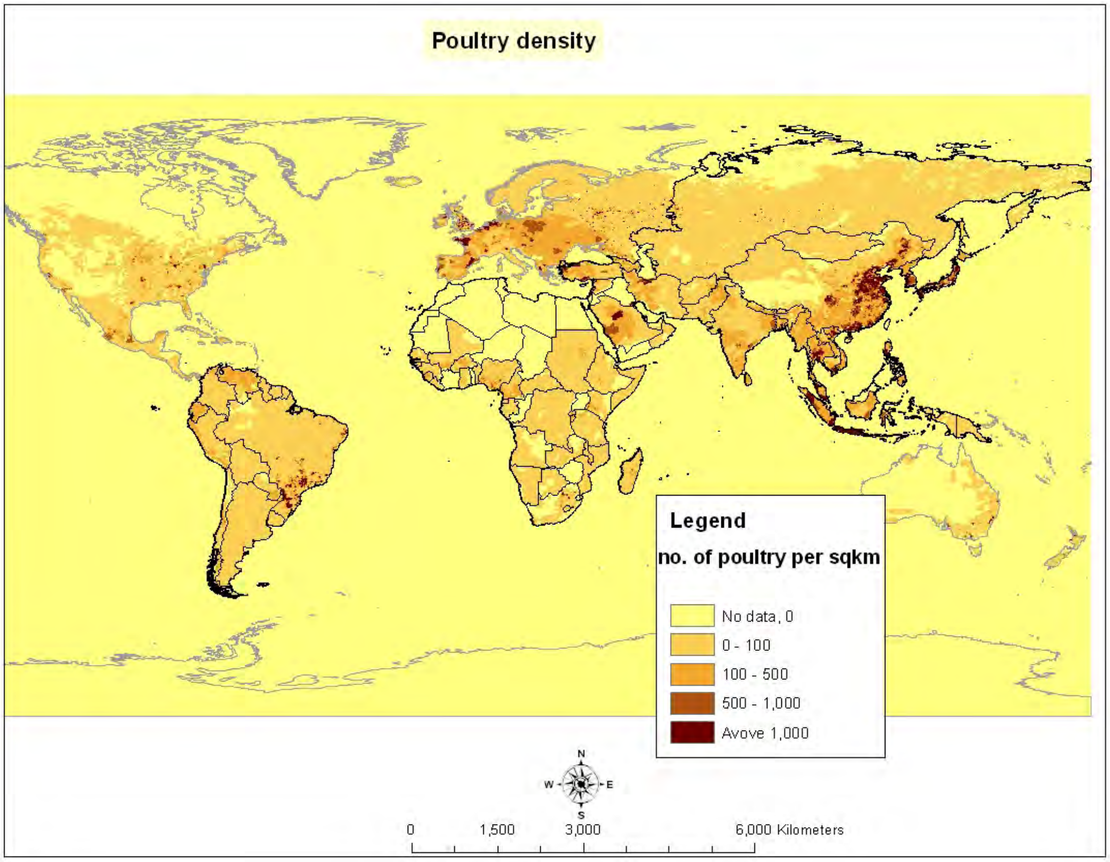


Figure 2.2 Global pig density (Robinson et al., 2011)

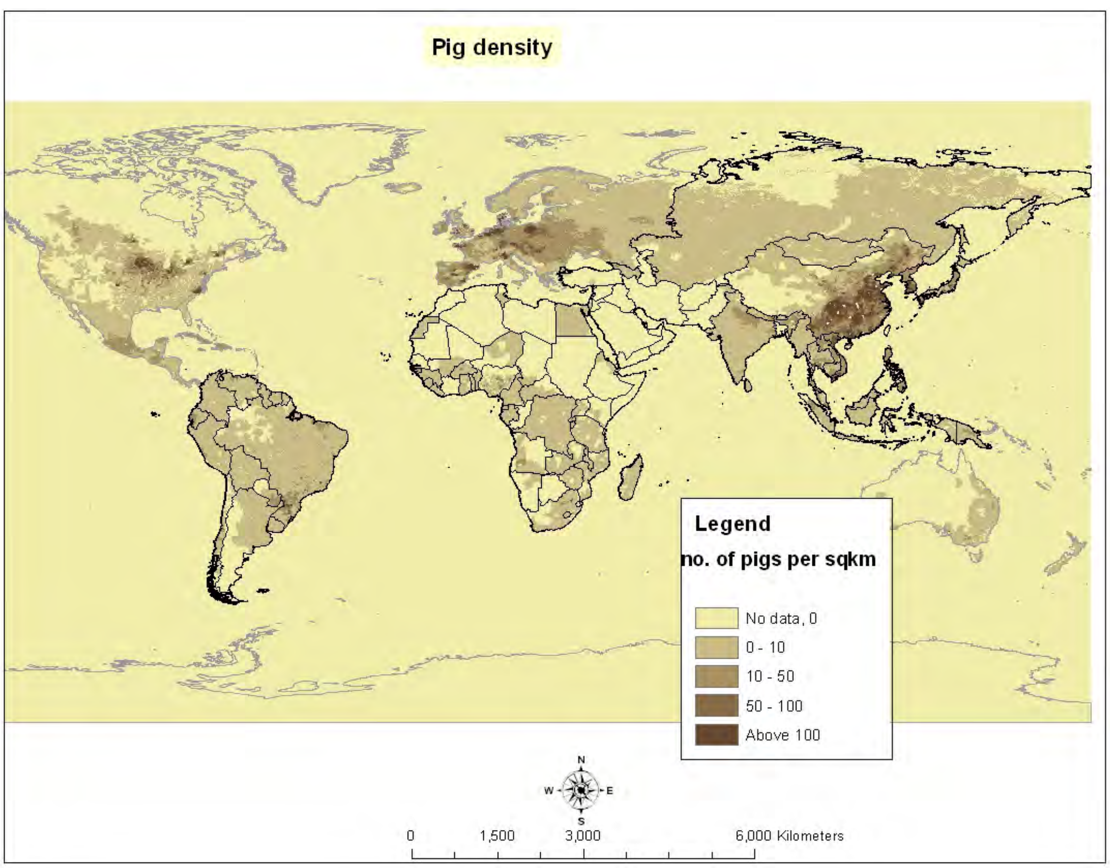
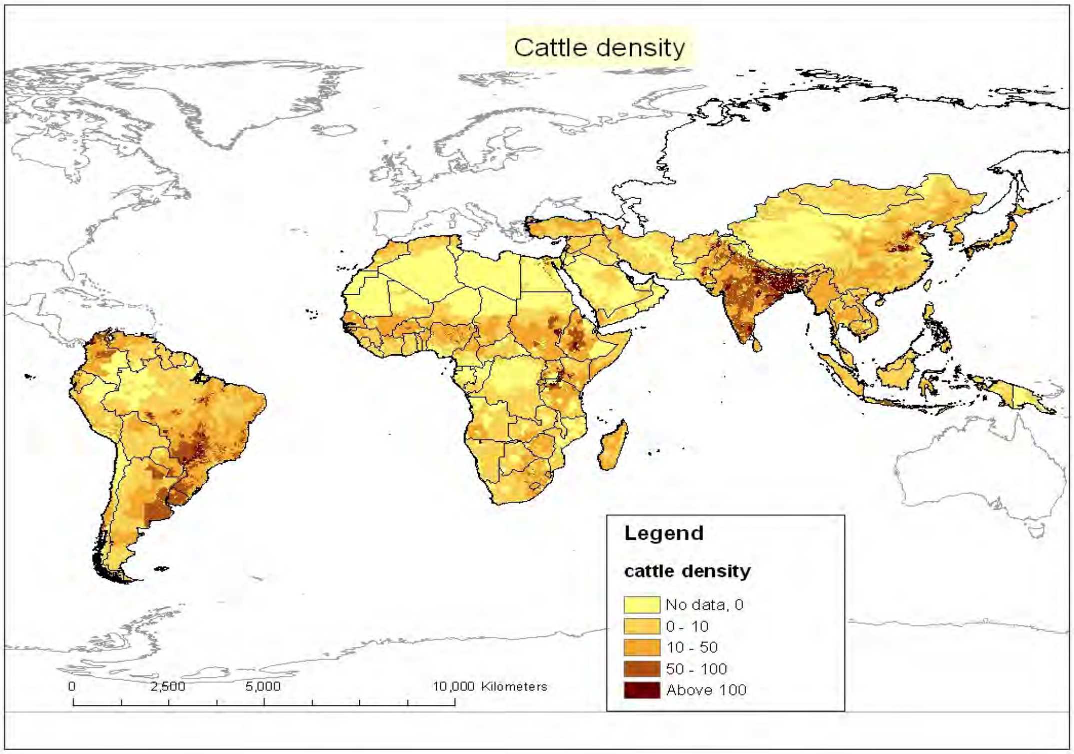


Figure 2.3 Global cattle density (Robinson et al., 2011)



2.3 Poverty and livestock

How many poor people depend on livestock? Where are they?

Livestock keeping had been variously regarded as a symptom of being poor, an important pathway out of poverty, and a transitional stage as burgeoning developing world populations shift from agriculture to urban livelihoods (Perry et al., 2010). Recent estimates suggest nearly 1 billion people living on less than two dollars a day are dependent to some extent on livestock (Staal et al., 2009). Over 600 million are found in South Asia, mostly in India. Sub-Saharan Africa has over 300 million poor livestock keepers, concentrated in East and West Africa, with fewer in southern and central Africa. A breakdown by region is provided in chapter 4.

What proportion of the poor depends on livestock?

Earlier estimates were around 70% of the rural poor depended on livestock (LID, 1999). Others have estimated that 40-50% of those living in poverty ($1.25 threshold) are at least partially dependent on livestock (Thomas & Rangnekar, 2004; IFAD, 2004). A more recent 12-country study supports this, finding that on average, around 68% of rural households in the bottom 40% as regards expenditure kept some farm animal compared to 65-58% of those in the 40%; in urban areas 22-26% of the poor kept livestock, and 8-12% of the well-off (Pica-Ciamarra et al., 2011).

To what extent do poor people depend on livestock?

Staal et al. (2009) analysed 92 case studies from the developing world and found that livestock contributions made up on average 38% of household incomes (33% of the income in mixed crop-livestock systems, and 55% of total income in pastoral systems). The 12-country study of Pica-Ciamarra et al. found livestock contributed on average 12% to household income, with no statistical differences between contribution in rich and poor countries. (This study over-represented emerging countries, which may explain the lower contribution of livestock compared to the study of Staal et al., 2009). There is strong evidence that poor people depend on livestock, but more research is needed on the extent and nature of this dependence.

Livestock provide many benefits besides income. These include traction, manure, food, social status as well as economic services such as insurance and guarantees. Several studies show that manure, while seldom marketed is highly valued in smallholder systems (ranking higher than milk in West Africa (Grace et al., 2009). A study in Kenya, found that non-marketed values comprised approximately 20% of the animals total perceived value (Ouma et al., 2003).

How much do livestock products contribute to nutrition in developing countries?
Across a range of developing countries, livestock products contribute 6-36% of protein and 2-12% of total calories (Nzuma & Randolph, 2008). In South Asia and East Africa dairy products account for most livestock product consumption; in the rest of Africa, dairy, poultry, beef and shoats are balanced, while in South East Asia poultry and pork predominate. Countries with low livestock consumption (e.g. Bangladesh) may offset this with high fish consumption.

What livestock do the poor keep?
Poorer households are more likely to keep small ruminants and richer to keep large ruminants. Poultry keeping tends to be evenly distributed across wealth groups. However, species ownership is system and country specific.

Which livestock systems contribute most value in poor countries?
Around half the value of production in sub-Saharan Africa is derived from cattle (55%), followed by poultry (25%) and small ruminants (20%). In South Asia these proportions were 61%, 21% and 18%, respectively (FAOSTAT, 2012). In both regions the arid/semi-arid zone contributed most to value of production. However, the trends are towards more value from poultry and pigs and more production from intensified systems. A recent comprehensive rural poverty mapping is the CGIAR Geographic Domain Analysis (2009). The most recent public domain maps on global poor livestock-keepers are those produced by ILRI in 2002 (Thornton et al., 2002).

2.4 Mapping poverty and livestock systems

Understanding the spatial distribution of livestock keepers can guide the allocation of resources as a first step in reaching the poor; identify areas of opportunity for livestock as a catalyst to growth; and, target hotspots of potential livestock-associated disease and environmental degradation. However, our knowledge of the location, characteristics and trends of change among poor livestock keeping populations is very patchy, both spatially and temporally. Here we outline a rapid broad- brush global assessment of spatial distribution of poor livestock keepers, and describe parallel activities in high-resolution poverty mapping for countries in East Africa using sophisticated econometric techniques pioneered at the World Bank.

In 2001 the UK Government's Department for International Development (DFID) commissioned a study to produce sets of maps locating the significant populations of poor livestock keepers in the world, and to assess in very broad terms how these populations are likely to change over the next three to five decades. These data are reported by Thornton et al (2002). The map presented in this document is updated using more current poverty estimates from World Bank's 2011 WDI with the majority of the information being from 2005-2010 yet with a few countries with estimates still from the 1990s. Several countries within each region also have no estimates and have to be extrapolated by region

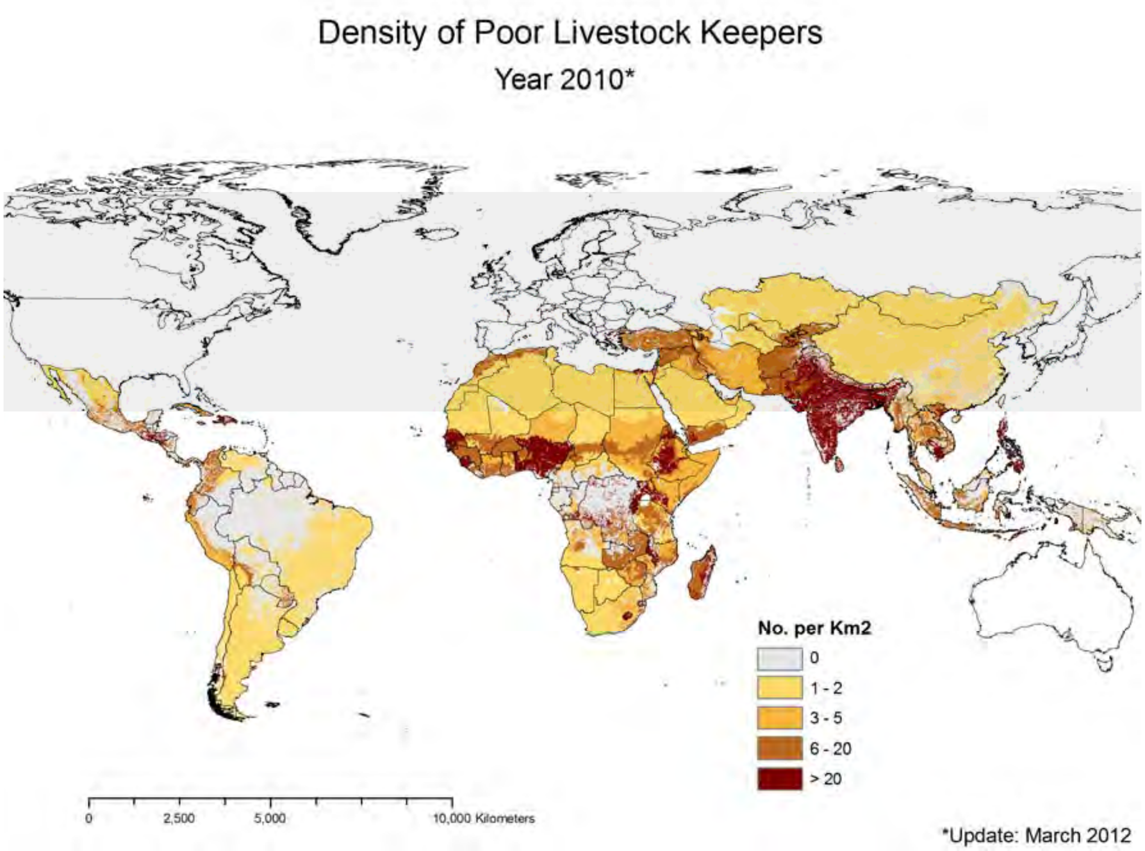
The Thornton et al (2002) study made use of existing data and spatial data layers, together with information from the literature and expert opinion. The central element of the analysis is a global livestock classification based on that of Seré and Steinfeld (1996), who present a typology based on mixed crop-livestock systems, livestock-only rangeland-based systems, and landless production systems. We defined the classification primarily in terms of landuse/cover and climate-based length of growing period (LGP), supplemented by existing global coverages of human population, irrigated lands, and urban areas. Human population scenarios to 2050 were developed for Africa, Latin America and Asia.

The study also provided a breakdown of poverty information by country and livestock production system that was available for most of the countries only at the national level including: World Bank rural and national rates and two internationally comparable poverty lines: less than 1$/day and 2$day. But this information did not include any information on how many of these poor were livestock keepers. So one additional layer was created by assigning differential poverty rates by broad livestock systems (mixed, pastoral and other) within each country providing at least some further sub-national distribution of the poor with livestock.

2.5 Maps of poor livestock keepers

The updated map of density of "poor livestock keepers" 2010 based on the methodology of Thornton et al. (2002) is shown in Figure 2.4. There are many assumptions and extrapolations involved in map development, however, despite caveats, various conclusions can be drawn from the analysis. In terms of numbers of livestock keepers, the critical regions remain South Asia and sub-Saharan Africa. The mixed farming systems (crop and livestock) contain large numbers of poor (over 1 billion), and numbers of poor people dependent to some extent on livestock are considerable. Mixed rainfed systems have more poor livestock keepers than mixed irrigated systems. Rangeland systems have least absolute numbers of the poor but the poor in this system have highest dependency on livestock. Almost half of the poor in rangeland systems are located in sub-Saharan Africa.

Figure 2.4 Density of poor livestock keepers in developing countries based on national data (updated March 2012)

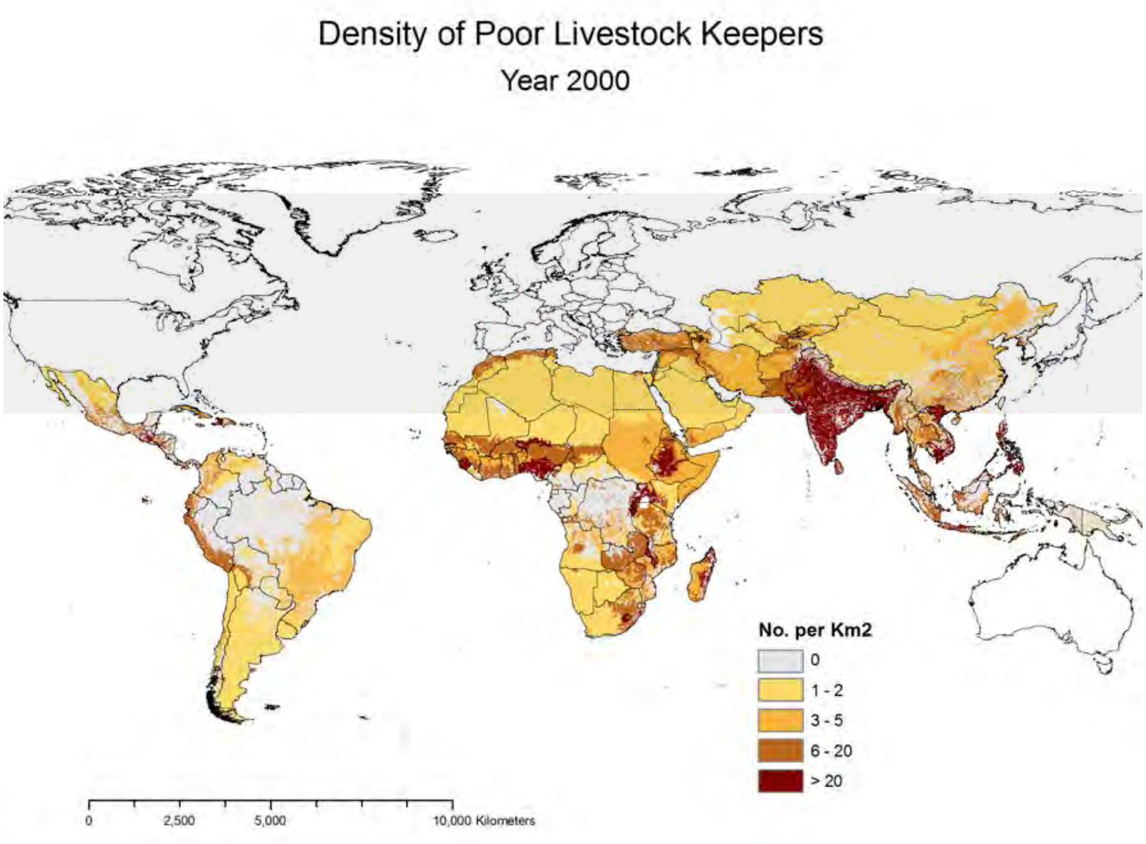


Some changes are evident since the map of 2002. There has been a marked decrease in the density of poor livestock keepers in South America and SE Asia. There has been some improvement, but to a lesser degree in francophone West Africa and South Asia

Change in number of poor livestock keepers

Because of different methods in developing the maps, the map of 2000 is not directly comparable with updates. Some changes are evident since the map of 2002. There has been a marked decrease in the density of poor livestock keepers in South America and South East Asia. There has been some improvement, but to a lesser degree in parts of francophone West Africa and South Asia. However, these improvments have been more than offset by increases in Africa, most of South Asia, the middle East and Central Asia. Overall, the number of poor livestock keepers is estimated to have by 56 million in the eight years from 2000 to 2008 (FAO, 2011).

Figure 2.5 Density of poor livestock keepers as mapped in 2002



The International Food Policy Research Institute IFPRI (Wood et al. 2009) have released their sub-national rural poverty rates that cover most of sub Saharan Africa, but not yet the rest of the developing world. We used these to prepare Poor Livestock Keeper (PLK) maps for the < $1.25/day and < $2/day poverty lines (Figure 2.6 and 2.7).

The two methods (national and sub-national) have broadly comparable results. In both maps, Ethiopia, Nigeria, the Great Lakes region, parts of West Africa and Malawi have the highest density of poor livestock keepers. However, the sub-national data reveals differences within countries. Because endemic zoonoses and emerging zoonotic events are geo-located, maps derived from sub-national data are more useful in exploring associations between zoonoses and poor livestock keepers (Figure 5.3).

Figure 2.6 Density of poor livestock keepers (<$1.25 a day) in sub-Saharan based on sub-national data (update May 2012)

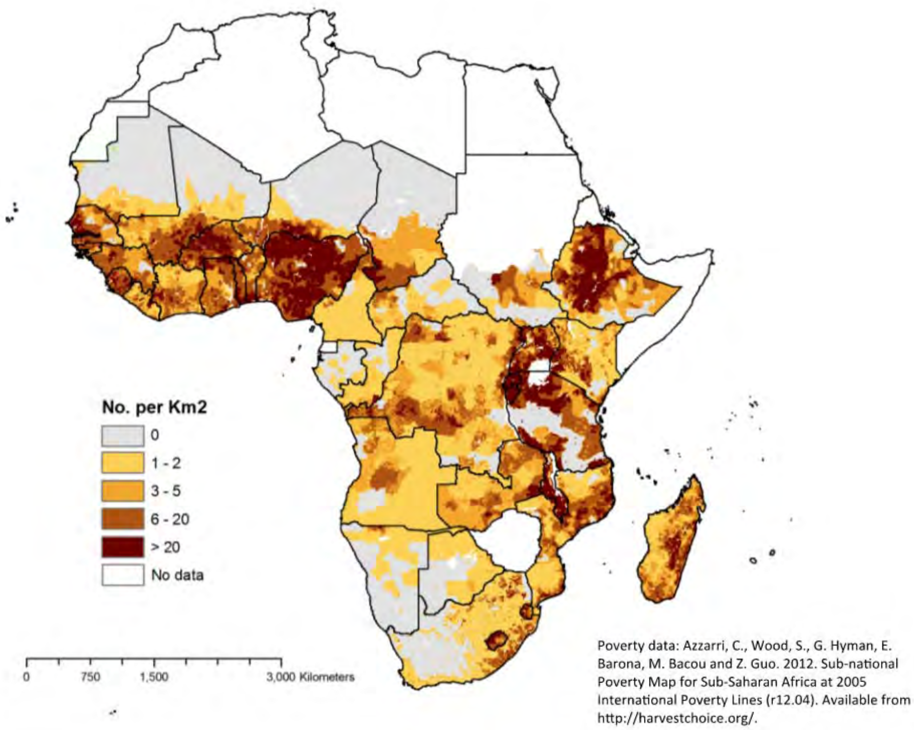
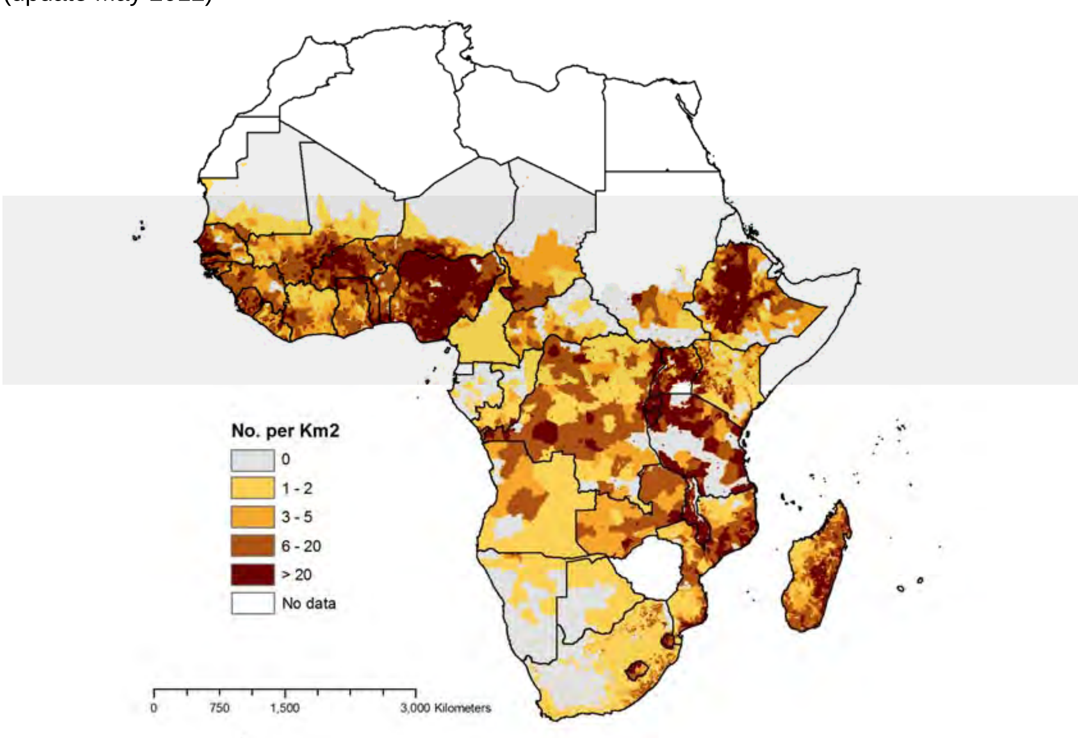


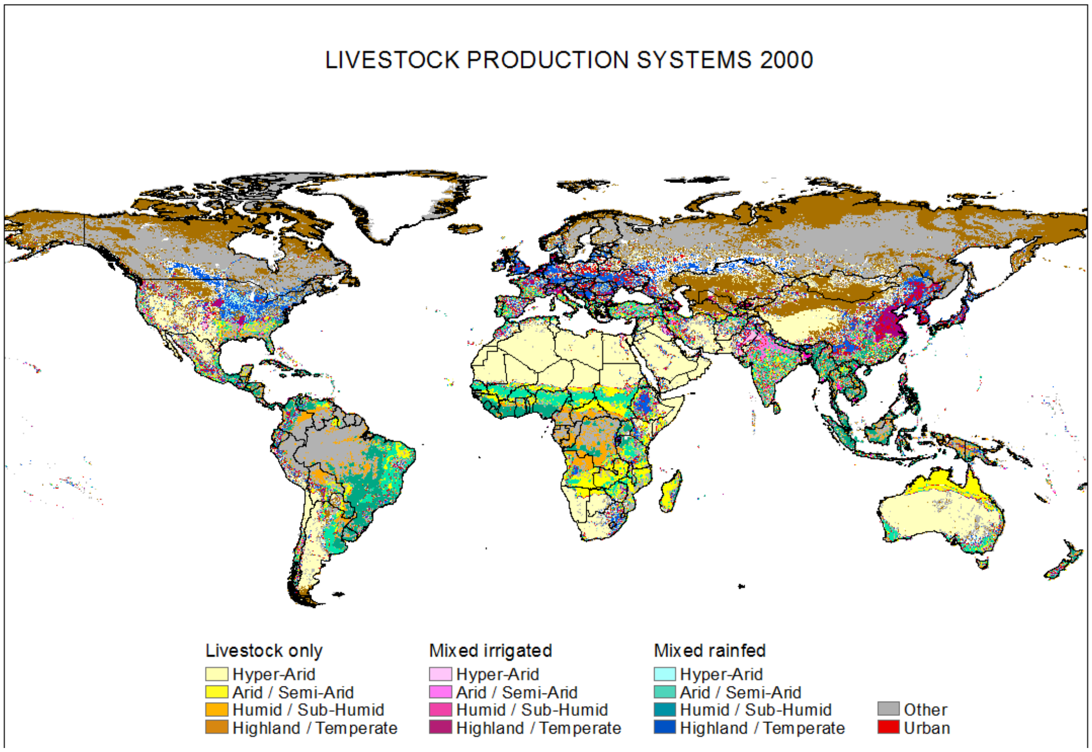
Figure 2.7 Density of poor livestock keepers (<$2 a day) in sub-Saharan based on sub-national data (update May 2012)

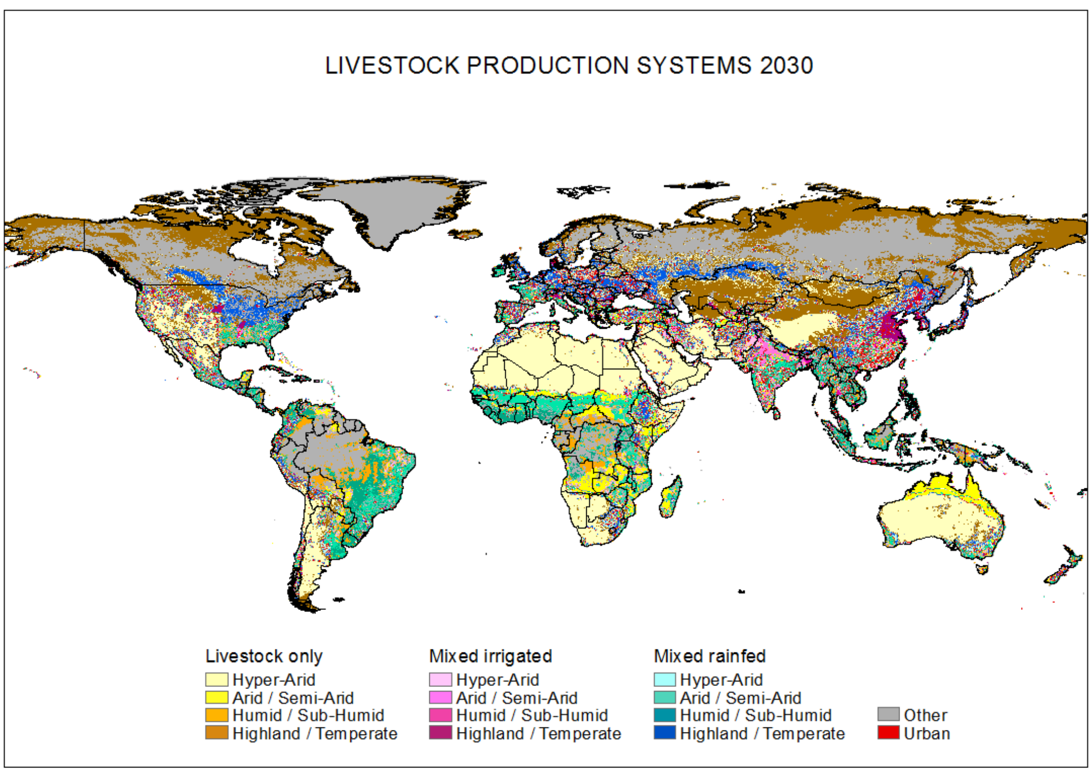


2.6 Maps of livestock system change

Livestock systems are changing rapidly in response to various drivers. Figure 2.8 shows estimates of livestock systems in 2000 and 2030 (Kruska et al., 2003, Hererro et al., 2008).

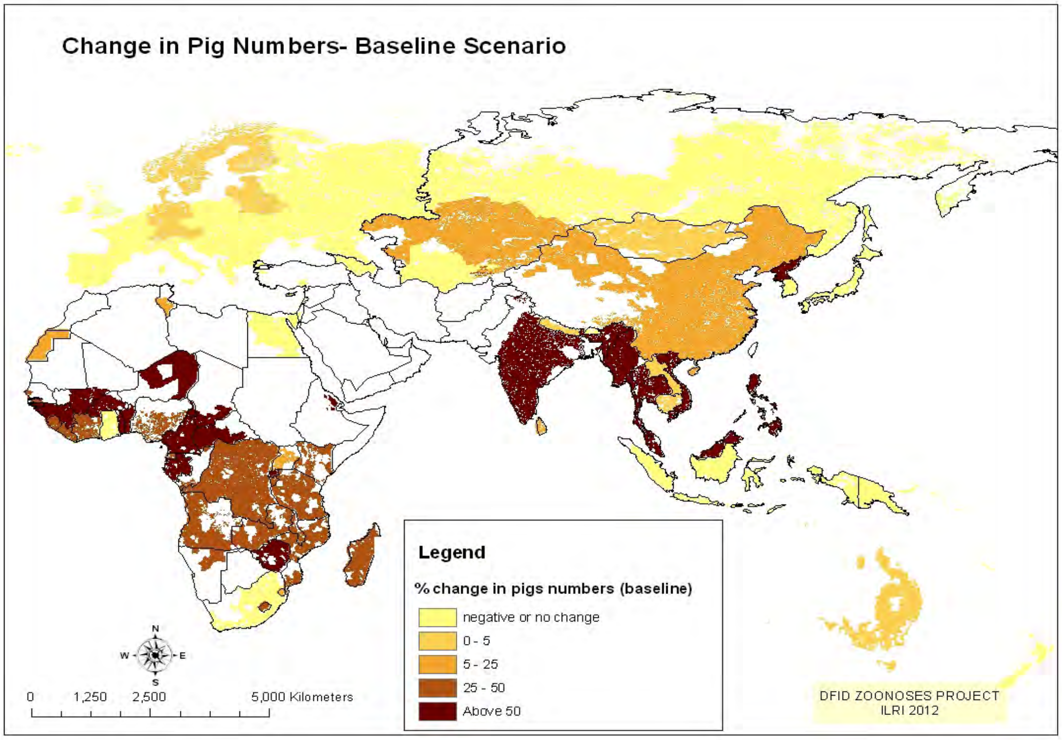
Figure 2.8 Farming systems in 2000 and 2030

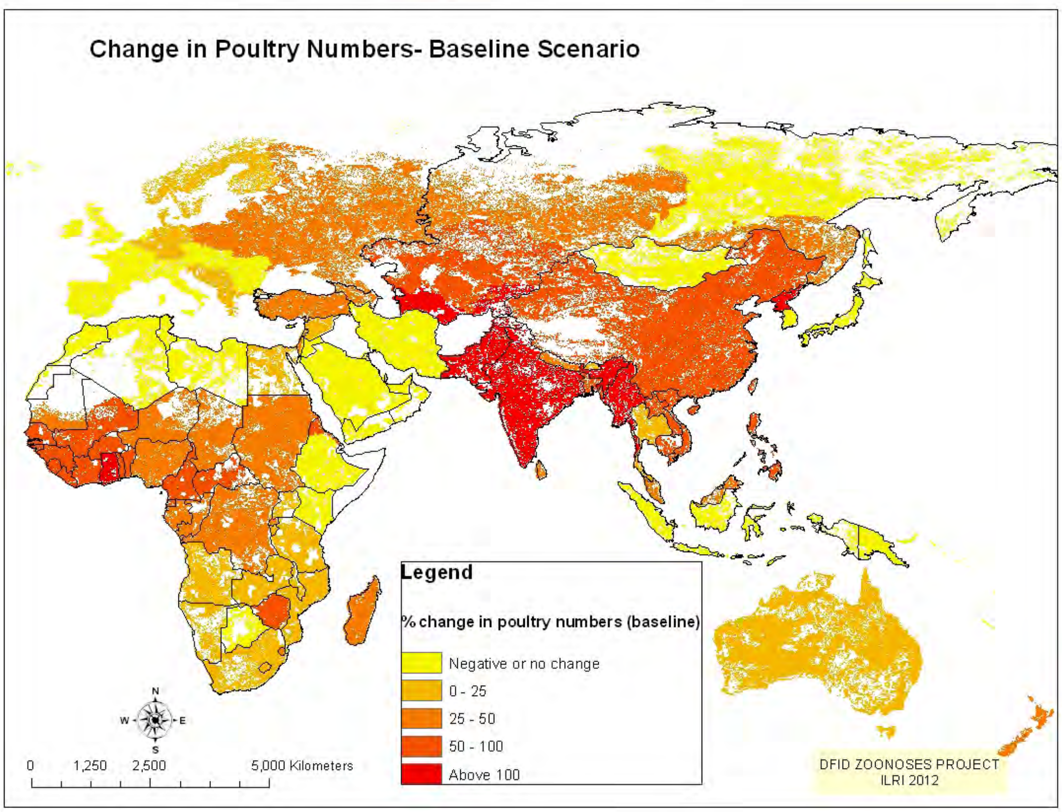




Herrero et al 2009 modelled growth in different livestock systems using the IMPACT model (Fig 2.9).

Figure 2.9 Changes in monogastric populations 2000-2030 (Herrero et al 2009)





Under the reference, or 'business as usual' scenario the hotspots in terms of rapid growth are in descending order, poultry in South and East Asia > poultry in South America > bovines in South and

East Asia > poultry in sub Saharan Africa = pigs in sub Saharan Africa. Figure 2.9 percentage changes in pig and poultry densities between 2000 and 2030 (Herrero et al 2009). These are used as a proxy for emerging livestock systems. These use estimates from the 'baseline scenario', that is the most probable development of the sectors.

Does changing livestock systems change the risk of zoonotic disease emergence?
The maps in Figure 2.9 show some of the geographical areas where change is most rapid; countries which are in the top 20 for both high numbers of monogastrics and rapid change are found in South Asia and South East Asia: Myanmar, India, Pakistan, Bangladesh, Thailand and China. Change in livestock systems extends beyond intensification of poultry and pigs. Rapid change and growth is often associated with erosion of the natural resource base. Globally, anthropogenic changes are driving climate change with implication for livestock keeping and zoonoses. These three change processes are discussed in this section: intensification, interface with wildlife and climate change.

Agricultural intensification and zoonoses
A systematic review of zoonoses at the livestock/wildlife interface recently commissioned by DFID examined evidence for links between livestock intensification and disease emergence. Evidence is as yet insufficient for definitive conclusions, and in some cases intensification is associated with less disease, overall intensification is linked with disease emergence and spread. Selection, breeding and management for increased productivity in livestock create host populations conducive to pathogen evolution and persistence (through lack of genetic diversity, high numbers and contact opportunities, stress-induced immunosuppression and other factors). This provides opportunity for "wild" microorganisms to invade and amplify or for livestock pathogens to evolve to new and more pathogenic forms. In addition, corollaries of intensification such as high livestock and pest densities, extensive transportation networks, sale of live animals for food and pets, landscape modification, poor waste management, and juxtaposition of agriculture or recreation with wildlife all contribute to "emergence" and shifting virulence of diseases (Grace et al., 2011).

The literature review conducted for this survey (chapter 4) found that zoonotic food-borne pathogens were markedly higher in poultry and pigs than in small ruminants and cattle. This suggests that as monogastric systems expand, so may food-borne disease.

Agricultural intensification is likely to have different impacts on the key zoonoses depending on their epidemiology. Probable impacts are discussed in chapter 3 and summarised here. Of the priority zoonoses, 9 are likely to become more of a problem with intensification, 4 are likely to decrease and for the remaining there is no clear link.

Table 2.1 Probable impact of intensification on priority zoonoses

Zoonosis	**Likely impacts of agricultual intensification**
Gastrointestinal (zoonotic)	Most gastro-intestinal zoonoses are food-borne and likely to increase with intensification and associated lengthening and branching of food supply chains. Many gastro-intestinal zoonoses causle little visible signs in animals reducing farmer incentives for control.
Leptospirosis	Leptospirosis is associated with smaller farms, and pasture-grazing especially with stagnant water. Intensification may reduce prevalence.
Cysticercosis	Associated with free-range, scavenging pigs. Intensification will reduce prevalence.
Tuberculosis (zoonotic)	Associated with larger farms and confined systems. Intensification likely to increase.
Rabies	No clear link. Most human transmission from dog bites or wildlife.

Leishmaniasis	No clear link. Transmitted by sandflies. Domestic dogs are the most important reservoir.
Brucellosis	Associated with larger farms and confined systems. Intensification will increase. However, artificial insemination, often associated with intensification, will decrease.
Echinococcosis	Associated with feeding offal to dogs. More common in extensive systems.
Toxoplasmosis	Some evidence this is more common in extensive systems. Associated with rodents.
Q fever	No clear link.
Trypanosomosis (zoonotic)	Intensification reduces risk by removing tsetse habitat and wildlife hosts
Anthrax	No clear link
Hepatitis E *	Extent of transmission from pigs not clear.
Chagas	*Most associated with extensive systems*
Chickungunya	*Associated with incursion into forest areas.*
Clostridium difficile disease	*No clear relation. Present in farm animals but role in transmission not clear*
Dengue fever	*Most transmission anthroponotic: livestock systems no clear role*
Ebola	*Intensification around bats is a risk*
Hanta disease	*Spread by rodents. Not farm associated*
Avian influenza	*Associated high poultry density – link with intensification not clear*
*Bov. Spongiform Encephalopathy^*	*Associated intensive systems*
Psittacosis	*No clear link*
Japanese encephalitis	*Associated with intensive rice systems*
Buffalo pox	*No clear link*
Rift Valley fever	*May increase with intensification and irrigation*

Zoonoses with a wildlife interface

Fourteen of the ‘top 25’ zoonoses have important wildlife reservoirs across many regions, including 8 of the ‘top 13’ zoonoses, namely: gastro-intestinal zoonoses, leptospirosis, rabies, leishmaniasis, toxoplasmosis, Q fever, trypanosomosis and anthrax. For some of the other zoonoses, wildlife may play an important role in some epidemiological circumstances. For example, tuberculosis associated with conservation areas in Tanzania and South Africa, brucellosis associated with buffaloes, and hepatitis E and cysticercosis with wild pigs. Where a wildlife interface exists, zoonoses control is much more complex (Grace et al., 2011). Other zoonoses in the ‘top 25’ but not ‘top 13’ with an important wildlife interface are: Chagas, Chickungunya, Ebola, Hanta disease, avian influenza, psittacosis and Rift Valley fever.

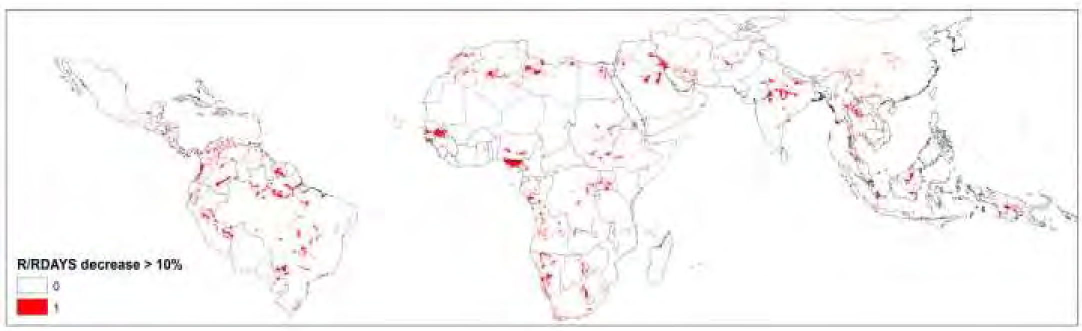
2.7 Climate change and zoonoses

There are several metrics for vulnerability to climate change (Cutter et al., 2009; Fussel et al., 2009). Tropical African countries and Asian coastal countries are usually among the countries considered most vulnerable to climate change. The CGIAR Research Program on Climate Change, Agriculture and Food Security (CCAFS) commissioned ILRI/ CCAFS to conduct a rapid assessment across the global tropics of the vulnerability of food security to climate change (Ericksen et al., 2011). The goal was to identify ‘hotspot’ locations where climate change impacts are projected to become increasingly severe by 2050 and food insecurity is currently a concern, using a range of indicators. The maps mainly focused on change with implications for crop growth but some of these changes also have implications for livestock production and disease.

Figure 2.10 and 2.11 predict areas where rainfall and flooding will increase. This is expected to increase the risk associated with vector-borne zoonoses including tick-borne and mosquito-borne diseases. It will also increase risk of bacterial pathogens associated with stagnant water and flooding (e.g. leptospirosis, anthrax, cryptosporidiosis).

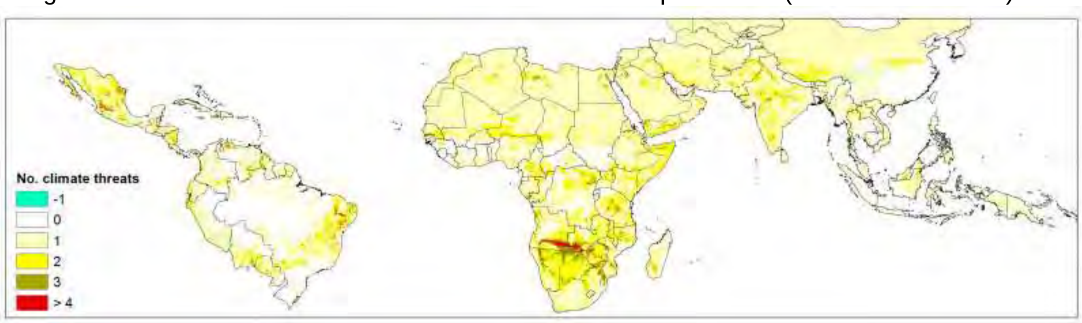
Figure 2.10 Areas where rainfall per day increases by 10% or more between 2000 and 2050 (Ericksen etlal 2011)

Figure 2.11 Flood frequency (Ericksen et al 2011)



The next map aggregates different thresholds that can stress production, including flips in: growing period, reliable crop-growing days, annual aveage temperature, annual average maximum temperature, maximum temperature exceeds 30 centigrade, changes in variablitly in rainfall, and increase in rainfall.

Figure 2.12 Number of climate thresholds that can stress production (Ericksen et al 2011)



In terms of exposure to multiple climate threats, southern Africa has the largest area exposed (across Namibia, Angola, Zambia, Botswana, Mozambique and South Africa) with multiple threats, followed by northeastern Brazil, Mexico, Guyana, Nicaragua, and small areas in Tanzania, Ethiopia, the DRC, Uganda, India, and Pakistan, as well as the Middle East.

While studies are starting to emerge on the likely effect of climate change on human disease, and changes in spatial dynamics of some animal diseases (e.g. blue tongue) are believed to be influenced by climate change, there is still little strong evidence on impacts of climate change on zoonotic disease in dynamic systems with multiple drivers. For example, as countries get warmer and wetter biological mechanisms would suggest that many diseases increase. However, if countries simultaneously get richer or invest more wisely in health care the net impact may be disease decrease (Perry et al., 2011).

The effects of climate change on livestock and non-vector-borne disease have, with some exceptions, received little attention. The climate-livestock-poverty nexus was reviewed by Thornton et al. (2008) and this section is largely based on their findings. Climate change may affect livestock disease through several pathways:

- Pathogens: higher temperatures and greater humidity generally increase the rate of development of parasites and pathogens that spend part of their life cycle outside the host. Changes to wind can affect spread of pathogens. Flooding that follows extreme climate events provides suitable conditions for many water-borne pathogens. Drought and desiccation are inimical to most pathogens.
- Vectors: vector-borne diseases are especially sensitive to climate change. Changes in rainfall and temperature regimes may affect both the distribution and the abundance of disease vectors, as can changes in the frequency of extreme events (outbreaks of Rift Valley fever have been linked to ENSO, for example).
- Hosts: some will be exposed to new pathogens and vectors as their range increases and impacts can be severe. Climate stress (heat, inadequate food and water) can also lower immunity.

Of the 13 priority zoonoses, cysticercosis, tuberculosis, rabies, brucellosis and echinococcosis are unlikely to show high climate sensitivity and food-borne zoonoses, leptospirosis and trypanosomosis are likely to show high climate sensitivity. It is less clear how climate change will affect the epidemiology of other priority zoonoses, although some evidence suggests there may be important negative impacts.

- Food-borne zoonoses: A recent extensive literature review concluded that campylobacteriosis and salmonellosis were most likely to increase with air temperature; campylobacteriosis and non-cholera vibrio infections with water temperature; cryptosporidiosis followed by campylobacteriosis with increased frequency with precipitation; and cryptosporidiosis followed by non-cholera vibrio in association with precipitation events. Listeria sp. was not associated with temperature thresholds, extreme precipitation events, or temperature limits (ECDC, 2012).
- Leptospirosis: Leptospirosis is considered one of the more climate sensitive diseases. Flooding and heavy rainfall have been associated with numerous outbreaks of leptospirosis around the world. With global climate change, extreme weather events such as cyclones and floods are expected to occur with increasing frequency and greater intensity and may potentially result in an upsurge in the disease incidence as well as the magnitude of leptospirosis outbreaks (Lau et al., 2010).
- Trypanosomosis: While climate will modify (generally decrease, but not everywhere) habitat suitability for the tsetse fly, the demographic impacts on trypanosomosis risk through bush clearance are likely to outweigh those brought about by climate change (Thornton et al., 2006).

- Q fever is transmitted in aerosols and climate change could affect survivability. Toxoplasmosis has rodent hosts and rodent populations are sensitive to climate change. Climate change and other environmental changes have the potential to expand the geographic range of the vectors and leishmaniasis transmission in the future. Anthrax is often associated with a combination of heavy rain and warm temperatures following a drought that encourages spores to germinate. These extreme events will be more common with climate change.

Chapter 3: Literature review of zoonoses of importance

Summary
We undertook a systematic literature review of the 13 zoonoses identified as important. Eight of these are 'endemic classical zoonoses' that is, zoonoses that are typically present across a wide range of communities at most times (although perhaps showing annual and inter-annual variability). In the case of bacterial food-borne zoonoses, we identified five diseases, which ranked highest on a number of recent assessments of impact (salmonellosis, listeriosis, toxoplasmosis, campylobacteriosis and disease caused by diarrhoeagenic Escherichia coli*). We also considered three epidemic or outbreak-associated zoonoses (rabies, leishmaniasis and anthrax) and hepatitis E, an emerging disease, which may have an important zoonotic transmission.*

For each disease we present information on prevalence, epidemiology, geographical hotspots and some key research questions and we estimated an 'endemic disease burden' score for all the countries for which information existed.

3.1 Methodology for systematic literature review
We generated search terms that incorporated certain key words, identified and screened abstracts, reviewed full papers and synthesised required information. Diseases were initially considered on the basis of their appearance in the top 13 list of zoonoses generated as explained in the previous chapter. These were: *Taenia solium* cysticercosis, leptospirosis, anthrax, brucellosis, echinococcosis, hepatitis E, leishmaniasis, Q fever, rabies, toxoplasmosis, trypanosomosis, tuberculosis, and food borne infections (caused by *Salmonella* spp., *Listeria monocytogenes*, diarrhoeagenic *Escherichia coli*, and *Campylobacter* spp.).

PubMed (www.ncbi.nlm.nih.gov/pubmed/) and CABDIRECT (www.cabdirect.org/) were used in doing the searches but also Google (www.google.co.ke/) including the Google scholar. Unpublished materials including student theses (mainly from the University of Nairobi) were accessed by visits. Related articles appearing during the active searches in PubMed were also utilized in sourcing for extra details, as well as from relevant references cited in the main papers reviewed. When available, the cited original papers were retrieved, reviewed, and relevant information retrieved. This also applied to major review papers providing a summary of the needed information and references for the original papers available. We used the same data as summarized in the review paper if the original paper was not available.

Search terms were formulated, by disease, and by country or region; different combinations, were either relaxed or broadened to capture more articles or were restricted to refine or limit the number of resulting articles. Different Boolean operators were used (including AND, OR, parenthesis) for specific PubMed and CABDIRECT searches. Phrases guided by key words were used for the Google searches. We also applied wildcard symbols, mainly * to broaden the results in some of the searches.

The first step involved screening the abstracts by title, abstracts not relevant for the project objectives were left out. The searches were originally limited to the last 10 years, but we also considered old studies if the search results were initially few. We considered studies conducted in Africa, South Asia and South East Asia. Some studies from the Middle East were also included. Those abstracts that were considered relevant (based on the title) were extracted into a word document and subsequently reviewed by a second person. Full papers linked to the relevant abstracts were extracted and reviewed. Prevalence information, if available, was extracted from abstract in cases where the full paper could not be accessed. Sources providing no information on the number of samples / subjects analysed were not considered- as the basis for the calculation of the prevalence estimates could not be established. Also excluded were papers with missing geographical locations for the specific studies.

An excel® database was developed to capture information extracted during the review process (including the different search terms used). Variables extracted included: country where the study was done / or where the results apply, geo-spatial location (the specific location or coordinates if given), number of herds studied, number of samples analysed, the specific diagnostic test(s) done, subjects (livestock species, food, humans), individual prevalence, herd prevalence, year data were collected and a description of the study population. Where multiple surveys were reported in one study, each survey was listed separately (e.g. if prevalence was estimated in cattle and sheep these were considered as two different surveys each with an associated sample size, species and prevalence). We distinguish between "community studies' which are conducted in the community and can be considered representative of it, and "high risk studies" which were conducted in high risk populations (sick people in hospitals, malnourished children, cattle which failed ante-mortem inspection, samples taken during an outbreak etc.). Maps were generated using data from community studies only.

We defined geographical hotspots as those which had a high prevalence confirmed in multiple surveys. The number of studies needed to consider estimates reliable varied from pathogen to pathogen depending on the number of studies available and is given in the results section of the different diseases.

In order to estimate the 'top twenty countries' for endemic disease burden we collated the geographical hotspots. We standardized scores for each disease so the country that had highest prevalence had a score of ten, and so on. We then summed scores for each disease by country.

To develop the maps of endemic zoonoses we collected on-locational or descriptive data on zoonoses using systematic literature review and details were documented in a MS Excel spread sheet. The study area covered entire Africa and Asia (South central Asia and South East Asia). The constitution of a spatially referenced database was performed by introducing locational or spatial data in the form of coordinates into the spreadsheet. These coordinates were approximated from the 'Geospatial location' section of the database and were sourced from existing GIS databases and occasionally from websites such as Google maps and www.longitude-latitude-maps.com.

The spreadsheet was then imported into the GIS software package ArcGIS v.10 (ESRI, Redlands). This software package allows for the seamless linkage of MS Excel spreadsheets to the GIS by using the coordinates columns, and these are imported as event data. The zoonoses locations were then mapped and the column 'prevalence' from the descriptive data used to map the magnitude of the prevalence as a percentage. For visualization purposes, mapping was done with a base map of agricultural farming systems on the background.

3.2 Results for systematic literature review- endemic zoonoses

We conducted a systematic review of brucellosis, tuberculosis, leptospirosis, trypanosomosis, cysticercosis, and Q fever and some bacterial food-borne diseases.

- Brucellosis – *the deceptive disease* – causes fever and occasionally chronic disease in people; mainly abortion and infertility in cattle, shoats and pigs
- Tuberculosis – *white plague* – a major cause chronic illness in people, causes wasting and illness mainly in cattle
- Leptospirosis – *swamp fever* – causes fever and occasionally jaundice in people and fever and infertility in cattle and pigs; wildlife important reservoirs
- Q fever – *the most contagious disease* – causes fever and occasionally death in people, carried by cattle, shoats, pets and wildlife, causes abortion in shoats
- Cysticercosis – *pork worm* – most common cause of adult-onset epilepsy in poor, pig-keeping communities, leads to carcass condemnation in pigs
- Trypanosomosis – *sleeping sickness* – cause of acute and chronic illness in people, historically caused severe epidemics, the most important disease of cattle in sub Saharan Africa; wildlife important reservoirs
- Bacterial food-borne disease – *the forgotten zoonoses* – major cause of gastrointestinal disease in people; some but not all cause illness in animals. Several have wildlife interface
- Echinococcosis – *cystic disease* - a major cause of illness in people and loss in sheep and goats from condemnation of carcasses

We obtained information from 1098 surveys covering around six million animals, ten million people and six thousand food or environment samples. Endemic zoonoses impose an important burden in all regions, although the distribution varies according to disease. Trypanosomosis is found only in sub-Saharan Africa, cysticercosis is rare (though not absent) from cultures where pigs are not kept, and brucellosis is associated with high populations of ruminants. Zoonotic food-borne diseases, the most important zoonoses, are at much higher prevalence in poultry and pigs than ruminants. Table 3.1 summarises the prevalence for important zoonoses by region and for all developing countries. It gives the overall prevalence (humans, livestock, wildlife, other animals) and the prevalence for humans and livestock separately.

Table 3.1 Prevalence (%) of important zoonoses by region

	North Africa, Near East	East Africa	Southern Africa	West Africa	South Asia	SE Asia	All developing
Brucellosis*	13%	8%	14%	16%	16%	2%	12
Tuberculosis^	9	8	5	7	17	0.2	7
Leptospirosis*	30	24	17	28	27	24	24
Q fever*	19	11	4	13	19	1	19
Cysticercosis^	Few pigs	12	23	16	14	12	14
Trypanosomosis^	Not present	9	12	10	N/A	N/A	10
Food-borne disease	25	27	21	30	18	25	25
Overall	**15**	**10**	**16**	**15**	**25**	**22**	**16**
Human	15	15	11	10	19	11	16
Livestock	15	10	16	16	17	18	15

*based mainly on seroprevalence, indicates current or recent cases (last 1-2 years)

^ based on parasitological tests, indicates current infections

Brucellosis – the deceptive disease

Pathogen

The most important species of *Brucella* are zoonotic: *B. abortus*, responsible for bovine brucellosis; *B. melitensis*, the main etiologic agent of ovine and caprine brucellosis and an increasing cause of cattle brucellosis; and *B. suis,* causing pig brucellosis.

Studies

259 studies were assessed covering 476,067 animals and 31,842 people and 537 food samples. 248 studies were from communities and 11 from high-risk groups (mainly people in hospitals).

Tests

Commonly used tests for brucellosis detect antibodies produced in response to infection. A combination of tests may be used to improve accuracy or ability to detect. The antibodies tested for generally persist for several months (IgG) or several years (IgM). Positive tests (to both antibodies) indicate the animal is currently sick, is chronically infected or has been infected in the last year or so. Hence positive tests are roughly equivalent to annual cases.

Prevalence

In community surveys, the prevalence was 13% in shoats, 13% in bovines, 7% in camels, and 5% in other species (chickens, pigs, dogs). Among livestock-keepers/abattoir workers prevalence was 11%, and among suspect hospital patients, 7%. A large study in India found that 2% of patients in the general hospital population tested positive for brucellosis.

Epidemiology

The main risks for people are occupational (contact with livestock) and consumption of dairy products. In some areas, brucellosis may be maintained in reservoir wild animal hosts (African buffaloes and North American bison) in other cases diseases spills-over to wildlife and if eliminated in cattle brucellosis will die out in wildlife. Brucellosis is more problematic in intensive systems than extensive and pasture-based systems.

Hot spots

Brucellosis is mainly a problem where ruminants are important (Africa and South Asia). Shoat-keeping communities are most at risk from *B. melitensis* considered the most pathogenic form.
Countries with multiple surveys (>=4) and high prevalence (>15%) include in descending order: Togo, Mali, Ivory Coast, Zambia, Niger, India, Sudan, Cameroon and Burundi (human and animal combined)

Impact

Sero-positive animals have higher rates of abortion, stillbirth, infertility, calf mortality and lameness. This is associated with lower milk yields (around 25% milk loss in aborted cows). Usually, infected females will abort only once, although they may remain infected their entire life. The losses are estimated at 6-10% of the annual value produced per animal (Mangen et al., 2002).

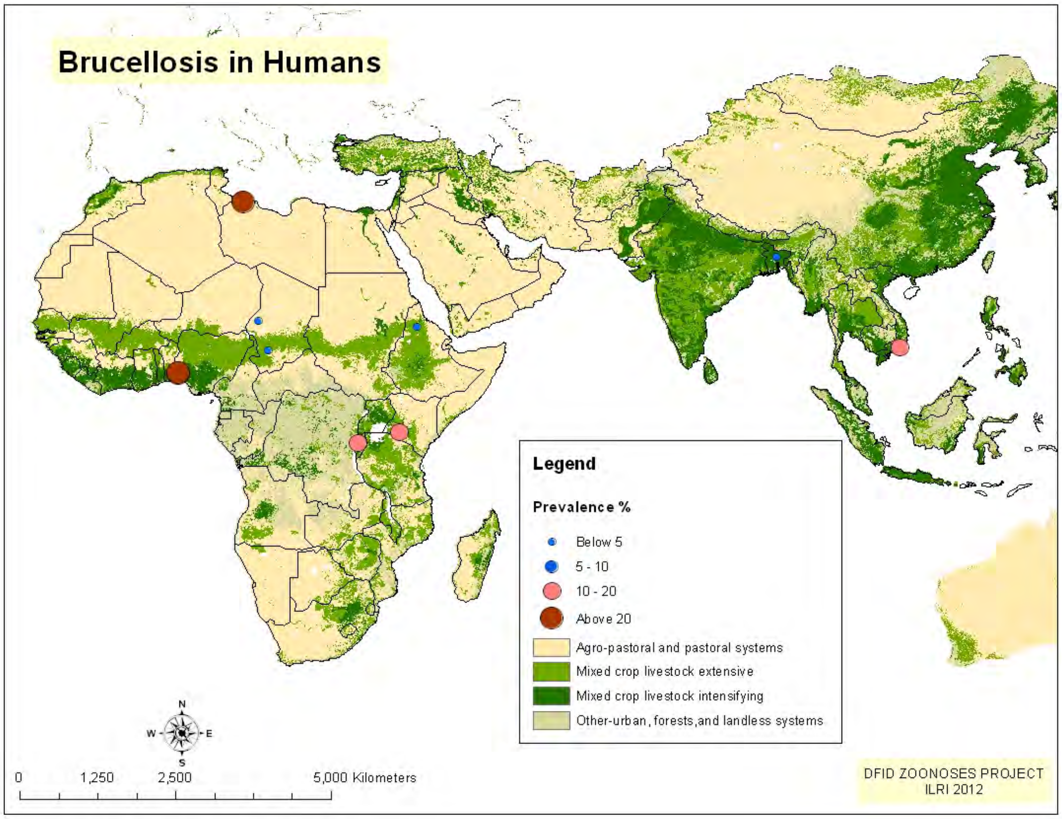
Agricultural losses have been estimated at $427 million per year for sub-Saharan Africa and $600 million for Latin America (Mangen et al. 2002; Seleem et al., 2009)
Human brucellosis usually presents as an acute febrile illness, often mistaken for malaria or typhoid. Chronic complications are not uncommon.

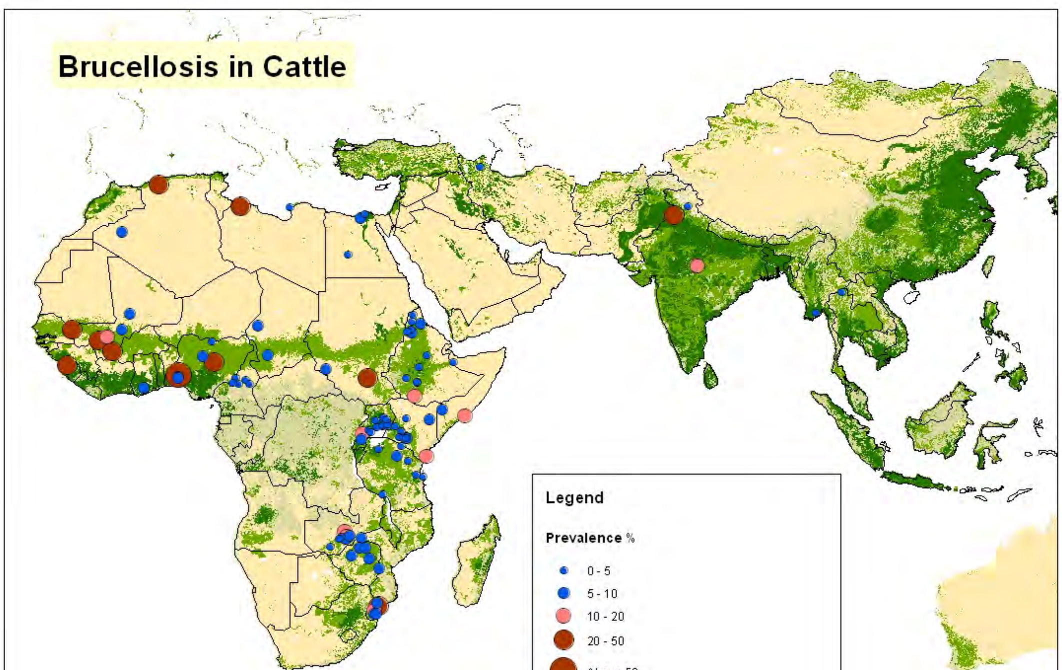
Key research questions

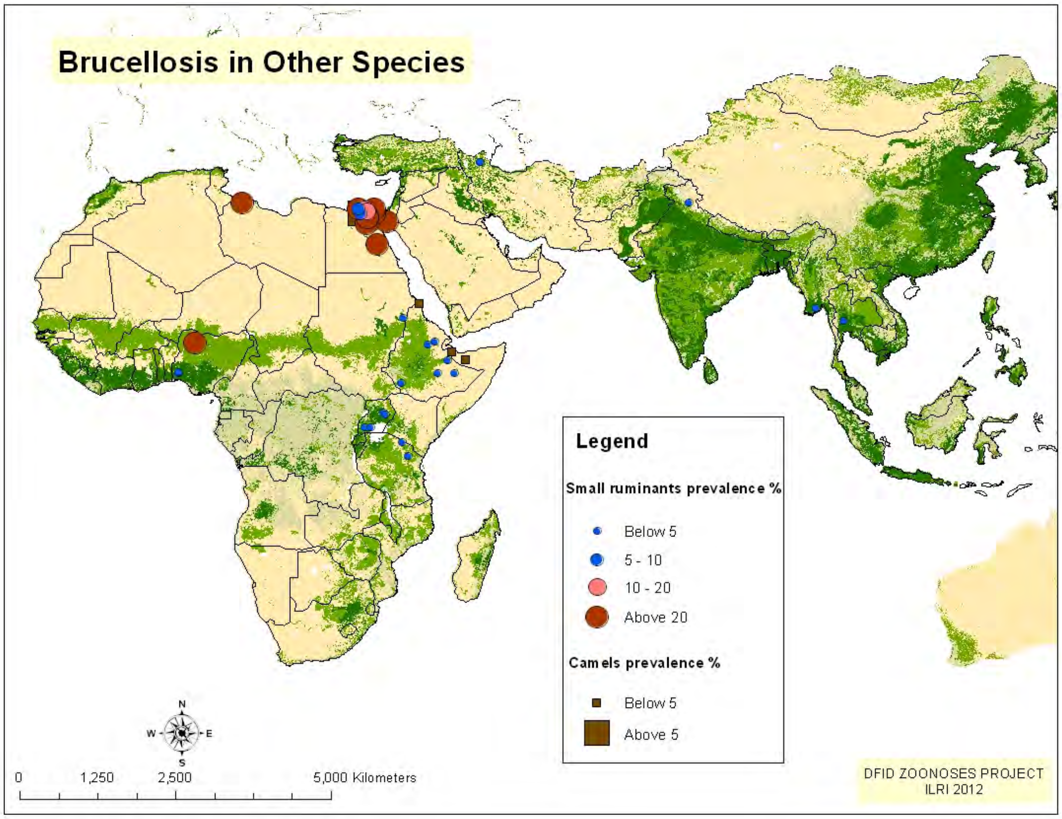
- Improving diagnosis in people, given widespread under-diagnosis and confusion with malaria
- Public-private partnerships for control – promising studies suggest that by combining human health investment and livestock sector investment, brucellosis can be controlled in a cost-effective way

- Role of wildlife in maintaining infection – wildlife have an important role in some circumstances. The extent of this is not known, nor are effective strategies for managing disease in wildlife populations
- Reducing risky behaviours around husbandry and consumption- much of the risk from brucellosis can be reduced by simple precautions applied to handling cattle and food.
- Developing a vaccine for *B. suis*
- Effective vaccination which can be distinguished from infection to aid in control

Figure 3.1 Brucellosis prevalence in community surveys







Tuberculosis – the white death

Pathogen

Worldwide and historically, most human tuberculosis (TB) is caused by *Mycobacterium tuberculosis*. *M. bovis* is responsible for cattle tuberculosis. It affects a wide range of animals and is responsible for zoonotic TB in humans. In west Africa, *M. africanum* causes up to half of human tuberculosis – it has characteristics intermediate between *M. tuberculosis* and *M. bovis* the agent responsible for bovine tuberculosis. Atypical mycobacteria are found in the soil and environment and can infect both people and animals.

Studies

110 surveys were assessed covering 336,152 livestock and 5,829 humans. 89 studies were community-based and 12 in high-risk populations.

Tests

The standard method for detection of bovine tuberculosis is the tuberculin test, which involves the intradermal injection of bovine tuberculin protein derivatives (PPD) and the subsequent detection of swelling at the site of injection. This may be performed using bovine tuberculin alone or as a comparative test using avian and bovine tuberculin. More recently, a gamma interferon test has been developed. Meat inspection is also used to detect tubercular lesions in cattle, but in developing countries is not very accurate. A large study in Ethiopia found routine inspection detected 3.5% carcasses with lesions whereas detailed meat inspection procedures identified 10.2% carcasses, a more than three fold difference (Biffa et al).

Positive tests are roughly equivalent to prevalence (or animals currently sick with TB).

Prevalence

Overall, 7.4% of livestock were positive. Overall prevalence was as follows: Bovines: 8%, camels 11%, shoats 2%, pigs 15%, wildlife 5%.

There were an estimated 12 million cases of human TB (prevalence) in 2010 (WHO, 2011). Twenty-two high burden countries account for approximately 80% of all new TB cases. An extensive literature exists on the prevalence of human TB but there is little information on what proportion is zoonotic, and our review concentrated on this. Table 3.2 summarises more recent studies from developing countries: on average 10.5% of human TB cases were associated with *M. bovis*. Our study suggests a higher overall prevalence than previous best estimates (3.1%)[5] but a strongly bimodal distribution: zoonotic TB is either very important or minor in a given context.

Table 3.2 Studies since 1999 on proportion of zoonotic TB

Country	Study	MTBC	M bovis	% M. bovis	Reference abbreviation	Year
Cameroon	15 district hospitals in Ouest	455	1	0.20%	Niobe-Eyangoh	2003
Djibouti	Unknown	85	1	1.20%	Koeck	2002
Egypt	Fever hospitals in cities	67	1	1.50%	Cooksey	2002
Ghana	Korle-Bu teaching hospital	64	2	3.10%	Addo	2007
Guinea-b	Unknown	229	4	1.70%	KŠllenius	1999
Madagascar	Antananarivo, Ansirabe, Fianarantsoa, Mahajanga	400	5	1.30%	Rosolofo-Razanamparany	1999
Nigeria	2 hospitals Ibadan	60	3	5.00%	Cadmus	2006
Nigeria	Lagos	91	4	4.40%	Idigbe	1986
Nigeria	3 hospitals Jos	50	10	20.00%	Mawak	2006
Tanzania	Arusha	34	7	20.60%	Cleaveland	2007
Tanzania	Pastoralist North & South	38	7	18.40%	Kazwala	2001
Tanzania	Arusha	34	7	20.60%	Mfinanga	2004
Uganda	Kampala	344	1	0.30%	Asiimwe	2008
Uganda	Kampala	234	1	0.40%	Niemann	2002
Uganda	Karamoja	10	3	30.00%	Oloya	2007
Uganda	Mbarara	69	0	0.00%	Byarugaba	2009
Bangladesh	Clinical	350	0	0.00%	Nakajima	2010
India	TB meningitis	37	24	64.90%	Shan	2006
India	EPTB hospital adjusted for prev EPTB in population	155	22	2.90%	Jain	2011
India	EPTB hospital adjusted for prev EPTB in population	115	53	12.60%	Prasad	2005
Pakistan	Hospital, Lahore	42	5	11.90%	Nawaz	2012

MTBC= Mycobacterium tuberculosis complex EPTB=Extra-pulmonary tuberculosis
Prev. = prevalence

Cattle can also be affected by *M. tuberculosis* and can in turn shed this in secretions and excretions. Cattle positive for *M. tuberculosis* to be a problem in South Asia: in one of the studies we reviewed, taking place in India, 7.1% of pharyngeal swabs from cattle were positive for *M. tuberculosis*. This

[5] Historically, *M bovis* was responsible for 5-30% of TB cases in the US, UK and Netherlands (Olmstead and Rhode, 2011; Cousins, 2001). Currently, zoonotic TB can be high in specific circumstances In California, during 1980--1997, 34% of culture-confirmed TB cases in were caused by *M. bovis.* However, many experts consider the role of zoonotic TB to be minor or negligible. The most authoritative review estimated that worldwide 3.1% of human TB cases are caused by *M. bovis* (Cosivi et al., 1998).

suggests that the burden of ‘zoonotic’ TB may be under-estimated as ‘human TB’ may be acquired from cattle.

M. bovis infects a range of African wildlife (high levels of infection have been found in the Kruger Park, Zambia and Serengeti). This is a potential source of infection to livestock and people, as well as a threat to wildlife. Where *M. b*ovis is established in wildlife hosts (e.g. badgers in the UK or possums in New Zealand) eradication is very difficult.

Epidemiology
Commonly found risk factors are close contact of animals (intensive and peri-urban systems), increasing herd size and presence of wildlife reservoirs. Important risk factors for zoonotic TB people are close contact with animals and consumption of raw milk. Prevalence appears to be higher on intensive farms.

Impact
Muller summarizes a range of early reviews from Europe and North America before control was widespread. Infected cattle lost 10% of milk production and 4% of meat production and infected cows had one fewer calf. Unfortunately, good economic data is missing from developing countries but similar losses could be anticipated. TB lesions are also an important reason for carcass condemnation but it seems likely that routine meat inspection misses most cases (Biffa et al., 2010).

Zoonotic TB has a similar course in people as non-zoonotic. Overall, one third of the world’s population is currently infected with TB. Of those infected with TB that do not receive treatment, about 5-10% will develop TB disease some time in their lives. Zoonotic TB is more likely to present as extra-pulmonary, and prevalence of extra-pulmonary TB is a crude proxy for zoonotic TB.

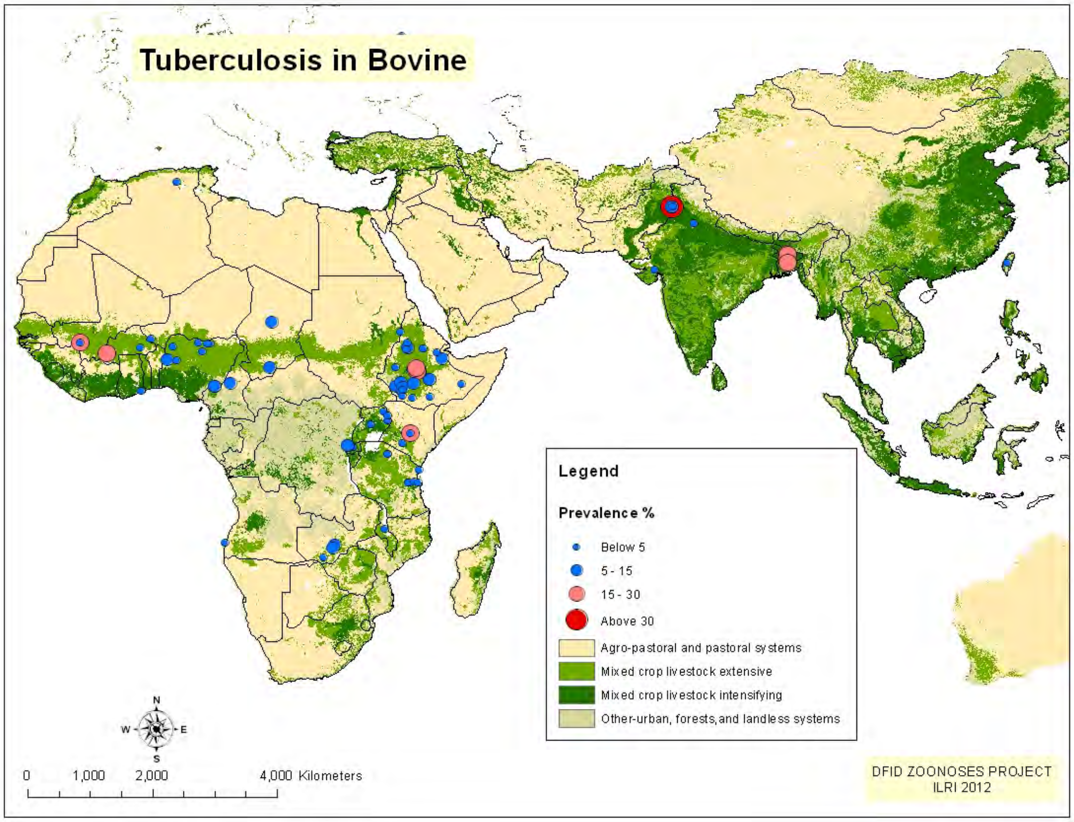
Agricultural losses worldwide have been estimated at $3 billion (Garnier et al., 2003).

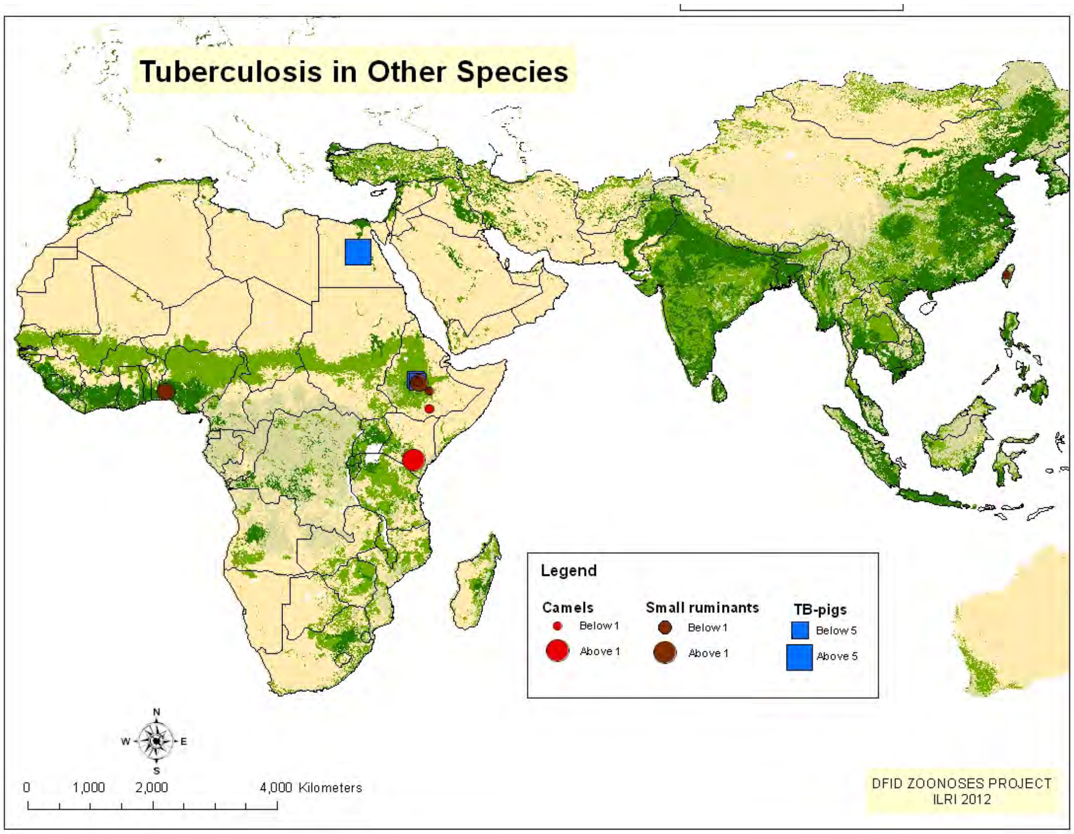
Geographical hotspots
Zoonotic TB is mainly a problem where cattle are important (Africa and South Asia). Dairying communities are most at risk.
Countries with multiple surveys (>=2) and high prevalence (>5%) include in descending order: Bangladesh, Burkina Faso, Pakistan, Ghana, Kenya, Mali, Cameroon, Chad, India, and Ethiopia.

Human TB (zoonotic 3-10%) is mainly localized in high burden countries: India, China, Indonesia, Nigeria, Bangladesh, and Pakistan.

Key research questions:
- *M. tuberculosis* (human TB) appears to be common in livestock in some areas (especially India). What is the significance for transmission?
- A zoonotic reservoir has been suspected for *M. africanum* – so far little evidence but not fully investigated
- TB is one of the most important and common human diseases. There is much uncertainty on the proportion of this attributable to *M. bovis,* and our review suggested that the proportion is higher than in previous estimates and most of a problem in South Asia
- Impact of *M. bovis* on cattle in Africa and South Asia. Much of the information on impact is derived from earlier studies in Europe or North America
- Wildlife-livestock interface in hotspots (Tanzania, Ethiopia, Zambia and South Africa)
- Understanding relation between intensification and disease: Cattle TB appears to increase with intensification and urban farming
- Controlling cattle *M. bovis* and *M. tuberculosis* in cultures that do not permit culling of cattle.

Figure 3.2 Tuberculosis prevalence in community studies





Pathogen
Leptospirosis is an infectious disease caused by pathogenic organisms belonging to the genus *Leptospira*. There are many serovars (>250) but typically only around 10-20 are found in a given region. Serovars can be grouped into 25 serogroups.

Tests
Microscopic agglutination test is the gold standard and was used by most of our studies. Paired serum samples are used to identify current or recent infection. Antibodies may persist for several years. Most of the surveys in our review were community based. For these, a positive result indicates current infection, chronic infection or infection in the last few years.

Prevalence
109 surveys were assessed covering 52,534 animals and 83,596 people. In community surveys the prevalence was 34% in swine, 29% in bovines, 14% in small ruminants, 16% in wildlife and 24% in people.

Among patients presenting with fever of unknown origins around 20% (7-57%) had leptospirosis. Among patients with suspected leptospirosis 60-90% had positive diagnoses

Epidemiology
Infected animals often become carriers. Wildlife are affected and can be important reservoir hosts. Risk factors for humans include presence of rodents, farm animals and floods. Risk factors for animals include smaller farms and extensive (pasture-grazing systems).

Geographical hotspots
Leptospirosis is mainly a problem in tropical countries where stagnant water can be found and where cattle, pigs or rodents are frequent. SE Asia has been regarded as a hot spot but fewer studies have been carried out in Africa.

Countries with multiple surveys (>=4) and high prevalence (>20%): Ethiopia, Vietnam, Nigeria, Egypt, and Malaysia.

Impact
In people, leptospirosis most often presents as a febrile illness. Around 5-10% of cases may develop jaundice or other complications and among these case fatality may reach 20%. SE Asia is considered a hot spot and in some areas is the second most common cause of fever after malaria.

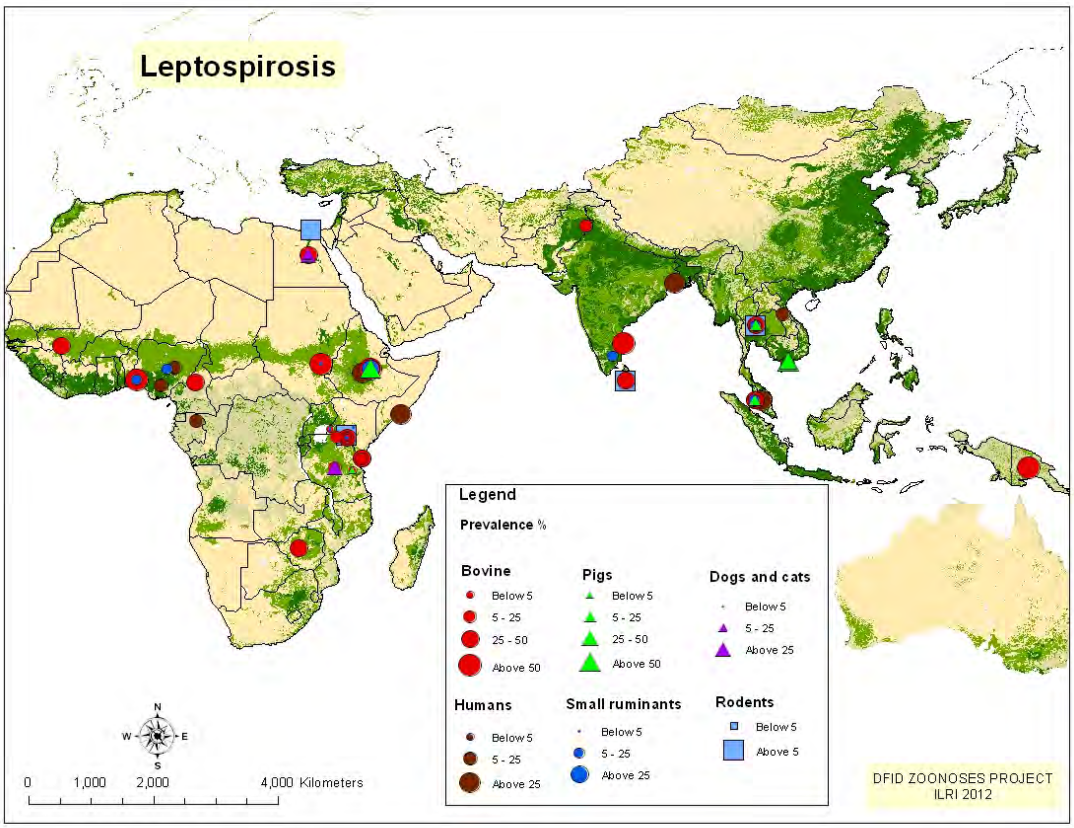
In livestock, leptospirosis is associated with abortion, still-birth, infertility and milk reduction in cattle and swine.
There is little good data on losses associated with leptospirosis in developing countries. In Australia, total loss was estimated at 2.2% at herd level (Holroyd, 1980).
In Vietnam, infection with some serovars correlated with one less live pig per litter, equivalent to 8% loss of production (Boqvist et al., 2002).

Key research questions

- Prevalence and incidence in Africa: leptospirosis has been considered most problematic in SE Asia, this study suggests it may be more important than suspected in Africa
- Leptospirosis as a misdiagnosis in people: like brucellosis and Q fever, leptospirosis is often under-diagnosed and better tests as well as awareness raising among the medical community and public is needed

- Context specific vaccination – vaccination is effective but needs to be adapted for the serovars present
- Understanding whether livestock or wildlife are main reservoir: in some studies livestock appear to be the most important reservoir, in others rodents. This has implications for control
- Risk reduction: human behaviour is important in decreasing risk
- Impact of climate change on extreme wet weather events and hence leptospirosis: leptospirosis is strongly associated with flooding and stagnant water

Figure 3.3 Leptospirosis prevalence in community studies



Trypanosomosis – sleeping sickness and 'the malaria of cattle'

Pathogens

Tsetse-transmitted trypanosomosis is an infectious disease unique to Africa and caused by various species of blood parasites. The disease affects both people (Rhodesian and Gambian sleeping sickness) and animals (nagana).

Test

The most common test in animals is direct microscopic examination of blood for parasites. Hence positive tests correspond to current infections.

Prevalence

103 studies were assessed covering 109,443 animals and 99,808 people. These were mostly parasitological studies so they represent current infections. In community studies, there was a prevalence of 10% among domestic animals and 5% among wild animals. Among humans (either suspect hospital patients or in focal areas for trypanosomosis) prevalence was 6%.

The WHO reports human trypanosomosis as highly spatially distributed: in the last 10 years, over 70% of reported cases occurred in the Democratic Republic of Congo (DRC). Angola, Central African Republic, Chad, Sudan and Uganda make up most of the remaining burden.

Epidemiology
Trypanosoma brucei gambiense (T.b.g.) is found in west and central Africa; it currently accounts for over 95% of reported cases of sleeping sickness and causes a chronic infection (Gambian sleeping sickness). Most transmission is anthroponotic and can be controlled effectively through interventions targeted at human reservoirs; however, animal reservoirs have a role in the epidemiology. Pigs are an animal reservoir and recently have been associated with the persistence and epidemics of sleeping sickness in Uganda, Equatorial Guinea and Cameroon. Other domestic animals and wildlife are also implicated.
T. brucei rhodesiense (T.b.r.) is found in eastern and southern Africa. Nowadays, this form (Rhodesian sleeping sickness) represents less than 5% of reported cases and causes an acute infection.

Agricultural expansion, deforestation and the removal of wildlife reduce the natural habitats and wildlife hosts of tsetse. Moreover, applications of insecticides to cotton and other crops may also reduce tsetse numbers and it is generally agreed that agricultural expansion/intensification is likely to reduce trypanosomosis challenge, at least in the short term (Bourne and Wint, 1994). However, in the short term there may be an upsurge in disease as tsetse, lacking alternative wildlife hosts, feed more on cattle.

Impacts
Acute sleeping sickness is a serious disease in people.

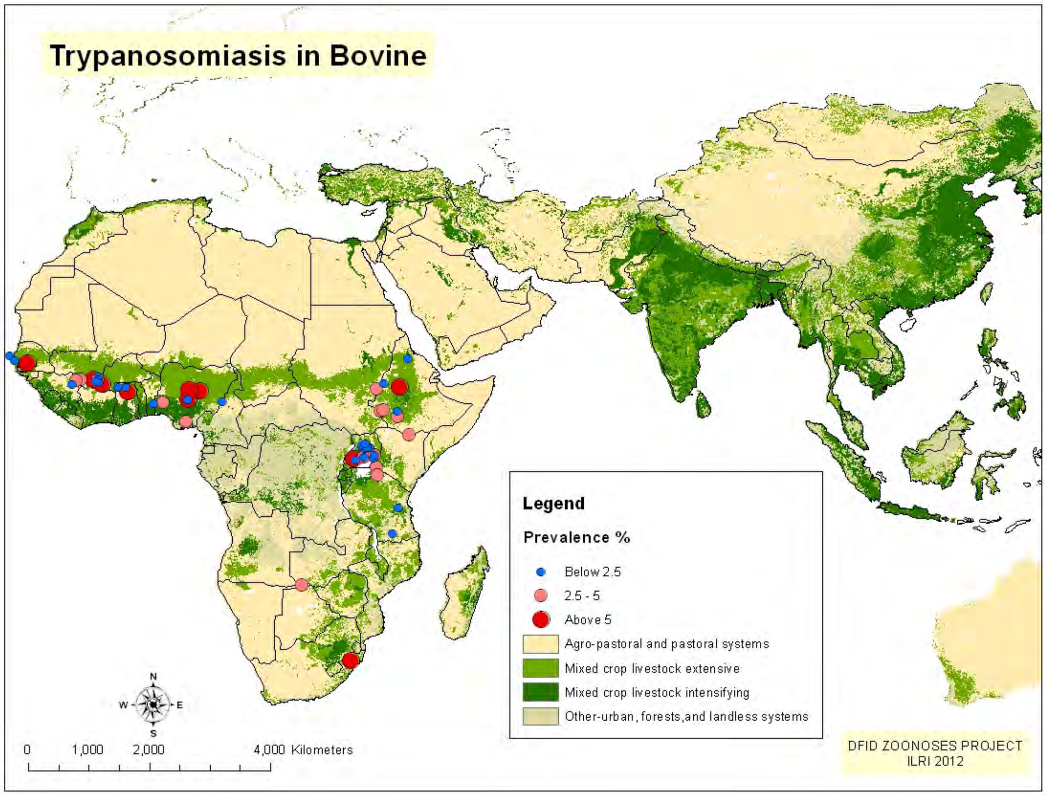
Trypanosomosis has serious health impacts in livestock. However, the non-zoonotic *T. congolense* and *T. vivax* are less pathogenic than zoonotic *T. rhodesiense*. Swallow (1999) summarises a number of studies and estimates reduced productivity of around 10-20% across a range of parameters (mortality, calving rate, milk, draft power).

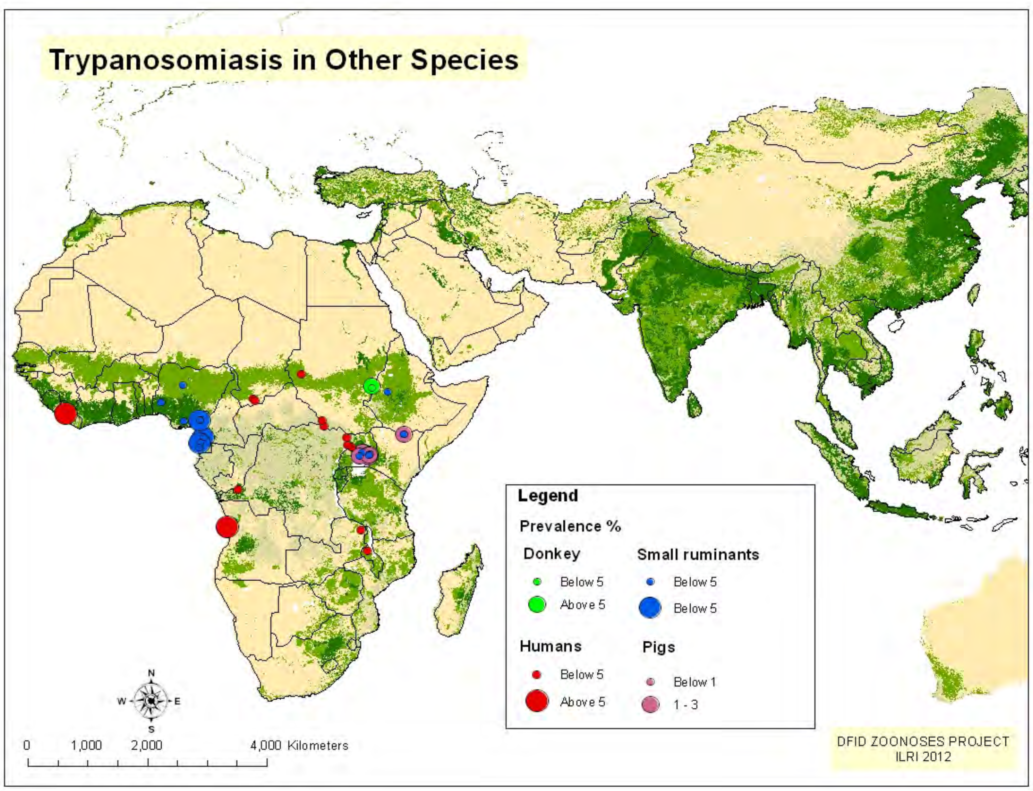
Geographical hotspots
Countries with multiple surveys (>=4) and high prevalence (>8%): Sudan, Mozambique, Tanzania, Ethiopia, Cameroon, Nigeria, and Burkina Faso

Key research areas:

- Arrest the northerly advance through Uganda of the zoonotic parasite *T. brucei rhodesiense,* which threatens to converge with *T. brucei gambiense*
- Farmer-and community-based management of disease: while technical highly effective, sustainability remains elusive
- Trypanocide resistance: an emerging problem across Africa which may also threaten the efficacy of human drugs
- Pen-side tests to allow better and more timely treatments avoiding cattle losses and slowing development of resistance
- Impact of climate, agricultural intensification and demography on disease dynamics
- Factors leading to massive human outbreaks as occurred historically at the start of the 20th century and to a lesser extent in the 1960s

Figure 3.4 Trypanosomosis (trypanosomiasis) prevalence in community surveys





Cysticercosis – pig tapeworm

Pathogen

Cysticercosis is a systemic parasitic infestation caused by the pork tapeworm (*Taenia solium*).

Tests

The tests commonly used for cysticercosis in pigs include meat inspection, lingual inspection and antigen ELISA tests. These indicate current infections. In humans, stool samples are also used to identify current tapeworm infections and imaging to identify brain cysts.

Prevalence

125 studies were assessed covering 349,923 pigs and 10,385,132 people. In community studies, the average prevalence in pigs was 17%. Among humans the prevalence in community studies was 11% (this combines people infected with Taenia solium as well as the much rarer cases of human cysticercosis). Among hospital patients and epileptics the prevalence was 12%.

Epidemiology

Humans are at risk not from consumption of pork with cysts but from consumption of tapeworm eggs shed by themselves or another human carrier. The disease persists in poor, pig-keeping communities where pigs have access to human faeces. Intensification would be expected to reduce prevalence of the disease.

Geographical

Hot spots: Rwanda, Congo, Chad, Togo, Nigeria, and Ghana (Geerts et al., 2004)

Impacts

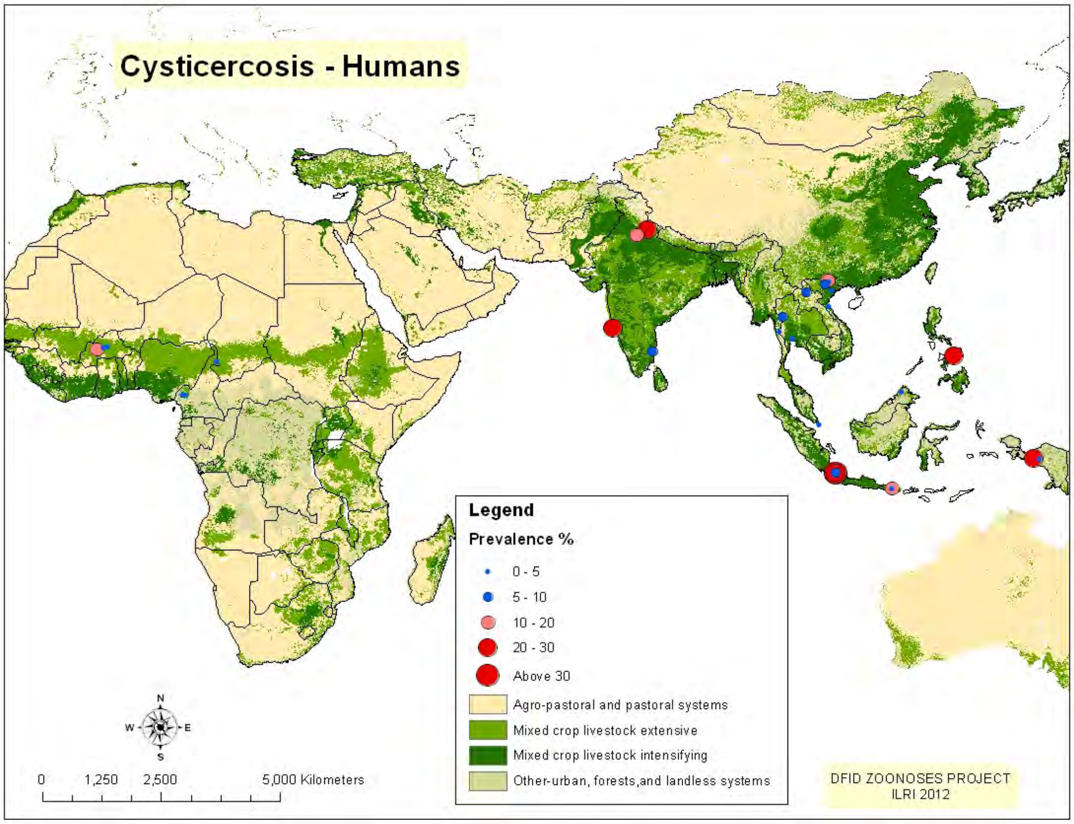
In some countries, pigs with visible infections (by lingual palpation or mucous membrane inspection) fetch a lower price. This was estimated as a 30% reduction in price in the Cameroon (Praet et al., 2003). A study in Tanzania estimated the price of healthy pigs at $45 and infected at $21: a reduction of 46% (CIRAD, 2012). Heavily infected pigs may be condemned during meat inspection; however, in many countries either smallholder pigs are not always inspected at slaughter or inspection is inadequate.

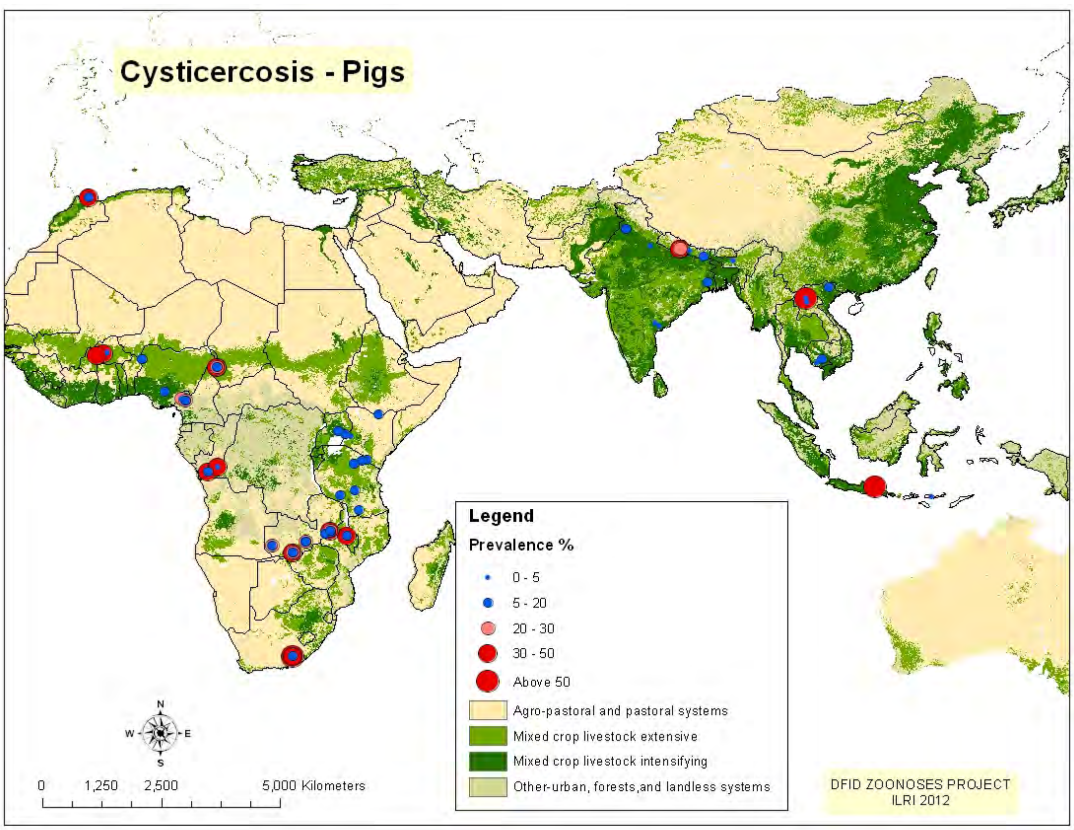
Cysticercosis is believed to be the most common cause of adult onset epilepsy in poor, pig-keeping communities.
In Cameroon, the cost of treatment of one cysticercosis patient (wage loss not included) was estimated at Euro 260 (Praet et al., 2003)

Key research questions

- Eradication of cysticercosis from an ecosystem: with the new vaccine as well as effective therapeutics, cysticercosis is eradicable but there have been no serious investments in Africa or Asia
- Pen-side tests for diagnosis of cysticercosis in pigs: a lateral flow test has been recently developed but requires serum (whole blood would be more convenient)
- More comprehensive and effective meat inspection: as for TB, it appears that because of financial incentives and dysfunctional systems, current meat inspection is not effective in poor countries
- Hotspots among marginalised pig-keeping groups;

Figure 3.5 Cysticercosis prevalence in community surveys





Q fever – the most contagious disease

Pathogen
Q fever is an infectious disease of animals and humans caused by a species of bacteria (*Coxiella burnetii*).

Tests
Most tests detect antibodies. Antibodies may persist for several years. Most of the surveys in our review were community based. For these, a positive result indicates current infection, chronic infection or infection in the last few years.

Prevalence
We accessed 81 surveys covering 27,252 animals and 11,023 people. In community studies, prevalence was as follows: bovines 28%, other animals (cats, dogs, horses and poultry) 26%, shoats 15%. Among febrile patients in hospitals, 0-40% (average 8%) had antibodies to Q fever.

Epidemiology
Coxiella burnetii is most frequently found in ruminants (cattle, sheep, and goats) but can also be detected in wildlife and companion animals. According to the literature (although not in our review) sheep appear to be infected most frequently, followed by goats and less frequently, cattle. Human cases are often associated with proximity to small ruminants (particularly at parturition or during abortions) and dry, windy weather. At least in Europe, here is no conclusive evidence in support of a link between an increased density of animals and/or farms and spillover from infected farms to humans (EFSA, 2010).

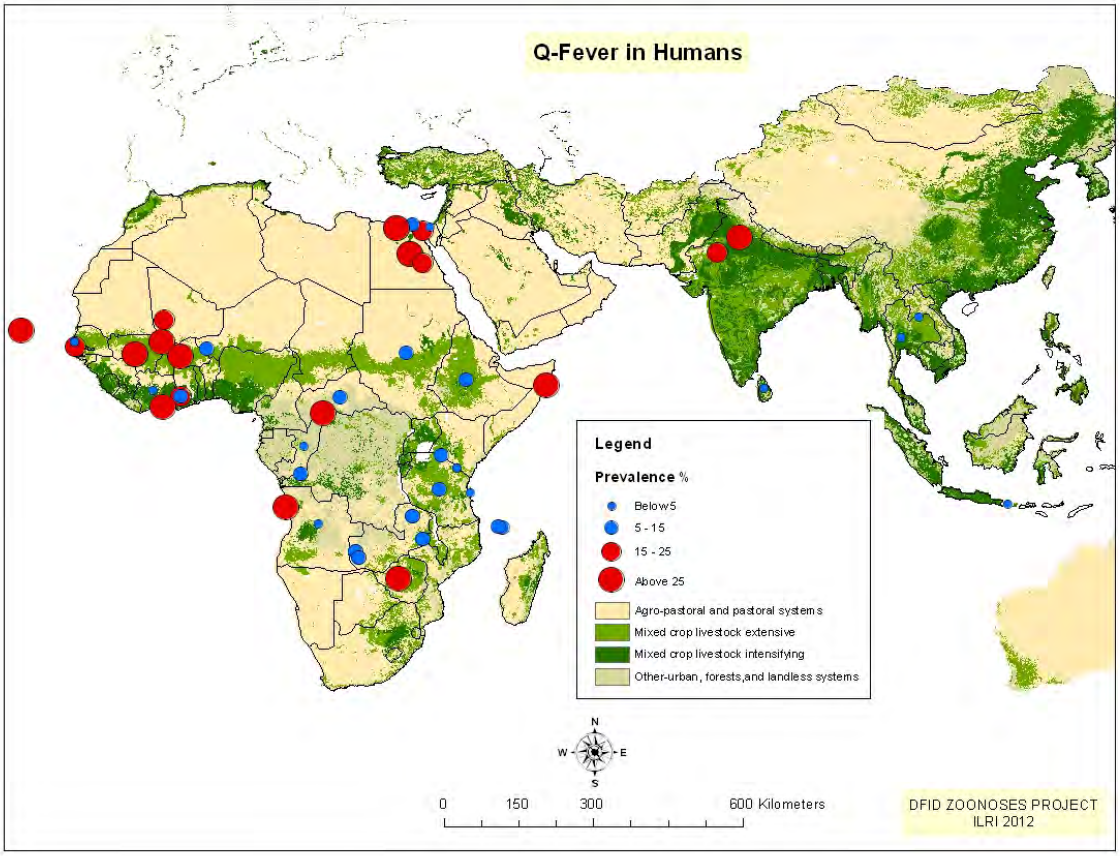
Geographical hotspots
Because Q fever has been investigated in few countries it is difficult to identify hotspots. Countries with high sheep populations would be expected to be at higher risk. Countries with multiple surveys (>=4) and high prevalence (>15%) include in descending order: Nigeria, Zimbabwe, India, and Egypt.

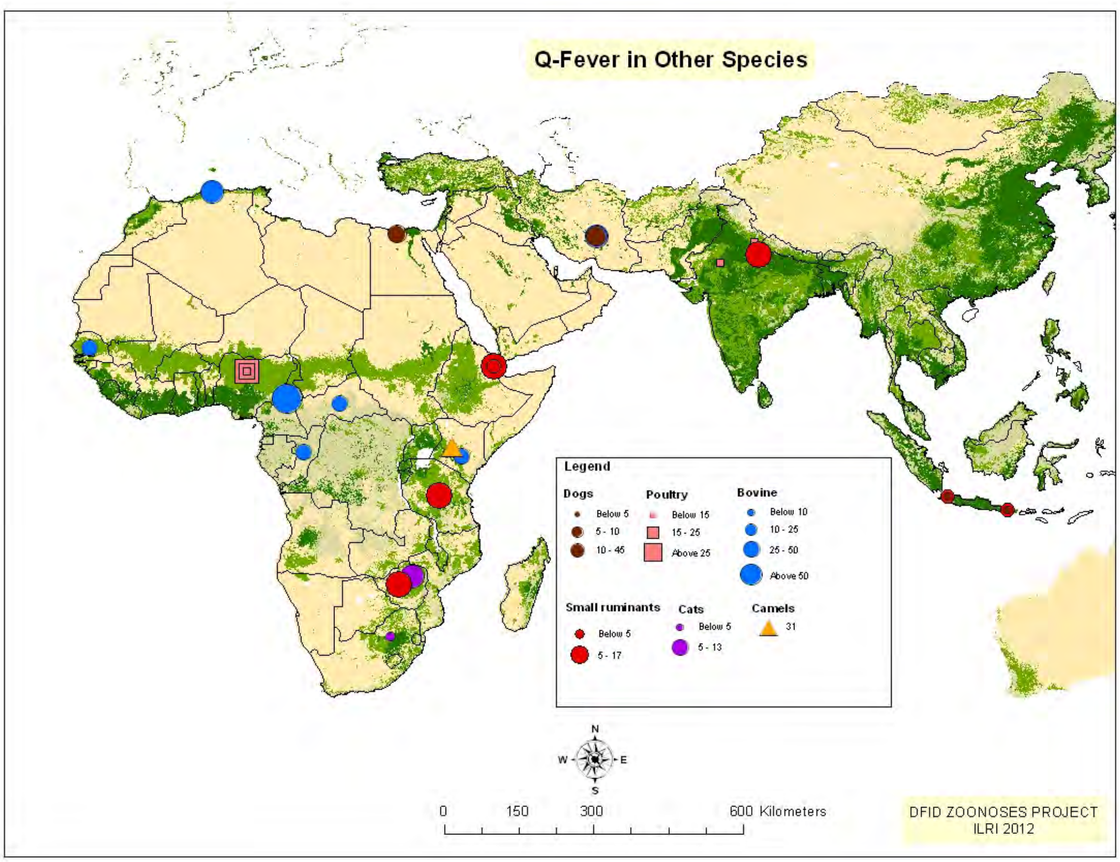
Impacts
Animals that carry this organism and shed it into the environment usually do not show any signs of disease. Infected ewes and does may abort or give birth to weak offspring. There is little data available on the economic impacts.

In people around 50% of infections may be asymptomatic; other patients have influenza-like symptoms, a minority have atypical pneumonia or hepatitis. In around 5% of patients, chronic infection establishes.

Key research questions
- Prevalence studies in more countries
- Economic impacts of Q fever in livestock
- Factors leading to outbreaks of Q fever in human populations
- High risk groups: pastoralists appear to have very high levels of Q fever – more studies are needed on prevalence and prevention in this group
- Q fever as an emerging disease
- Vaccination to manage Q fever in high risk populations

Figure 3.6 Q fever prevalence in community surveys





Bacterial food-borne disease – the forgotten zoonoses

Pathogen

In this category we include the bacterial zoonotic diseases, which are transmitted mainly through food. We reviewed *Salmonella*, toxigenic *Escherichia coli, Listeria, Campylobacter* and *Toxoplasma* which are among the most important causes of food-borne disease as well as hepatitis E, an emerging zoonosis. Other zoonoses of somewhat lesser importance not reviewed are: *Staphylococcus aureus*, *Bacillus cereus*, and *Clostridium spp*. In this section, we do not include the previously considered classical endemic zoonoses that are often food-borne (brucellosis, Q fever, zoonotic tuberculosis) but have other important transmission pathways. We did not consider non-zoonotic diseases associated with animal source foods (typhoid, rotavirus disease, scarlet fever, giardiasis, shigellosis etc.). We call these 'forgotten' zoonoses because health experts, decision makers and the public are often unaware of the important role zoonoses play in food-borne infections.

Tests

A variety of tests were used. In most cases, a positive result indicates current, recent or chronic infection.

Prevalence

We accessed 258 surveys covering 27,425 animals and 263,995 people and 4,208 food or environmental samples. In community studies, prevalence was as follows: bovines 16%, shoats 20%, pigs 30%, poultry 36%, other animals 17%, food 31%. Among people in the community prevalence was 21% and among high-risk groups prevalence was 20%.

Geographical hotspots

Countries with multiple surveys (>=4) and high prevalence (>15%) include in descending order: Tanzania, South Africa, Gambia, Vietnam, Nigeria, Senegal, India, and Egypt.

Impacts

Some of these diseases can have impacts in animals (salmonellosis, listeriosis, toxoplasmosis). However, in many cases strains pathogenic to people are not pathogenic to animals which means farmers have less incentives for control.

In people, food-borne disease is an important cause of illness and economic loss. There is no good information on the proportion of gastrointestinal disease burden associated with food-borne zoonoses in developing countries. In developed countries, the proportion varies from 30-50% (Grace et al., 2008). Food-borne pathogens also cause other health problems, less common but more serious (e.g. kidney failure, septicaemia, abortion, encephalitis etc.); around 2-3% of people with acute food-borne zoonoses may also go on to develop serious complications (Lindsay, 1997). The health burden of these is considered to at least equal the burden due to gastrointestinal illness.

Key research questions

- Impact of food-borne bacterial diseases in livestock
- Managing food safety in the informal sector where most of the poor buy and sell but food safety regulation is not working
- Gender and food safety – much of food purchase, processing, and handling is done by women but they are often not engaged in food-safety programs
- Relation between food safety and food security
- Attribution – how much food-borne illness is due to zoonotic disease or agricultural products
- High risk groups –the young, old, pregnant and immunosuppressed are especially vulnerable to food-borne disease and special targeting is needed to reach them

Figure 3.8 Food borne disease prevalence in community surveys

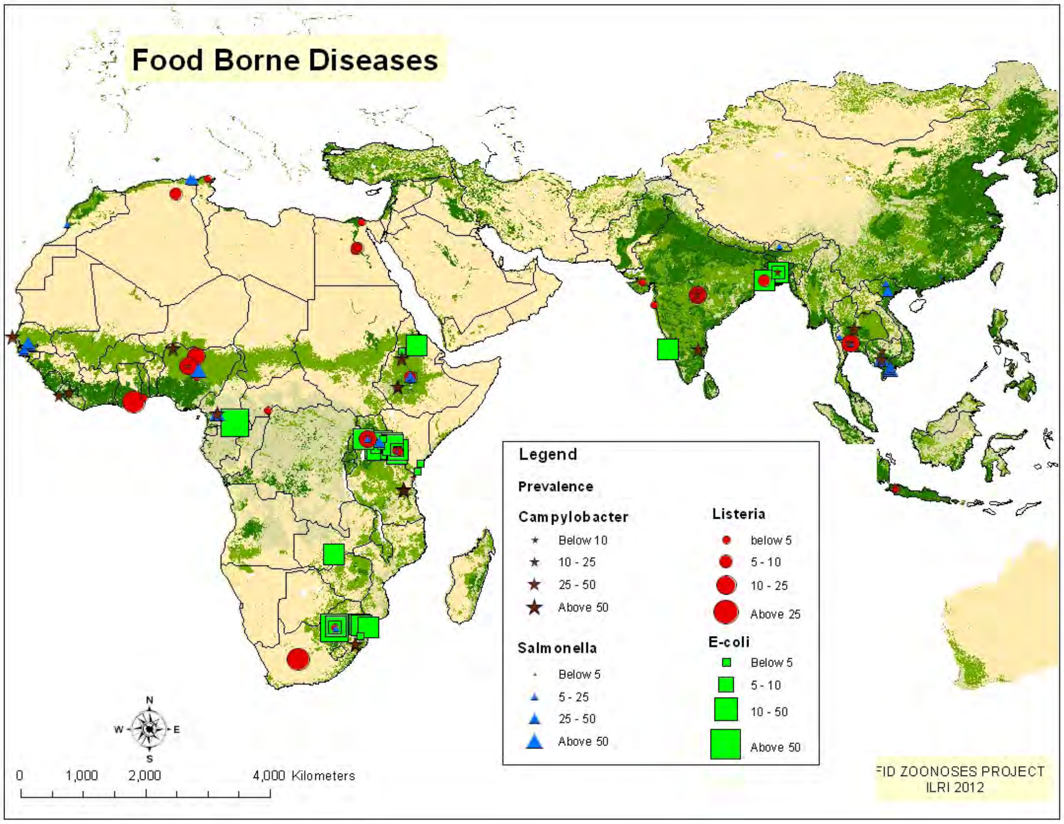
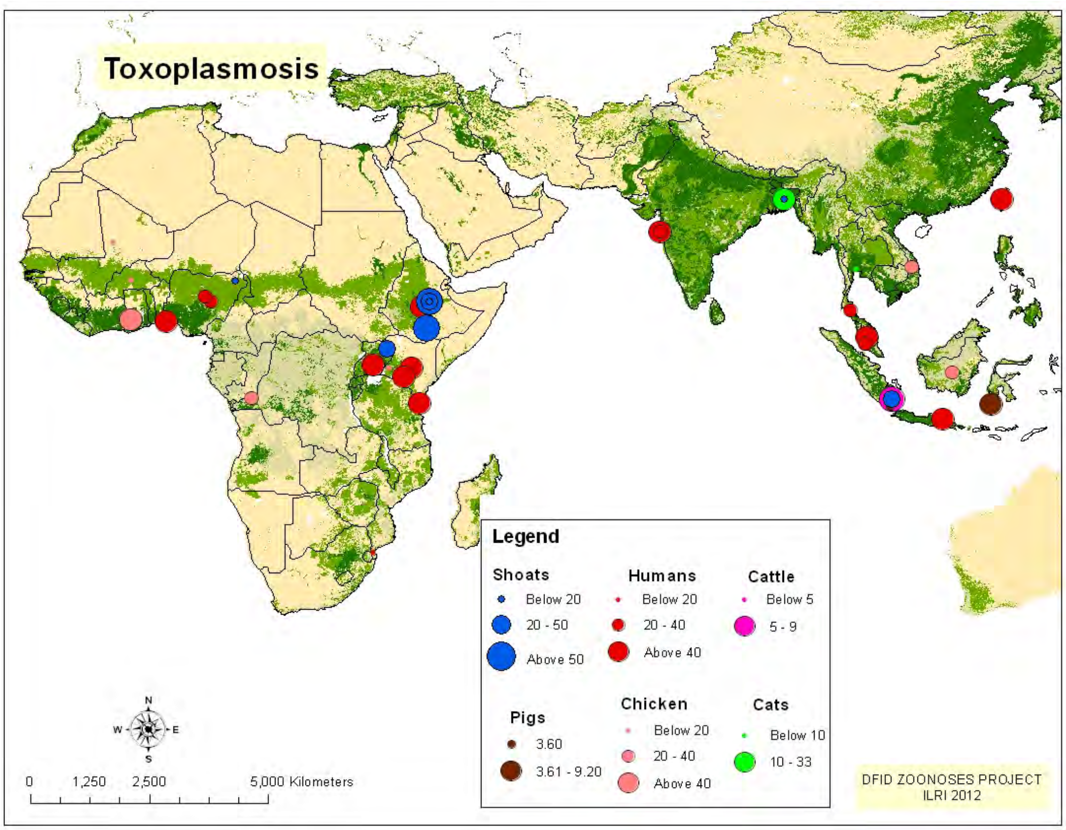


Figure 3.9 Toxoplasmosis prevalence in community surveys



Echinococcosis – cystic disease

Pathogen

Cystic echinococcosis (CE) in humans is caused by the larval stage of *E. granulosus, E. ortleppi, E. intermedius* or *E. canadensis*. All these parasites have canines (usually domestic dogs), as definitive hosts and a variety of ungulates, particularly farm animals, as intermediate hosts. Man is generally an aberrant intermediate host in which the hydatid cyst develops, usually in the liver or lungs as a space-occupying lesion, which can result in considerable morbidity

Prevalence

We did not review echinococcosis in depth; however, a comprehensive assessment has recently been carried out by Budke et al. (2006).

Epidemiology

Cystic echinococcosis (CE) is a condition of livestock and humans that arises from eating infective eggs of the cestode *Echinococcus granulosus*. Dogs are the primary definitive hosts for this parasite, with livestock acting as intermediate hosts and humans as aberrant intermediate hosts.

Geographical hotspots

More than 90% of human cases occur in the 8 endemic regions in North Africa-near East and China. In descending order: China (Tibetan plateau), Turkey, India, Iraq, Iran, and Afghanistan

Impact

A preliminary estimate of the annual global burden of CE has suggested approximately 1 million DALYs are lost due to this disease (Budke et al., 2006). This is likely to be a substantial underestimate (Craig et al., 2007). In addition the losses to the global livestock industry is around $2 billion lost annually and cost of illness is around the same.

We conducted a systematic review for toxoplasmosis but have not included the information here because of some epidemiological complexities. For toxoplasmosis, high prevalence may be associated with less risk, because the most vulnerable group (pregnant women) are exposed before they are pregnant. For hepatitis E there is some uncertainty over the extent of zoonotic transmission.

Key research questions

- Control of echinococcosis in remote and insecure regions
- Relation between toxoplasmosis prevalence and risk: as toxoplasmosis is most serious if encountered by a naïve pregnant women, it may be that cultures where exposure to toxoplasmosis is very high (e.g. France) have less disease burden than cultures where exposure is low
- Prevalence of toxoplasmosis
- Changing behaviours that increase exposure to toxoplasmosis and echinococcosis
- Zoonotic component of hepatitis E

3.3 Top twenty countries for endemic zoonoses burden

Twenty-eight countries appeared in the 'geographical hotspots' listing. To be considered a geographical hotspot for a disease, a country had multiple surveys (human and animal combined, but only community surveys) with a high average prevalence (table 3.2). (The cut-off prevalence varied with disease reflecting that for different diseases, different prevalences are considered high[6]). The country with the highest prevalence is ranked as 1. The ranking for each disease is shown in Table 3.2 as well as the number of surveys and cut-off prevalence the ranking was based on.

Table 3.2 Geographical hotspots for zoonotic disease (country)

	Brucellosis	Tuberculosis	Leptospirosis	Cysticercosis	Q fever	Trypanosomosis	Food-borne bacteria
1	Togo	Bangladesh	Ethiopia	Rwanda	Nigeria	Sudan	Tanzania
2	Mali	Burkina	Vietnam	Congo	Zimbabwe	Mozambique	South Africa
3	Ivory Coast	Pakistan	Nigeria	Chad	India	Tanzania	Gambia
4	Zambia	Ghana	Egypt	Togo	Egypt	Ethiopia	Vietnam
5	Niger	Kenya	Malaysia	Nigeria		Cameroon	Nigeria
6	India	Mali		Ghana		Nigeria	Senegal
7	Sudan	Cameroon	.			Burkina Faso	India
8	Cameroon	Chad					Egypt
9	Burundi	India					
		Ethiopia					
	4+ surveys, prev. >15%	2+ surveys, prev. >5%	4+ surveys, prev. >20%	Geerts et al.	4+ surveys, prev. >15%	4+ surveys, prev. >8%	4+ surveys, prev. >15%

To calculate the countries with the highest burden of endemic zoonoses we gave each country a weighting according to its ranking for average prevalence for each disease (the country with the highest prevalence for the disease got a weighting of ten). Weights were added across the diseases (so a higher score represents a higher average prevalence summed across all the endemic zoonoses considered). The countries with highest burden of endemic zoonoses are shown in Table 3.3. (This ranking is probably biased towards countries with better university and research infrastructure as they conduct and publish more studies: for example, there are many more studies from Nigeria than from the Central African Republic).

Table 3.3 Countries with most zoonotic disease hotspots

Country	Score	Country	Score	Country	Score
Nigeria	27	Cameroon	10	Pakistan	8
Ethiopia	17	Chad	10	Zimbabwe	8
Tanzania	17	Rwanda	10	Zambia	7
Togo	15	Ghana	9	Kenya	6
India	14	Mozambique	9	Niger	6
Mali	14	South Africa	9	Senegal	4
Vietnam	14	Congo	8	Malaysia	2
Sudan	13	Egypt	8	Burundi	1
Bangladesh	10	Gambia	8		
Burkina Faso	10	Ivory Coast	8		

[6] To give an extreme example, for a rare disease like rabies one in 100,000 animals might be considered a high prevalence, while for a common disease like brucellosis one in 5 animals might be considered high.

3.4 Outbreak zoonoses

We retrieved papers on three of the outbreak zoonoses that appeared in the ‘top 13’ zoonoses listing. These were: rabies, anthrax and leishmaniasis.

Rabies

Twenty-one papers were accessed on rabies. These were not useful for assessing prevalence or cases but were consistent with the geographical patterns of rabies.

Most rabies cases are concentrated in high-risk countries in Africa and Asia. (Bangladesh, India, Myanmar, Pakistan, China Egypt, Sudan, Ethiopia, Tanzania, Ghana).

Anthrax

Thirty-five papers were accessed on anthrax. They were not useful for assessing prevalence or cases but were generally consistent with the geographical patterns of anthrax.

There are approximately 10-100 thousand human incidences annually throughout the world with significant numbers of cases in Chad, Ethiopia, Zambia, Zimbabwe and India

Leishmaniasis

Paper retrieval was not useful in assessing prevalence. Most leishmaniasis is zoonotic, but anthroponotic transmission is more important in outbreaks, 90% of human visceral leishmaniasis cases occurring in South Asia, Sudan, Ethiopia, and Brazil and 90% of cutaneous leishmaniasis cases occurring in Afghanistan, Algeria, Iran, Saudi Arabia, Syria, Brazil, Colombia, Peru, and Bolivia.

Other important outbreak pathogens that were not in the ‘top 13’ list but did appear in the ‘top 25’ were:

- Rift Valley fever virus
- Hanta virus
- Ebola virus
- Chickungunya virus.

Avian influenza was also in this list, a zoonosis that is endemic in some regions (Indonesia, South China, Egypt and possibly elsewhere), but in most countries occurs as outbreaks, which are controlled (rich countries) or burn out (poor countries) (Bett et al., in press).

These five pathogens (including avian influenza) are all caused by viruses and are characterised by high case fatality but low burden of disease. Together they cause around 15,000 deaths a year which is trivial in comparison to the top 13 zoonoses (causing 2.5 million deaths a year). Currently humans are mainly spill-over hosts and there is no sustained anthropogenic transmission (human-to-human). However, if these pathogens were to mutate to allow easy human-to-human transmission while maintaining their high case fatality the impacts would be enormous. Hence, these diseases are of interest not so much because of their burden of disease but because of potential to become diseases with higher burden. Smallpox, bubonic plague, HIV-AIDS, malaria and measles are examples of former zoonoses that jumped species with civilisation-altering impacts (Wolfe et al., 2007).

Perry and Grace (2009) argue that many negative impacts of zoonoses and emerging diseases are from inappropriate responses by authorities, farmers and general public rather than disease itself. This was especially evident in the avian influenza pandemic, when outbreaks led to large changes in purchasing behaviour, which probably had little impact on mitigating risk. Similarly, the reluctance to support commodity-based trade is prejudicial to developing countries without any commensurate benefit in reducing human health risk.

The map was extracted from HealthMap (www.healthmap.org). It shows all disease reports between Jan 1st 2010 and May 2nd 2012 of the endemic zoonoses considered in this report. The sources used were: ProMed, FAO, OIE, Eurosurveillance, Google.

Figure 3.10 Outbreaks of five important zoonotic diseases 2010-2012 as aggregated and reported by HealthMap (www.HealthMap.org)

(Extracted from HealthMap, www.healthmap.org)

In all 200 reports are cited, on the HealthMap site, distributed as follows: leptospirosis (124), trypanosomosis (24), brucellosis (20), Q fever (12) and bovine tuberculosis (10). Between Jan 1st 2010 and Dec 31st 2010 there were only three reports for brucellosis and all were in people. As explained in Chapter 2 this implies under-reporting of actual new cases by several orders of magnitude.

3.5 Global burden of disease

The original Global Burden of Disease Study (GBD) was commissioned by the World Bank in 1991 to provide a comprehensive assessment of the burden of 107 diseases and injuries and ten selected risk factors for the world. Burden of disease is calculated using the disability-adjusted life year (DALY). This time-based measure combines years of life lost due to premature mortality and years of life lost due to time lived in states of less than full health. The GBD represents the most authoritative source of information on human illness.

There are some challenges in using the GBD to assess zoonoses.

- Firstly, zoonoses (especially in poor countries) are widely unreported, and under-reporting is relatively greater for zoonoses than for non-zoonotic diseases of comparable prevalence (Schelling et al., 2007). As the GBD report is based on national information for levels of mortality and cause of illness, this under-reporting is reflected in the GBD.
- Secondly, several zoonoses with considerable burdens are not included in the GBD assessment. For example rabies, echinococcosis, cysticercosis, leptospirosis and brucellosis
- Thirdly, the GBD is organised around diseases and not pathogens or transmission pathways. For example, diarrhoeal diseases, among the highest causes of morbidity and mortality in poor countries, comprise one category. Although the majority of important diarrhoeal pathogens are zoonotic (Schlundt et al., 2004) it is not currently possible to identify the zoonotic component of diarrhoeal disease from GBD figures

In order to use the GBD to estimate disease we made some assumptions:

- Tuberculosis: we took the conservative estimate of Cosivi (1998) who estimated worldwide the proportion of TB caused by M. bovis at 3.1%. This literature review suggests the proportion is higher. A higher proportion is also consistent with historical data.
- Diarrhoeal diseases: we assumed 33% of diarrhoea disease is due to zoonotic pathogens. In developed countries, several reviews (Schlundt et al., 2004, Flint et al., 2005) argue the majority of gastrointestinal disease burden is due to zoonotic pathogens (>50%). However, given the lack of evidence for developing countries we took the conservative estimate of 33%.
- Trypanosomosis, Chagas disease, leishmaniasis: Japanese encephalitis: are all considered as zoonotic.
- Schistosomiasis: cases in regions where the zoonotic species *Shistosoma japonicum* predominates are considered zoonotic.
- Dengue is not included. Although dengue is a zoonosis and the sylvatic cycle (monkey-mosquito) has important implications for disease eradication, most transmission is human-to human.
- Tetanus is not included. Tetanus is a sapro-zoonoses and the load of toxins in the environment is largely the result of contamination with ruminant faeces. However, most human burden is from contact with the environment and not animals.
- Respiratory disease is a major cause of human sickness and death and a certain proportion is due to zoonotic diseases such as Q fever. We did not include these as no reliable estimates could be found.

For zoonoses recorded in the GBD, 68% of the burden is made up of just 13 countries (Figure 3.1). There is a very high correlation (99%) between protein energy malnutrition[7] and burden of zoonoses indicating the strong relation between poverty, dependence on livestock, and zoonotic disease.

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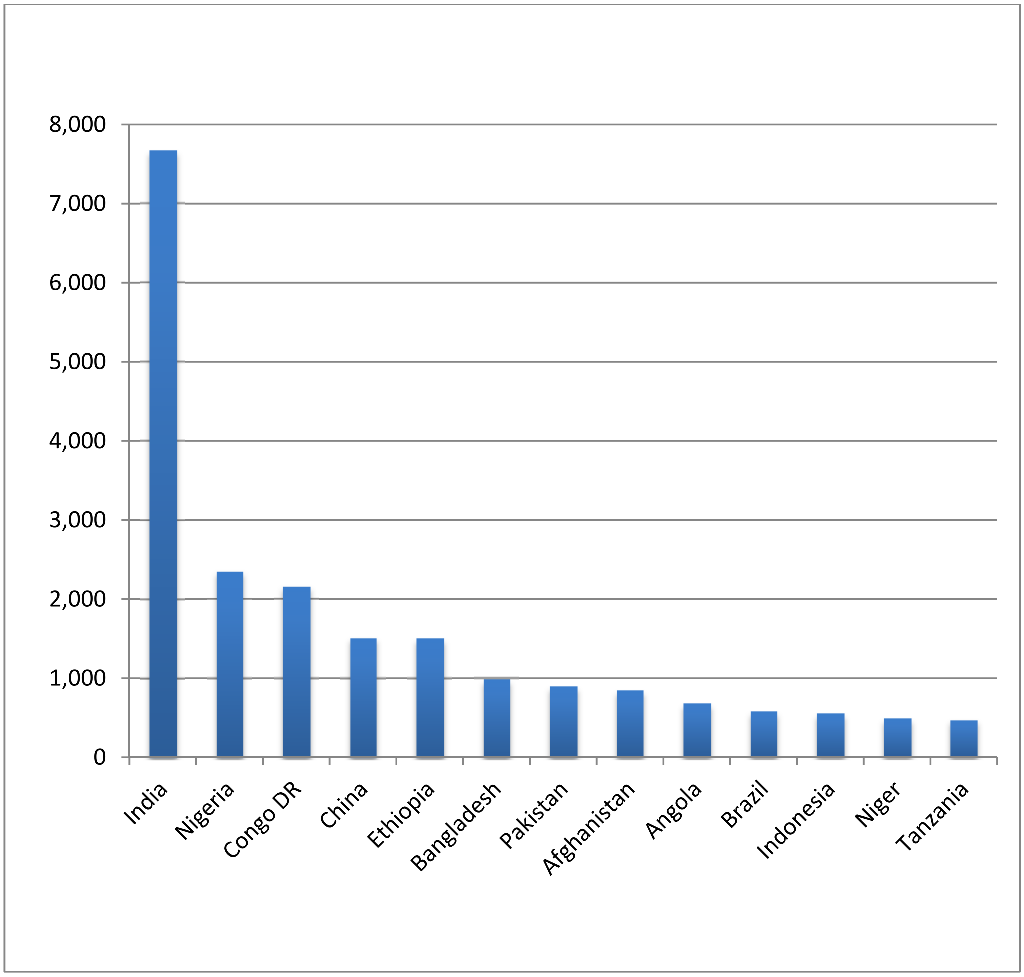
[7] Protein-energy malnutrition is a nutritional deficiency resulting from either inadequate energy (caloric) or protein intake and manifesting in either marasmus or kwashiokor. Marasmus is characterised by wasting of body tissues, particularly muscles and subcutaneous fat, and is usually a result of severe restrictions in energy intake. Kwashiokor affects mainly children, is characterised by oedema (particularly ascites), and is usually the result of severe restrictions in protein intake. However, both Types can be present simultaneously (marasmic kwashiokor) and mask malnutrition due to thepresence of oedema.

Figure 3.11 Health burden of zoonoses in million disability adjusted life years (DALY)



From Global Burden of Disease, World Health Organisation, 2008

3.6 Comparing systematic literature review to in country literature search

Introduction and summary

In this review we extracted papers mainly in English (with a minority in French) from medical and agricultural databases available on line. Systematic literature reviews which only include some languages and which depend on major databases risk missing important information. Hence, we conducted a study in Vietnam to review literature for three of the key zoonoses (Data provided by HSPH).

154 papers were identified of which 117 were in Vietnamese and only 27 in English.

Methods

We used a large range of Vietnamese scientific journals, library documents, as well as meetings with key researchers on zoonoses, and open sources.

•Vietnamese journals on preventive medicine, practical medicine, public health, veterinary sciences and techniques, agriculture and rural development

•Institution libraries: Vietnam Medical Information Centre (MOH), National Institute of Hygiene and Epidemiology, National Institute of Malariology Parasitology and Entomology, National Institute of Animal Husbandry.

•University libraries: Hanoi Medical University, Hanoi School of Public Health, Hanoi University of Agriculture

•Key researchers/research groups from institutes and universities

•Conferences proceedings

•Web sites: Ministry of Health, Ministry of Agriculture and Rural Development

The process of creating the search strategy consisted of two steps: (i) identification of key concepts characterizing the research questions and (ii) generation of a list of search terms that reflected the key concept. The main concept identified was zoonotic diseases in Vietnam. For this concept a number of subject terms and keyword terms were identified, which was then combined for the search:

The overall search term components considered to define “zoonotic diseases” AND “Vietnam” for the search, were: (i) population surveyed (human or animal), (ii) prevalence and (iii) laboratory techniques. Diseases were searched by their common names, as well as the names of the causative agents. The keywords were used both English and Vietnamese, for examples:

- English: “Cysticercosis” AND “Vietnam” or “Taeniasis” AND “Vietnam”
- Vietnamese: “Sán dây lợn” or “Bệnh lợn gạo”

English papers: we searched online databases of Science Direct, Pubmed and Web of Science with keywords of disease name or names of the pathogens in the fields of title/keywords/abstract.

All the electronic copies and hard copies papers were scanned and reviewed from their title and abstract to see if the papers are relevant to research on zoonotic diseases in Vietnam. After 2 screening rounds, many zoonoses were identified from research done. However, due to the time constraint and to respond to the TOR, we decided to select 3 zoonotic diseases, including cysticercosis (pig tapeworm), leptospirosis, and Salmonellosis for in-depth review. For each of the paper related to the selected diseases, we collected key information on i) location of the study, ii) on human or animal or both, iii) robustness of research design, iv) analysis method, v) prevalence. It happened also when a paper reporting different values for different sample analysis (e.g. milk, serum or both), these were treated separately to have different prevalences of the targeted samples.

Results

We found 50 papers, project reports and student's thesis study related to cysticercosis, including 47 in Vietnamese and 3 in English; 64 papers, project reports and student's thesis study related to salmonellosis, including 40 in Vietnamese and 24 in English; 40 papers, project reports and student's thesis study related to leptospirosis, including 30 in Vietnamese and 10 in English.

Conducting an in-country review covering Vietnamese journals, libraries and conference proceedings dramatically increased the number of papers and samples. It also revealed papers on less commonly studied aspects (e.g. cysticercosis in animals other than pigs and leptospirosis in wildlife) which were missed by the systematic, web-based, mainly English language review.

For four of the six comparisons, the prevalence estimated by systematic and in-country review were similar, but for two there was a marked discrepancy (27% prevalence of cysticercosis in people versus 4% and 57% prevalence of leptospirosis in livestock and companion animals (domestic) versus 14% in the systematic and in-country reviews respectively). The much smaller number of studies in the systematic review makes it likely that these are less accurate.

However, while 60% of the papers in Vietnamese were judged to have a 'moderate' or 'weak' methodology, only 37% of the papers in English were so judged.

Table 3.4 Comparing data on cysticercosis from a systematic review and an in-country review

	Systematic review			In country review		
	People	Pigs	Other	People	Pigs	Other
Studies (number)	6	1	0	23	19	10
Community studies (number)	5	1	0	23	17	10
Prevalence (%)	27.4	9.9		3.8	10.8	24.6
Samples for prevalence (no.)	1,434	323	0	27,298	5,015,261	493,803

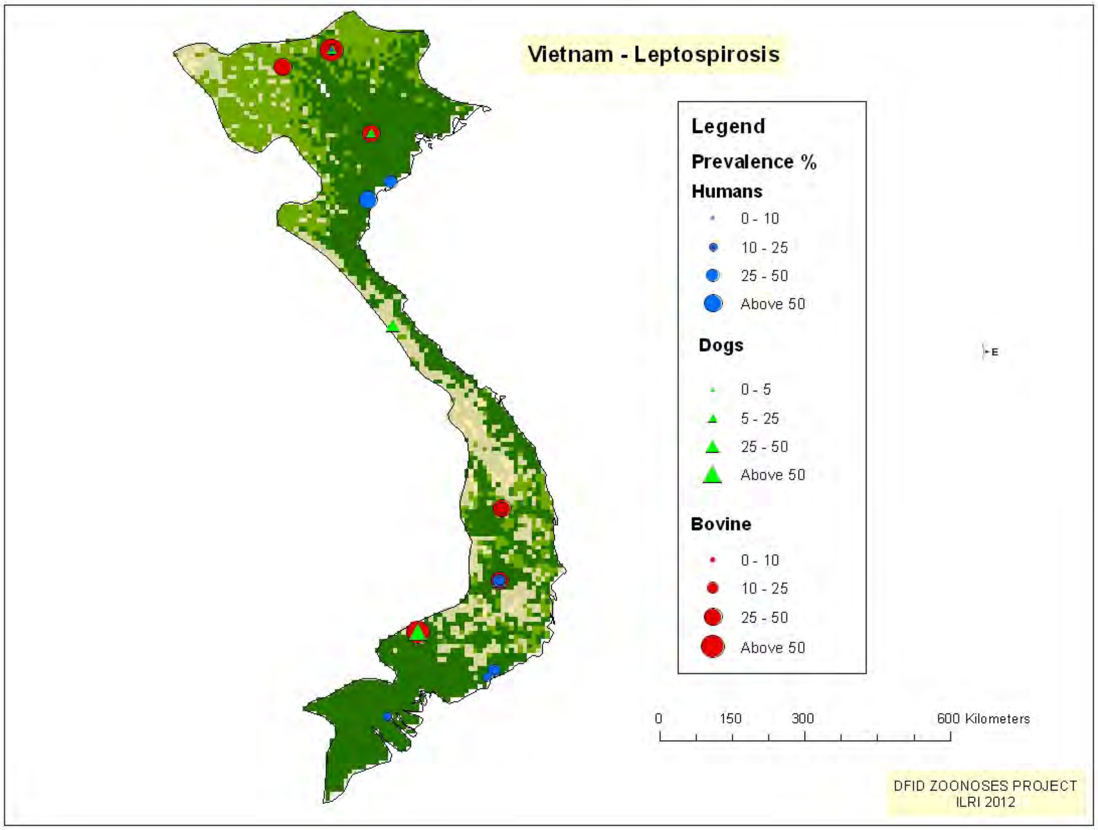
Table 3.5 Comparing data on leptospirosis from a systematic review and an in-country review

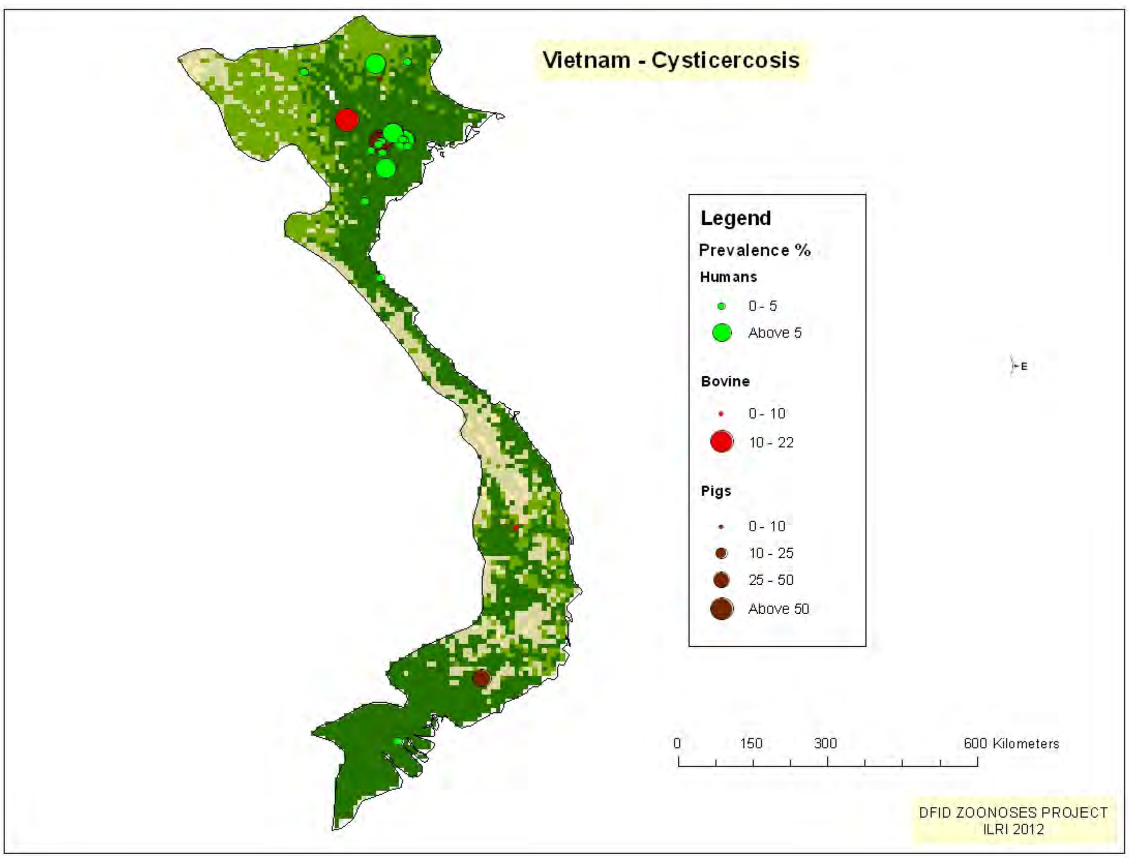
	Systematic review			In country review		
	People	Domestic	Wildlife	People	Domestic	Wildlife
Studies (number)	1	3	0	58	167	5
Community studies (number)	1	3	0	43	166	10
Prevalence (%)	12.8	57.0		12.1	13.6	7.7
Samples for prevalence (no.)	961	456	0	7,085	22,506	1,047

Table 3.6 Comparing data on salmonellosis from a systematic review and an in-country review

	Systematic review			In country review		
	People	Animals	Food	People	Animals	Food
Studies (number)	1	11	6	18	167	58
Community studies (number)	0	11	6	7	166	58
Prevalence (%)	n/a	13.1	39.2	16	51.8	31.9
Samples for prevalence (no.)	n/a	6831	980	2099	106,910	22,269

Figure 3.12 Leptospirosis and cysticercosis in Vietnam identified from in-country review





3.7 Interpretation of the review of endemic and outbreak zoonoses

As well as the likely existence of large amounts of missed literature because literature review was based on English/French publications indexed on online databases, other weaknesses and potential biases include:

- Many zoonoses have never been looked for in many places, and published literature reflects research infrastructure as well as disease prevalence
- Zoonoses which are more difficult to detect or test for (e.g. campylobacteriosis, listeriosis) are under-represented because they are rarely investigated
- We generally used data from the last 10 years. For several zoonoses, information exists for 30 or more years. However, given rapid changes in farming systems as well as changes in diagnostic techniques we thought this might be less reliable.
- Some surveys don't distinguish to species level making it impossible to distinguish between zoonotic and non-zoonotic pathogens
- Surveys focus on presence rather than transmission: so *Mycobacterium tuberculosis* will usually be classified as non-zoonotic although it is possible that the human victim acquired the infection from livestock
- Most surveys only report on one pathogen
- Varying sensitivity and specificity of surveys because of different tests used making direct comparison difficult
- Often little information on sampling and some community surveys may have considerable selection bias although authors claim sampling was representative
- In general, studies with fewer samples and country estimates based on fewer studies appear to over-estimate prevalence. This may be because researchers focus on areas they think may have a problem even if this is not always reported in the survey
- Some areas are over-represented (near universities) and many under-represented
- Some countries are under-represented because of less capacity in assessing zoonotic diseases
- In the current analysis small samples have as much weight as large samples. We planned to construct weighted prevalences by sample size and extrapolate to populations at risk but time did not permit (confidence intervals could also be given)
- We class slaughterhouse surveys as 'community' that is representative of the livestock population. In some places, sick animals are less likely to be slaughtered but in others they are more likely

Suggestions for overcoming these problems and improving our understanding of zoonoses of importance to the poor:

- Further analysis of the data collected to allow better extrapolation to agro-ecosystems and investigate risk factors
- Conduct large scale, probabilistic, stratified surveys to accurately determine prevalence of key pathogens
- Conduct surveys in regions where pathogens are likely to be present but data is lacking (risk-targeted)
- Collect economic and behavioural data to understand the impact and risk factors for key pathogens
- Develop better, cheaper diagnostics that can detect multiple pathogens
- Support bio-repositories for pathogens with meta-data allowing investigation of epidemiology and risk factors

Chapter 4: Updated map of emerging zoonotic disease events

Summary

The study searched for papers on zoonotic disease emergence events since 2004. Out of 43 new or newly identified events, most are viral and zoonotic from wild animal hosts. Although, the mappable zoonotic new events (n = 30) are globally spread across every continent, there may be clusters in northeast US, South America, Europe and South East Asia. These trends likely reflect surveillance differences with perhaps a trend to higher representation in developing countries reflecting increased attention over this period. Combined with existing data on zoonotic EID events from 1940-2004 (n = 202), the clearest potential hotspots are USA and Western Europe, which may reflect historical surveillance differences. Countries with most events are USA, UK, Australia, and France. (Chapter prepared by IOZ)

4.1 Introduction

Novel pathogens continue to emerge worldwide, the majority of which are zoonotic. ILRI engaged Zoological Society of London and Ecohealth Alliance to produce updated high resolution maps of zoonotic human emerging infectious disease (EID) events, by 1) extraction from the database used in Jones *et al*. (2008), and 2) further collection of EID events to update the database until 2012.

4.2 Methodology for updating map of emerging zoonotic disease events

We review the zoonotic human EID events in Jones *et al*. (2008), and methods for data collection and mapping of new events.

1) Jones *et al*. (2008) EID database. The data from Jones *et al*. (2008) covers 335 human EID events occurring between 1940 and 2004, 216 of which were zoonotic. In the Jones *et al*. (2008) analysis, an EID event was defined as the first emergence of a pathogen in a human population as a result of either increasing incidence, virulence, geographic range, drug resistance, or any other cited factor in case reports and literature. Single case reports were excluded, as were those with uncertain data quality. Separate pathogen strains were not considered as separate events, with the exception of drug resistant strains. For the maps presented in Jones *et al*. (2008), the location of each EID event was geo-referenced to point localities where possible, based on locations given in data sources (e.g. a village, or a hospital). These data were then converted to give each pathogen a location in a one decimal degree global grid. However, 95 of these events could only be traced to larger areas such as subnational units (e.g. states) or whole countries. To standardise for further analysis in the paper, one grid cell in these areas was selected via a random draw to represent the location of a particular EID. One of the random draws was selected for the maps presented in the paper.

For the purposes of this report, we mapped all those events that had a point locality, and where only subnational unit location information was available, we assigned an EID event to the weighted centroid of that area calculated using the 'Generate Centroid' function in HawthsTools 3.27 for ArcMap 9.3. Where only country information was present, these data were excluded from the maps. A total of 172 events were mapped (Fig. 1a).

2) Further data collection of EID events. We made slightly different assumptions when collecting new data than in the original Jones *et al*. (2008) protocols, based on updated criteria and suggested changes to the definition of “emerging” since 2008. We only considered emerging pathogens to be those completely novel to humans, or having novel virulence in humans or novel drug resistance. Geographic range, incidence and any miscellaneous factors were excluded. Furthermore, single case reports are *not* excluded, in contrast to the previous map. Separate strains or subspecies are once

again only considered in the context of virulence and drug resistance. We have also extended our criteria to cover issues not addressed by Jones et al. (2008). We excluded any events from non-natural infections (for example, accidental inoculation of laboratory workers), and we accept novel pathogens not yet given certified scientific names. Additionally, we explicitly definite an event as zoonotic if there is evidence the pathogen has an animal host or vector, or if it is cited in the literature as a likely zoonosis. Much assumption of zoonotic status is based upon transmission/natural hosts of closely related pathogens. Zoonoses were sub-classified by host type into one of four groups: 1) wildlife hosts only, 2) non-wildlife (i.e. domestic) hosts only, 3) both host types, 4) unknown. Finally, we accepted any diagnostic method (e.g. serology, microbial culture, DNA) as evidence of human infection (or animal infection for evidence as a zoonosis).

Initial leads on new EID events were obtained by various search methods including; 1) searches in peer-reviewed journal articles using Web of Science v5.0 (search terms = [novel OR new] AND human AND pathogen AND [emerging OR outbreak]); 2) searches in the ProMED reporting archives (search terms = [novel OR new] AND human); and 3) expert suggestion (EcoHealth Alliance and colleagues). Initial searches were conducted in articles from 2004 onwards, although no date restriction was made in accepting EID events or their supporting references. From initial leads, further information was found via follow-up of references. Once a potential EID event was identified, we extensively traced literature on the pathogen both backwards and forwards to find the first chronological *case* (not the first chronological report). Data were not recorded if the pathogen could not be assigned a single, feasible spatiotemporal origin (for example, many novel human viruses have recently been discovered that were then found in populations worldwide and/or historical samples, giving no clear emergence time or location). Following Jones *et al*. (2008), we recorded multiple fields of interest including details of pathogen taxonomy, transmission mode, known hosts, pathogenicity, data quality and any miscellaneous notes, in addition to geographic location. This information was generally unavailable for pathogens described very recently (in the past 10 years or so) because they have not yet been studied in detail, though no exclusions were made based on missing supplementary data.

4.3 Results: new zoonotic emerging disease events

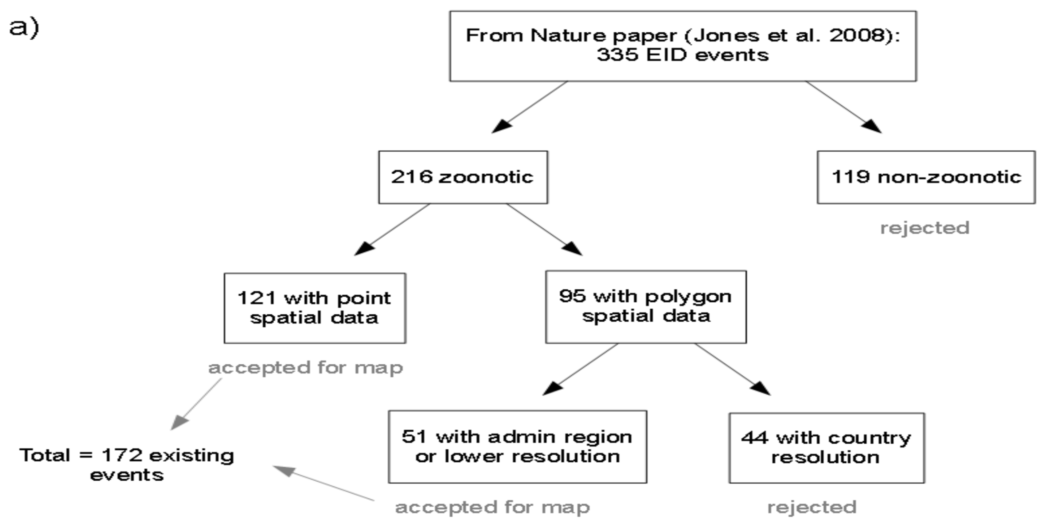
We identified 43 new EID events, 34 of which were zoonotic (Fig. 4.1b). Mapping of the new EID events followed that above for the previously gathered events. Point localities were all mapped were exact coordinates were given in the source and the exact coordinates were found using Google Earth v6.2. if only textual geospatial information was given. The locality of weighted centroids was assigned to EID events with only sub-national unit and EIDs with only country localities were excluded. In total, 30 new EID events were retained.

The majority of these new EID event pathogens are viruses, with several bacteria and only two protozoa (Table 1). Three events were due to drug-resistant strains, and only one due to a newly virulent strain. Although data was collected with a perspective to continuing from where Jones *et al*. (2008) left off, 15 EID events occurred pre-2004, 7 of which are from the 1980s or 1990s. This likely includes previously unidentifiable outbreaks that have only been classified using modern techniques. 17 of the 30 EID event pathogens in Table 1 have identified reservoir hosts or at least known animal infections (11 wild, 2 domestic, 4 both host types). However, most are recently discovered, therefore natural hosts for the remaining 13 will no doubt take time to locate and confirm.

4.4 Maps of zoonotic emerging disease events

To remap the combined previous and the new EID events, we created a one decimal degree grid using HawthsTools 3.27, and used ArcMap 9.3’s ‘Spatial Join’ tool to assign each EID event point to a single grid cell. New zoonotic EID events were mapped and labelled (Fig. 4.2) (n=30). Although the events are globally spread across every continent, there may be potential clusters of new or newly identified EID events in the Northeast US, South America, Continental Europe, and Southeast Asia. Only one grid cell contained more than one event, which was in Cameroon, containing Human T-lymphotrophic viruses 3 and 4, which were discovered simultaneously (Table 1). Previous EID events were mapped in combination with the new events (n=202) (Fig. 4.3). Again, events are present across most of the inhabited world. In contrast to the new events, the clearest potential hotspots are now the USA, and Western Europe, which likely reflects historical differences in surveillance and reporting. As in Jones et al., the maximum number of events in any grid cell was 6, occurring in Central London, UK. Separate maps were also produced for those events with wild hosts, and non-wild hosts (Fig. 4.4 4.5). Similar patterns were present for each, with the most noticeable difference being that very few EID events from non-wild hosts occurred in Africa or South America. Maps were also produced to illustrate breakdown of events in each grid cell by zoonotic host categorisation, drug resistance, and type of data (see Figure 3).

Figure 4.1. Tree diagrams illustrating data structure for EID events from 1) Jones et al. 2008, and 2) this update, with respect to zoonotic status, spatial data quality of entries, and whether data was accepted or rejected for the new maps contained in this report.



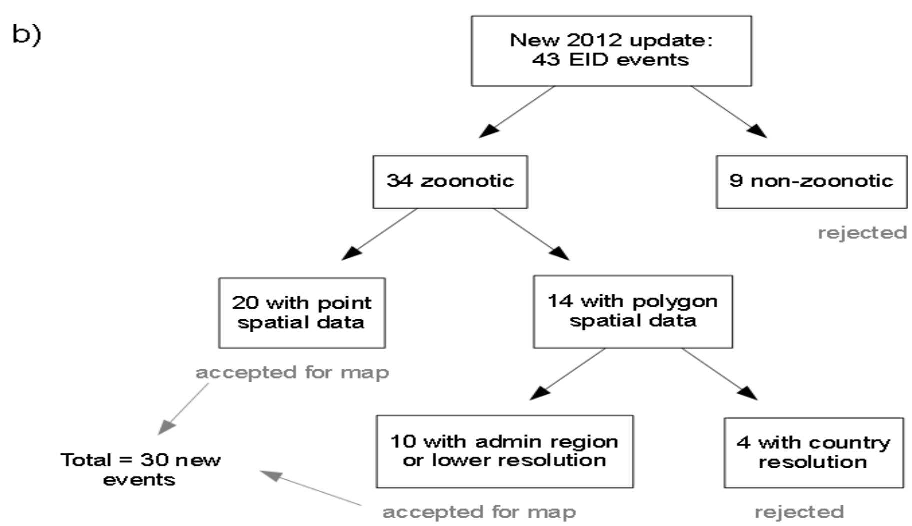


Figure 4.2 New zoonotic disease events identified in 2012 and not previously mapped

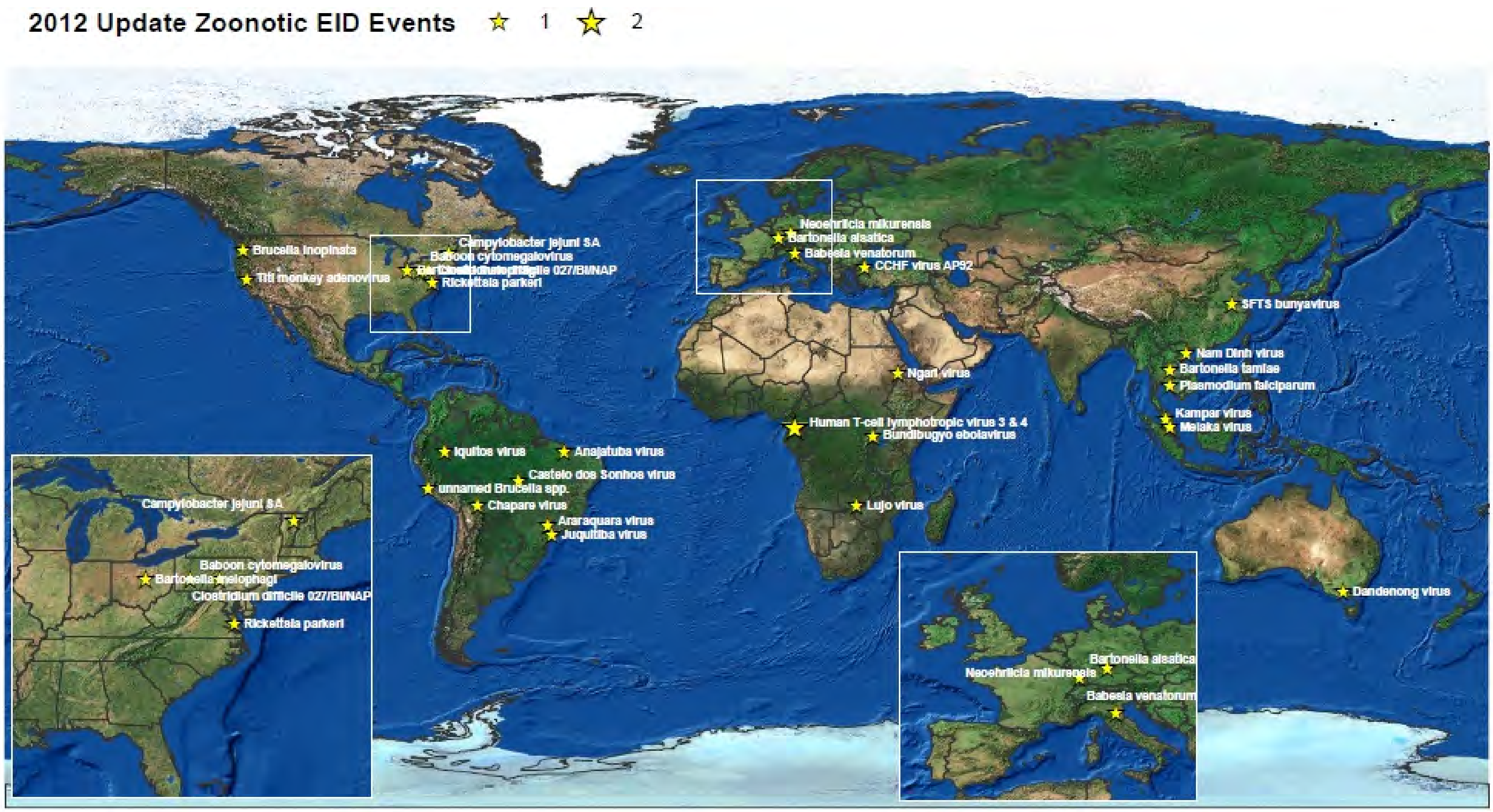


Figure 4.3 Previous zoonotic emerging disease events were mapped in combination with the new events

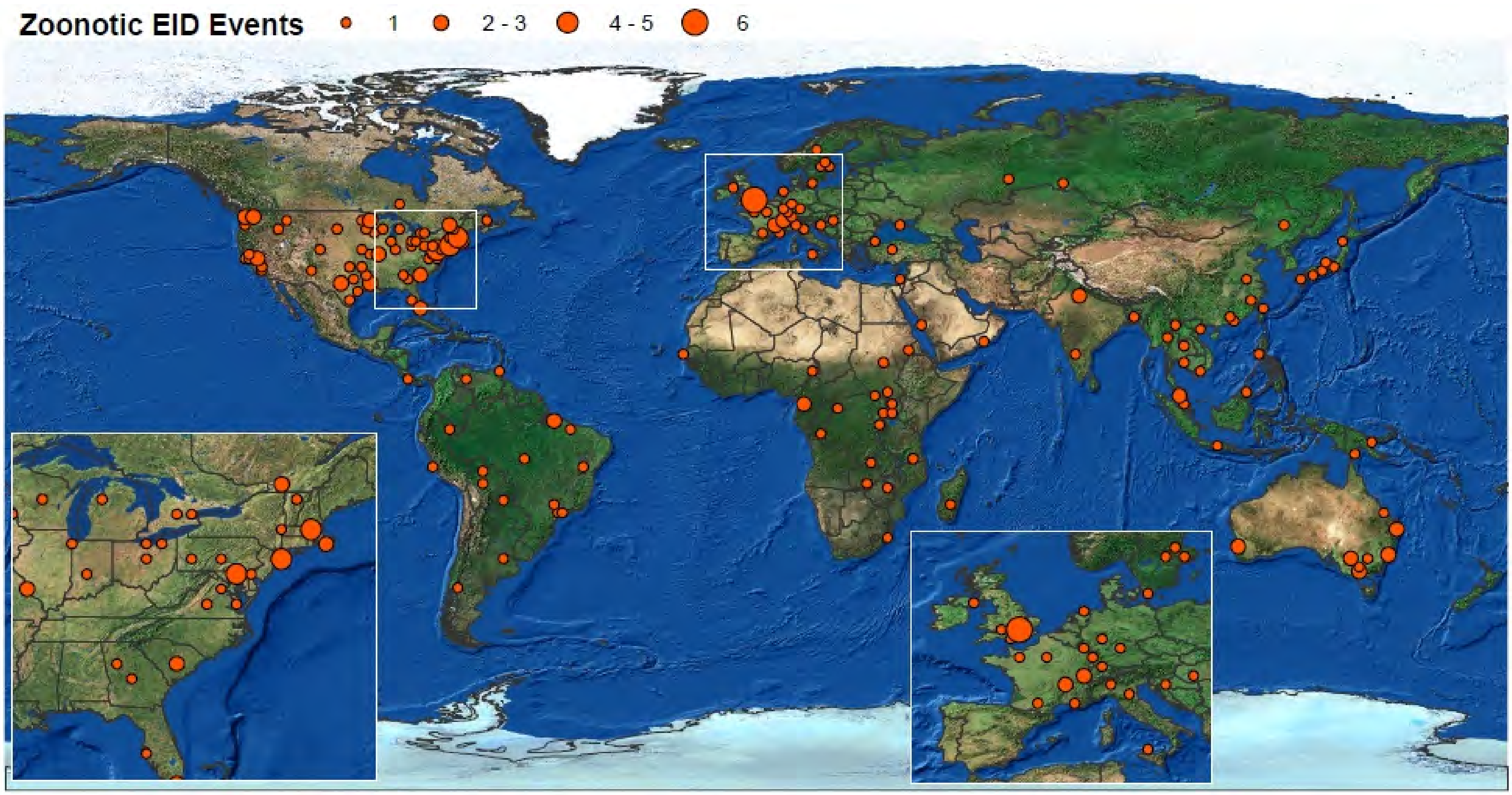


Figure 4.4 Zoonotic emerging disease events with wildlife hosts

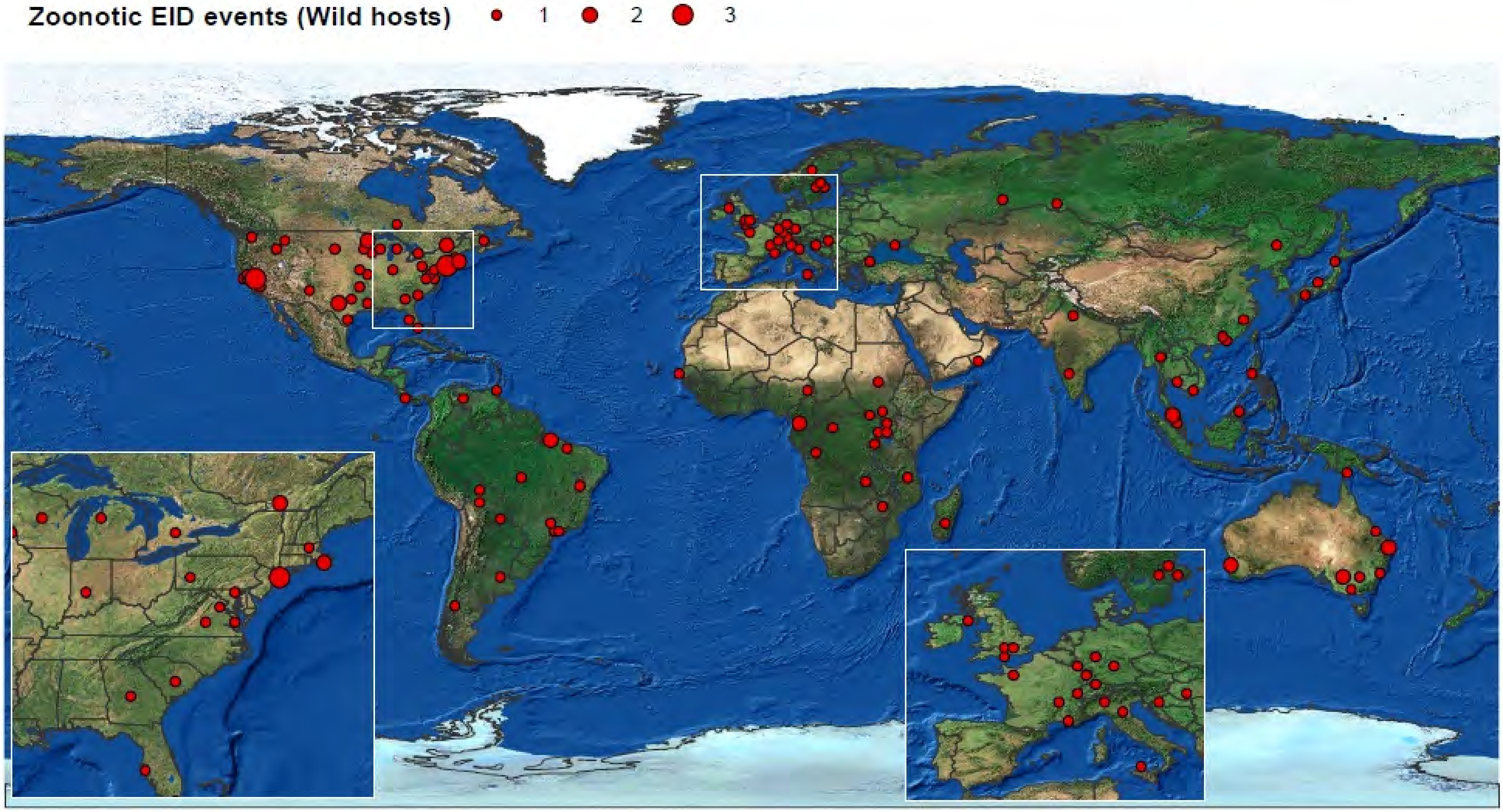


Figure 4.5 Zoonotic emerging disease events with non-wildlife hosts

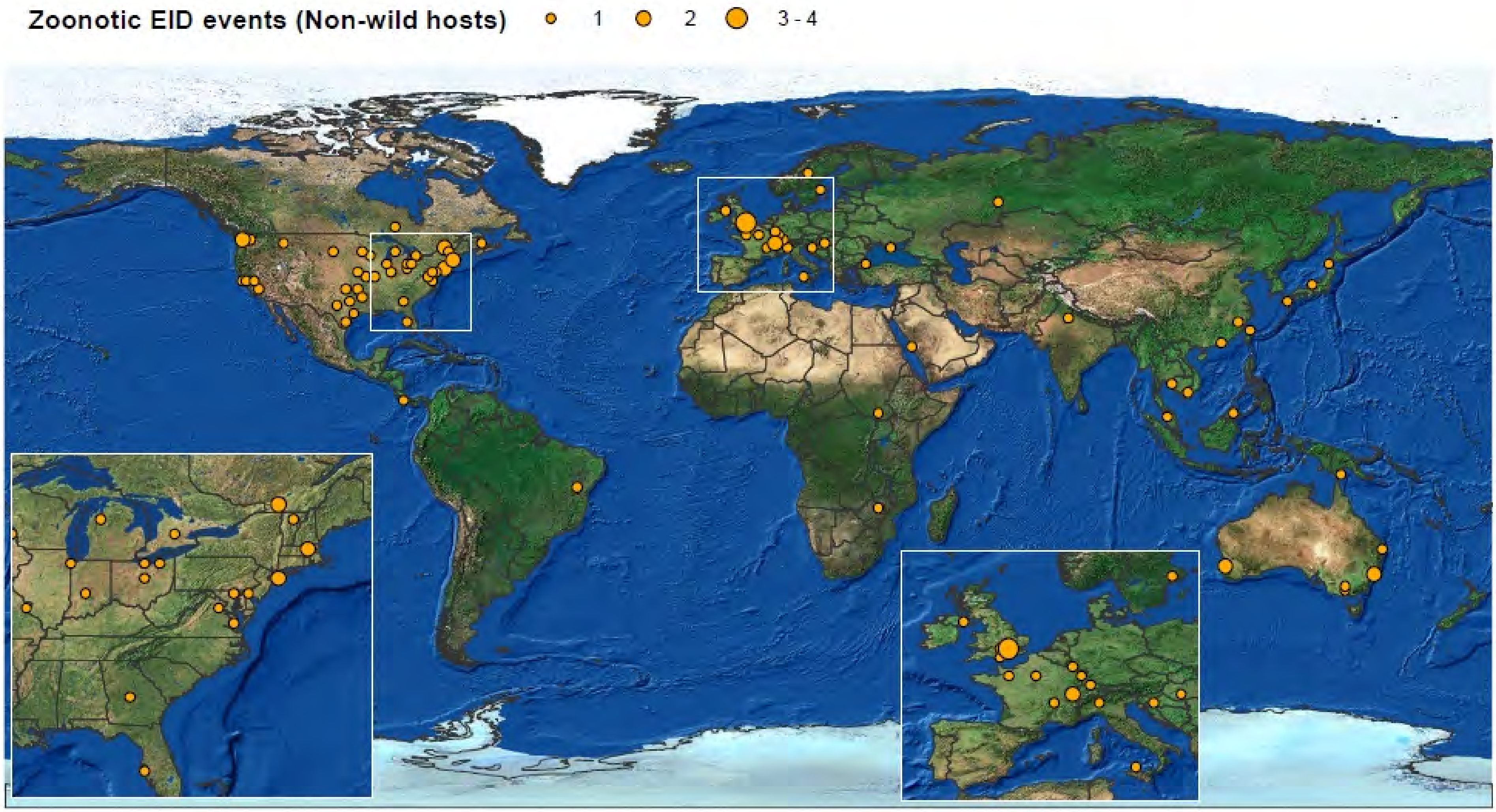


Figure 4.6 Maps of all zoonotic emerging infectious disease events (n = 202) stratified by potential variables of interest. Size of circles denotes number of events in each one degree grid cell, and colour denotes breakdown of events in terms of type of zoonotic host

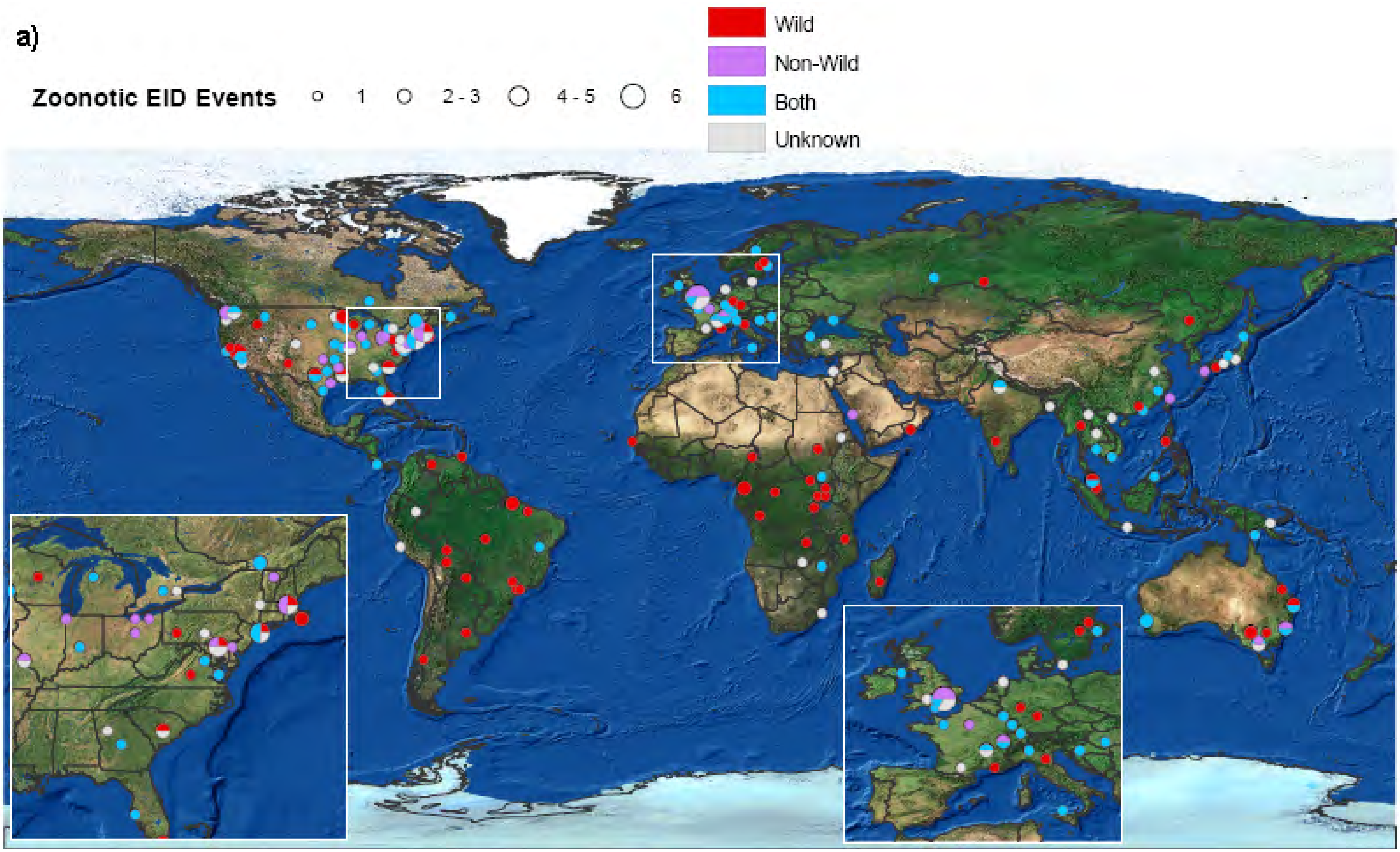


Figure 4.7 Maps of all zoonotic emerging infectious disease events (n = 202) stratified by potential variables of interest. Size of circles denotes number of events in each one degree grid cell, and colour denotes breakdown of events in terms of drug-resistant events

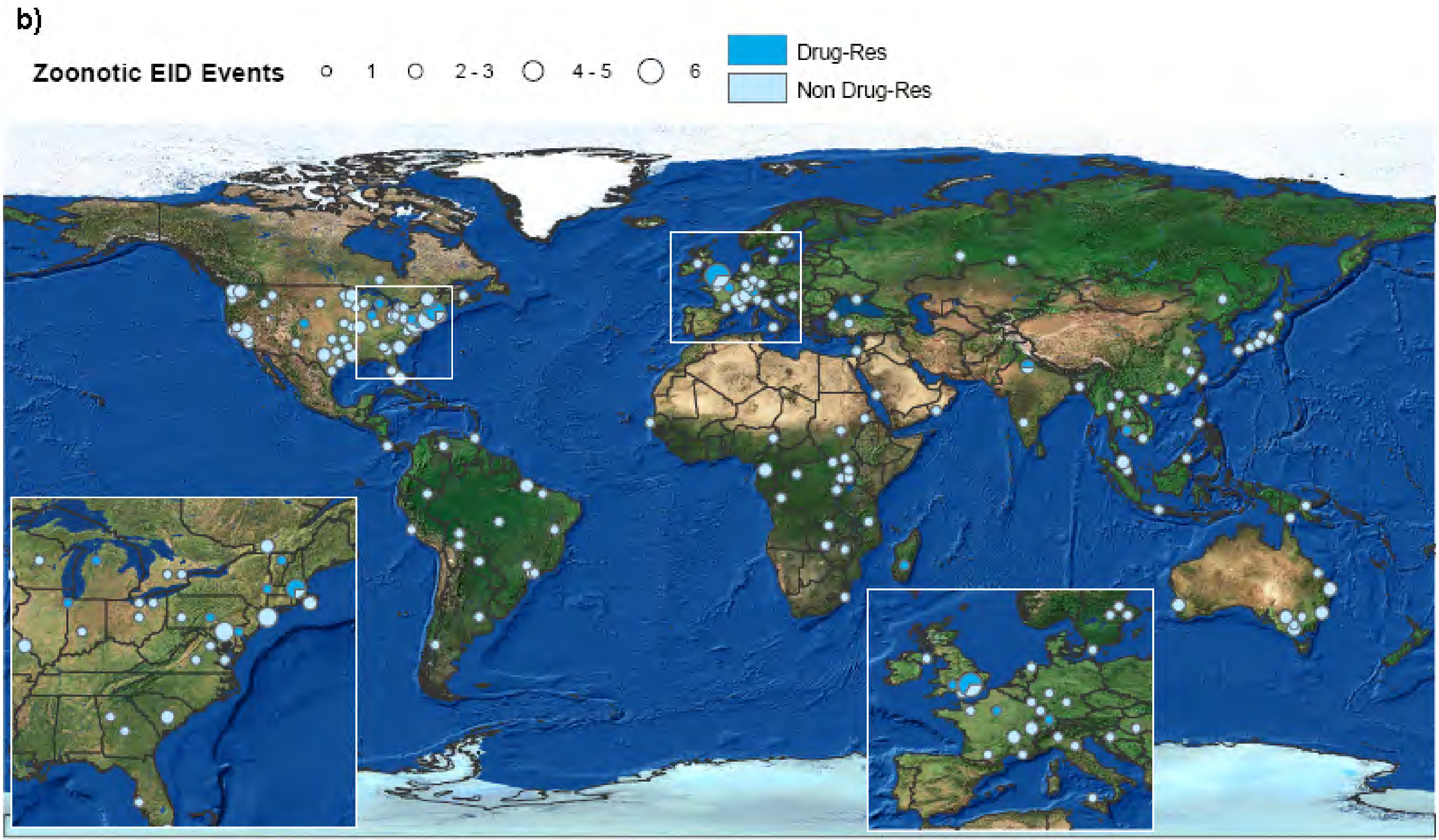
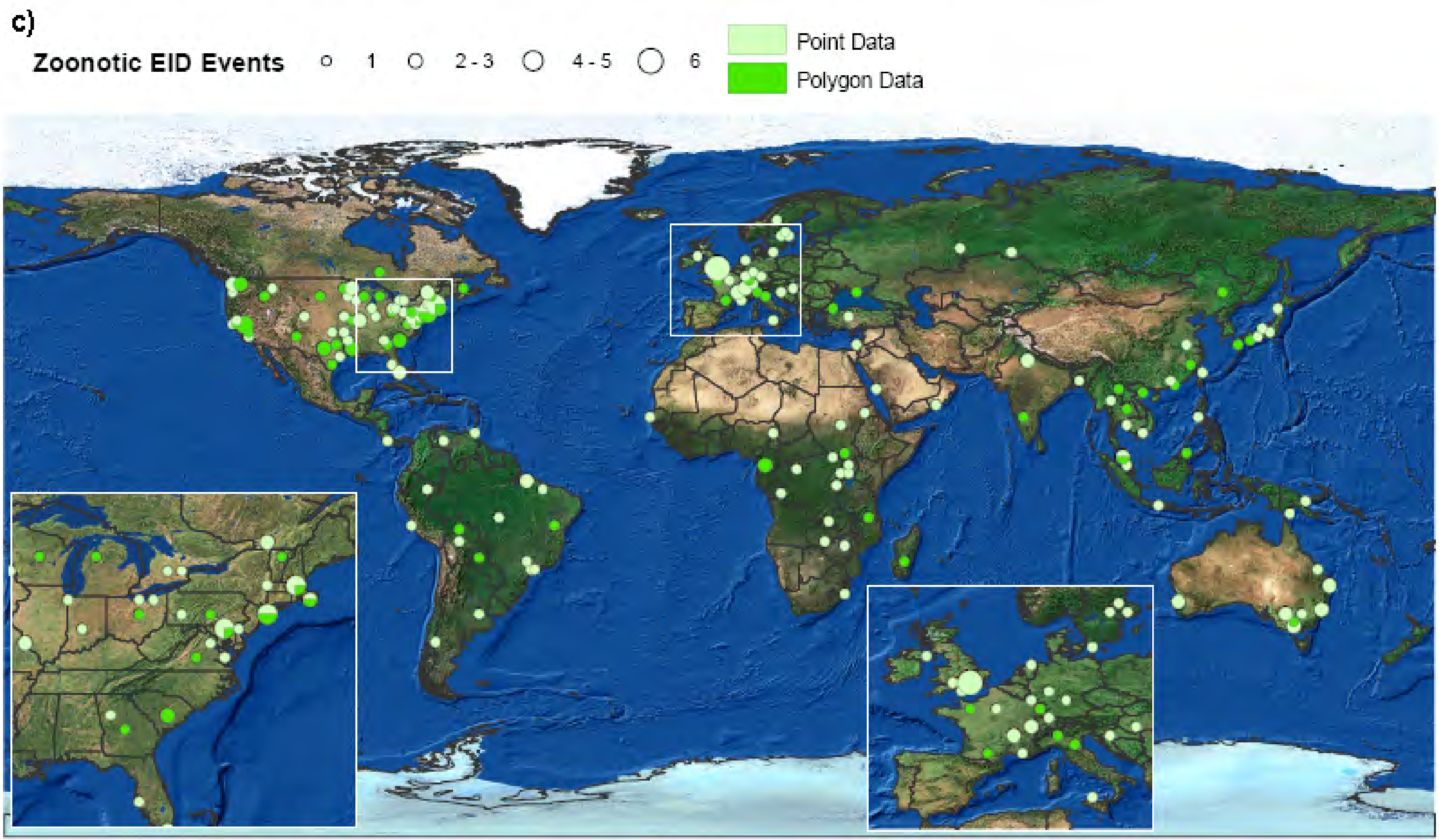


Figure 4.8 Maps of all zoonotic emerging infectious disease events (n = 202) stratified by potential variables of interest. Size of circles denotes number of events in each one degree grid cell, and colour denotes breakdown of events in terms of spatial data resolution (see also Figure 1).



4.5 Conclusion on zoonotic emerging infectious disease vents

We have geo-located and mapped a total of 202 zoonotic emerging infectious disease events, 30 of which were newly collected during this contract. High-resolution maps are provided for all events, as well as events stratified by type of zoonotic host, and other potential classifiers of interest. Potential hotspot trends could broadly reflect surveillance differences, although the higher representation of developing countries within the new events may suggest increasing research focus or improving diagnostic technology

(Note: Is the world becoming sicker or are we just better able to detect disease? The last decades have seen dramatic improvements in biological disease detection with dozens of new potential pathogens anticipated by 2020. At the same time innovations in information management are increasing awareness of disease outbreaks. Perry et al. (2011) explore this in a recent review and conclude that there is evidence for increased emergence of disease in recent decades, although this is not historically unprecedented: major epidemiological transitions also occurred during the Neolithic when livestock were domesticated on a wide-scale, during the age of exploration when Old World pathogens were introduced to the New World, and to a lesser extent with increased global travel in the nineteenth century).

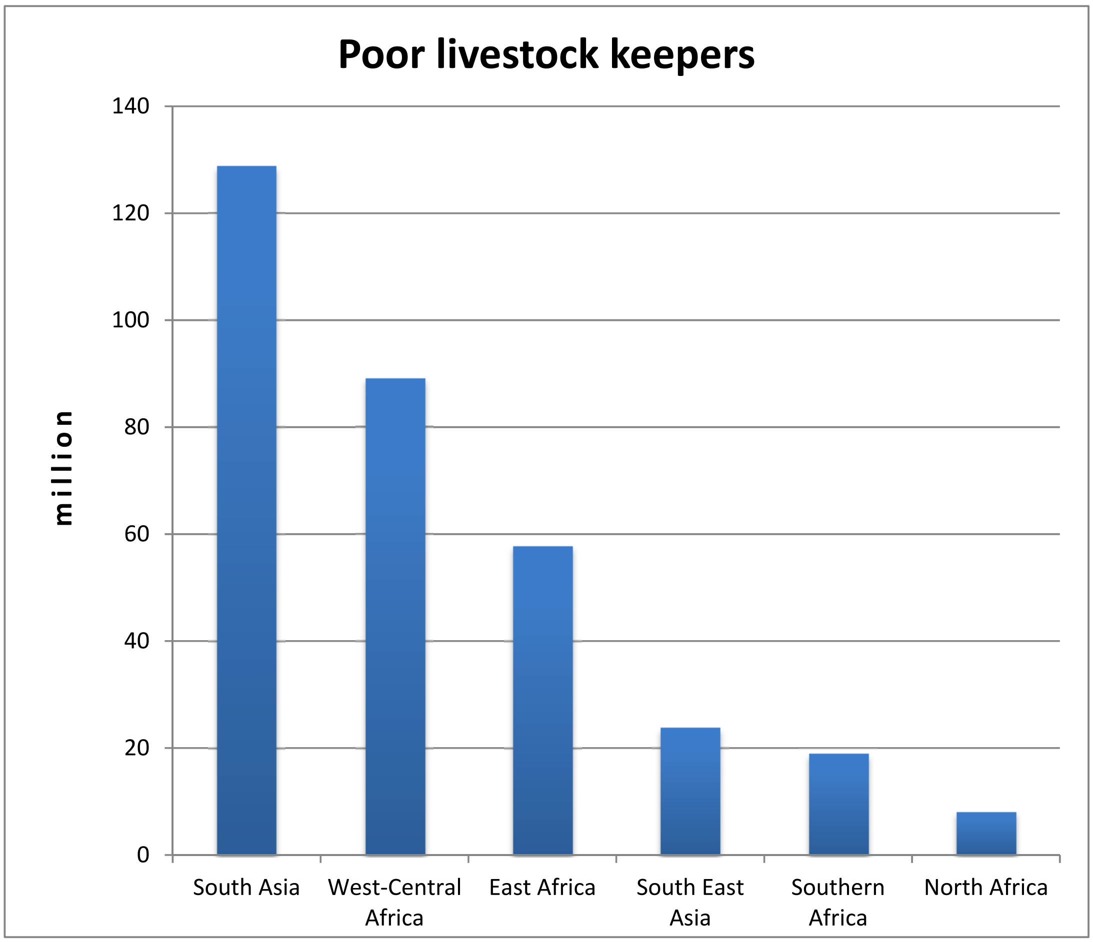
Chapter 5: Poor livestock keepers in livestock systems

Summary
We also updated the regional maps based on the national poverty data showing:

- Agro-ecosystems
- Numbers of cattle, sheep, goats and pigs
- Human population
- Poor livestock keepers

The maps and tables are shown in the this section as well as a summary of regional characteristics relevant to the review.

Figure 5.1 Poor livestock keepers (million) by region



East Africa
Countries: Sudan, Ethiopia, Eritrea, Djibouti, Somalia, Kenya, Uganda, Rwanda, Burundi, Tanzania

Fig 5.2: Eastern Africa region: Farming systems (Herrero et al 2009, Notenbaert et al 2009)

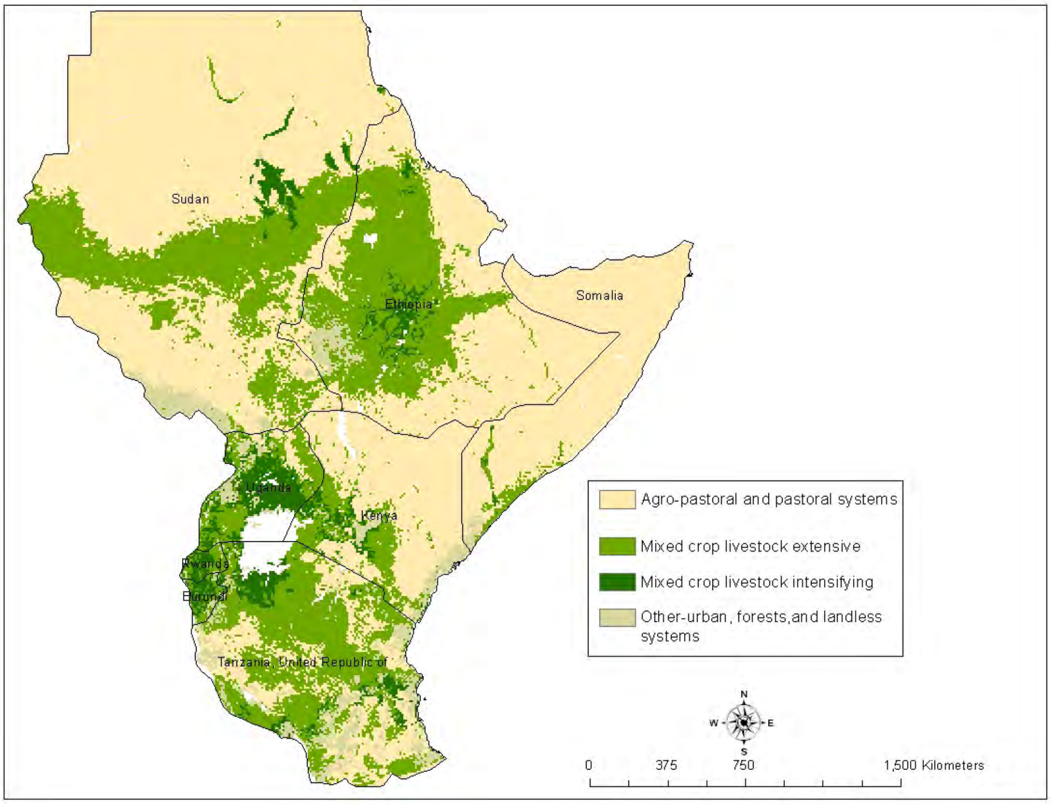


Table 5.1: Species population by farming system in Eastern Africa (Herrero et al 2009)

Farming system	Agro-pastoral and pastoral	Mixed extensive	Mixed intensifying	Others	Total
Bovines	32,239,100	59,221,300	13,481,300	4,479,000	109,420,700
Goats	35,603,000	31,020,500	6,699,100	3,082,780	76,405,380
Sheep	34,404,700	29,999,200	4,893,750	2,254,030	71,551,680
Pigs	85,169	433,390	543,184	183,700	1,245,443
People	30,608,700	76,115,200	37,649,000	14,669,900	159,042,800
Poor livestock keepers	12,125,100	31,719,400	11,281,600	2,740,620	57,866,720

East Africa is characterised by:

- Poor livestock keepers 36% of the population; cattle are relatively important.
- Mixed extensive systems predominate but agro-pastoral /pastoral are more important than most other regions. Pastoralists have high vulnerability to zoonoses.
- Zoonoses with a wildlife interface are important.
- Rapidly dairy development in highlands: bringing risks of brucellosis, tuberculosis and milk-borne diseases.
- Rapid growth in pig production in Uganda brings risks of emerging disease such as Ebola.
- Intra-regional trade important for the horn of Africa (shoats), and of interest to Ethiopia.
- High zoonoses burden in Ethiopia and Tanzania.
- Insecurity in Somalia and possibly South Sudan with implications for zoonoses.

Southern Africa Region
Countries: Zambia, Malawi, Mozambique, Zimbabwe, Botswana, Swaziland, Lesotho, South Africa

Fig 5.3: Southern Africa region: Farming systems (Herrero et al 2009)

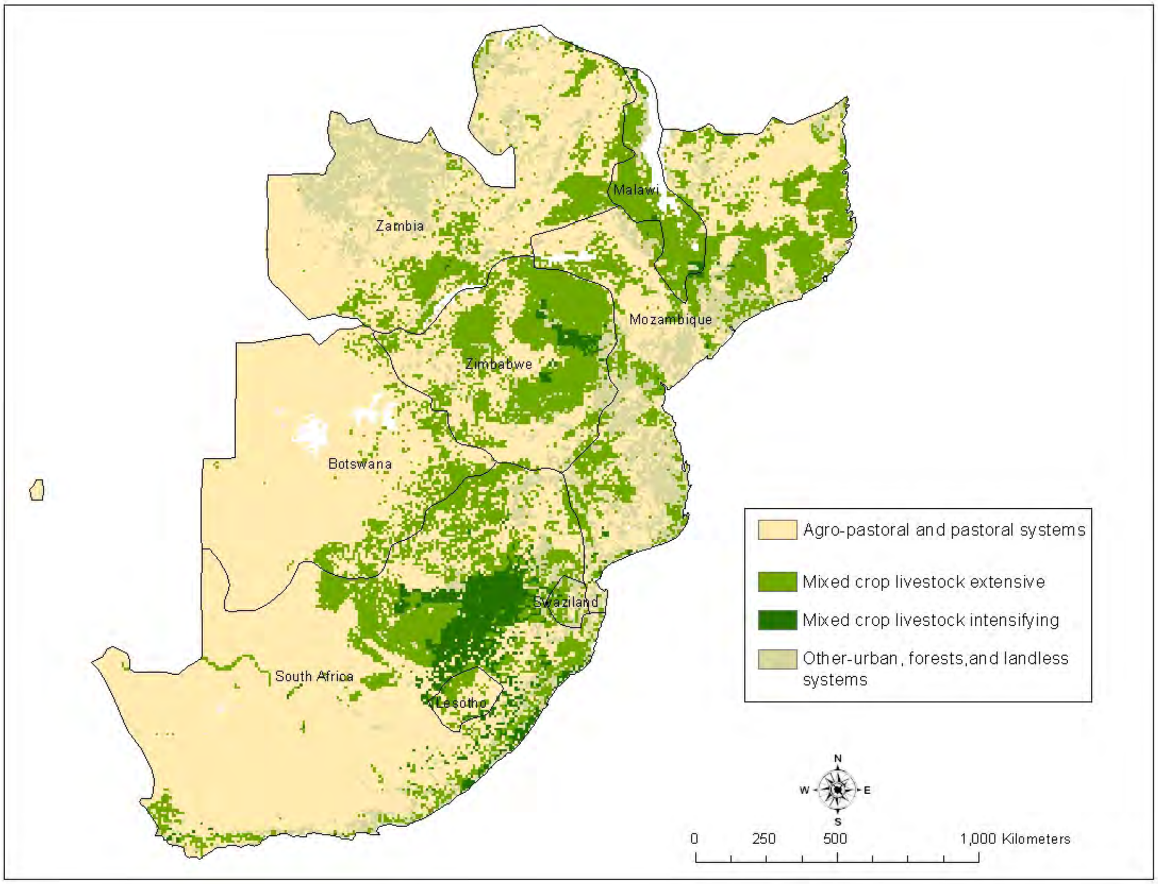


Table 5.2: Species population by farming system in SA (Herrero et al 2009)

Farming system	Agro-pastoral / pastoral	Mixed extensive	Mixed intensifying	Others	Total
Bovines	9,611,320	8,532,650	2,307,420	1,746,690	22,198,080
Goats	7,300,510	6,164,890	643,834	1,301,330	15,410,564
Sheep	9,611,320	8,532,650	2,307,420	1,746,690	22,198,080
Pigs	696,286	1,300,700	840,703	215,223	3,052,912
People	17,757,100	32,350,900	5,730,630	16,532,100	72,370,730
Poor livestock keepers	6,286,600	10,182,200	783,379	1,650,570	18,902,749

Southern Africa is characterised by:

- Poor livestock keepers 26% of population. Lowest in SSA; Cattle relatively important
- Agro-pastoral /pastoral more important. Pastoralists have high vulnerability to zoonoses.
- Zoonoses with a wildlife interface are important. Current interest
- Significant commercial ranching and farming, with better animal health and zoonoses control. Some countries with export potential
- Better animal health services and disease reporting systems than most other SSA regions
- Wide regional variation in farming systems, zoonoses and response capacity

West Africa region

Countries: Mauritania, Mali, Niger, Chad, Senegal, The Gambia, Guinea Bissao, Guinea, Sierra Leone, Liberia, Ivory Coast, Burkina Faso, Ghana, Togo, Benin**,** Nigeria, Cameroon

Fig 5.4: West Africa region: Farming systems (Herrero et al 2009)

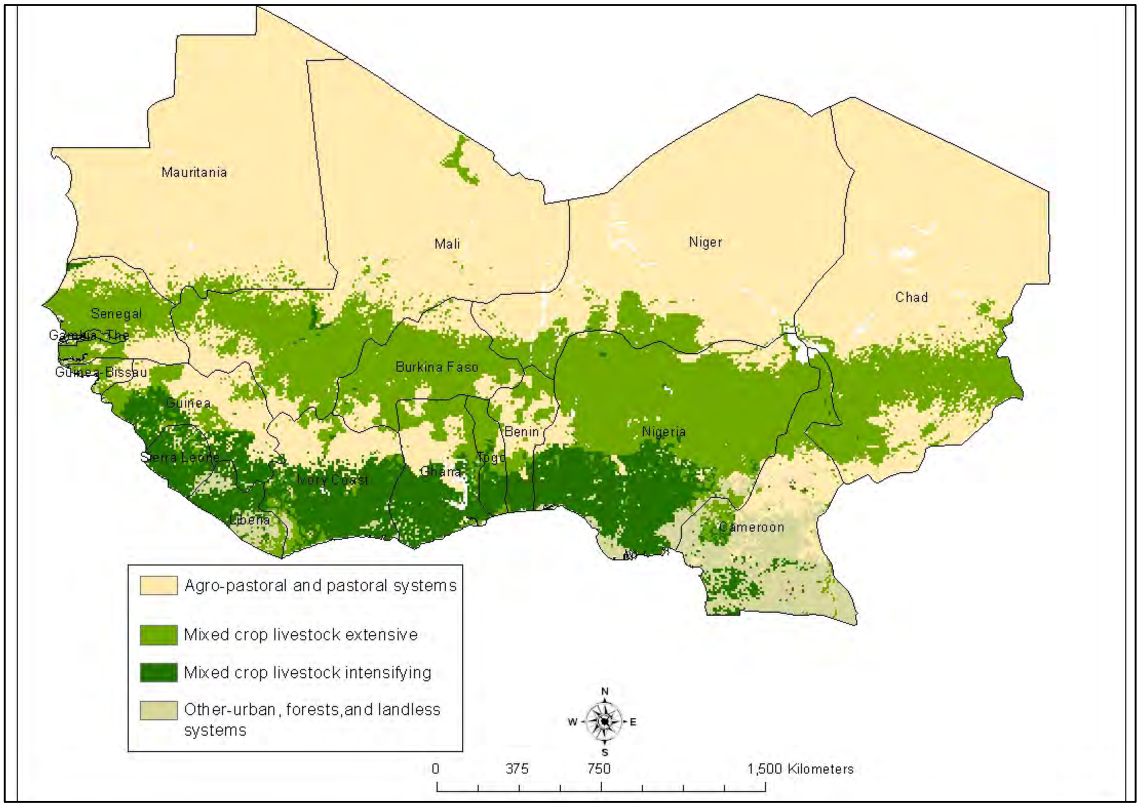


Table 5.3: Species population by farming system in WA (Herrero et al 2009)

Farming system	Agro-pastoral /pastoral	Mixed extensive	Mixed intensifying	Others	Total
Bovines	13,458,000	28,220,300	2,403,490	1,034,530	45,116,320
Goats	19,936,400	37,553,900	16,816,900	2,603,100	76,910,300
Sheep	13,841,500	29,747,800	8,505,920	2,024,590	54,119,810
Pigs	810,597	2,598,830	2,518,430	1,367,550	7,295,407
People	18,540,400	80,711,100	72,559,700	13,249,700	185,060,900
Poor livestock keepers	11,343,700	38,161,100	19,231,600	2,011,420	70,747,820

West Africa is characterised by:

- Poor livestock keepers 38% of the population; highest in SSA. Goats (followed by sheep) relatively most important species
- Mixed extensive more important, but mixed intensifying more important than other regions of SSA. Pastoralism/agro-pastoralism mainly in the Sahel.
- Cattle important for traction, but tsetse a major barrier. Trypanotolerant cattle important in the some areas. Little dairying and reliance on imported dairy products. Traditional dairying in the Sahel has high risk of milk-borne zoonoses because of cultural practices.
- Also high imports of poultry. Slow growth in livestock production.
- High zoonoses burden in Nigeria and sub-humid coastal countries.
- Insecurity in several countries

North Africa region
Countries: Western Sahara, Morocco, Algeria, Tunisia, Libya, Egypt

Fig 5.5: North Africa Region: Farming systems (Herrero et al 2009)

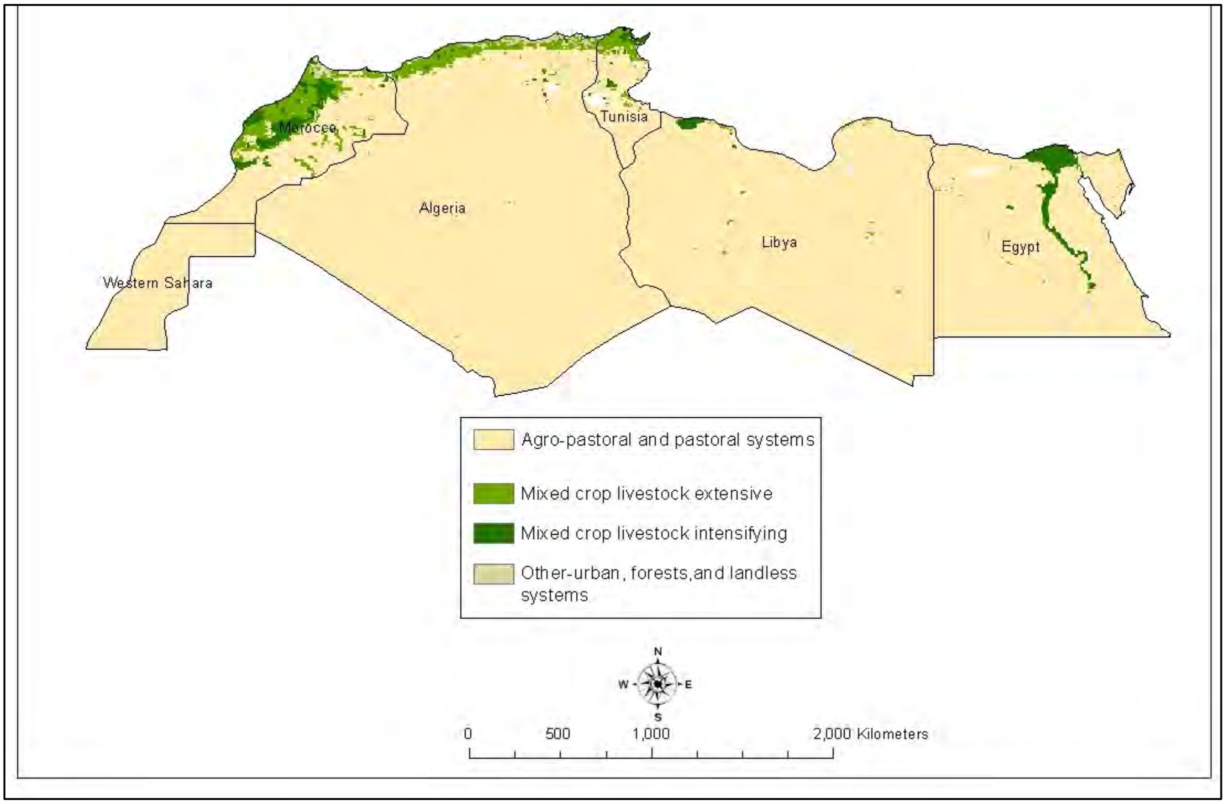


Table 5.4: Species population by farming system in NA (Herrero et al 2009)

Farming system	Agro-pastoral pastoral	Mixed extensive	Mixed intensifying	Others	Total
Bovines	2,008,120	1,595,520	2,367,870	462,762	6,434,272
Goats	6,325,060	1,667,820	1,881,460	578,935	10,453,275
Sheep	23,411,000	10,130,600	5,593,700	1,606,520	40,741,820
Pigs	2,321	477	26	0	2,824
People	23,570,000	14,934,900	51,341,000	5,623,850	95,469,750
Poor livestock keepers	4,946,850	916,512	2,088,880	203,899	8,156,141

Northern Africa is characterised by:

- Poor livestock-keepers 8% of the population. Lowest in Africa.
- Relatively high urbanisation and higher development indices
- Sheep by far the most important species, followed by goats and then cattle. Only region where sheep pre-dominate. Pigs rare.
- Pastoralism/agro-pastoralism the most important system. Unlike elsewhere in Africa, mixed extensive is the least important.
- Intensive production important in many countries – especially poultry.
- Extremely high poultry numbers and density along the Nile allow avian influenza to persist and a risk factor for other poultry disease

Central and SE Africa

Countries: Central African Republic, Equatorial Guinea, Gabon, Congo, Congo DR, Angola, Namibia (this region is included in West Africa for the review of endemic zoonoses)

Fig 5.6: Central and SE Africa region- Farming systems (Herrero et al 2009)

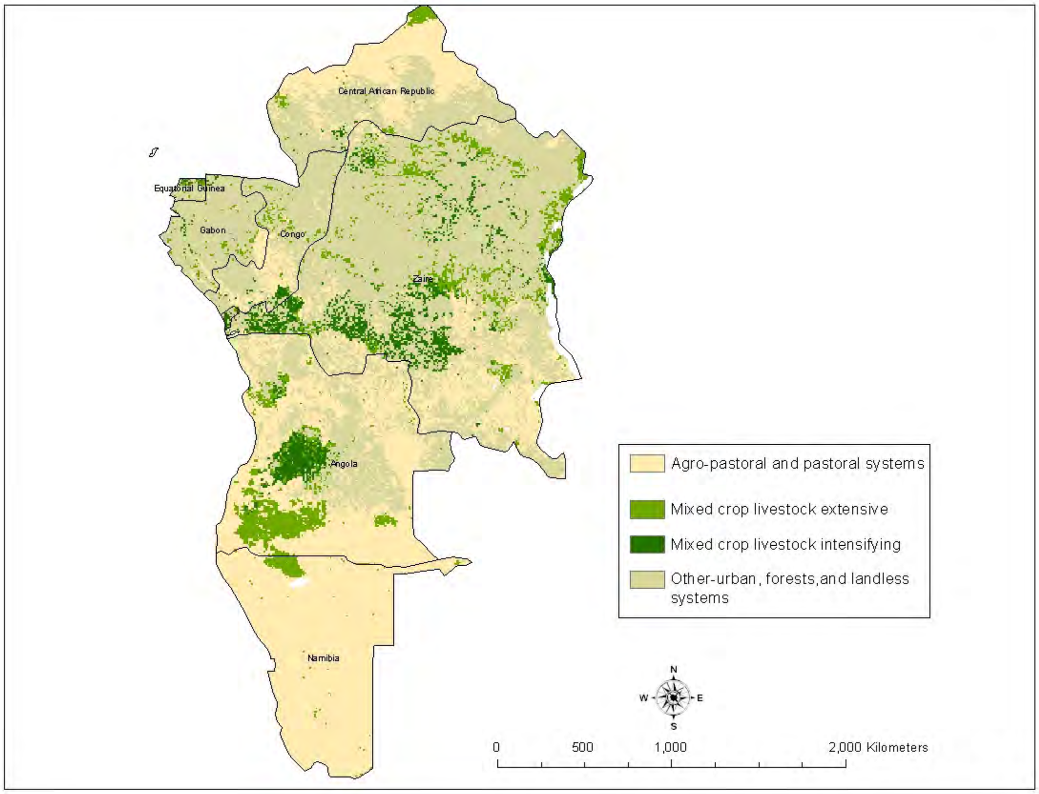


Table 5.5: Species population by farming systems in Central and SE Africa (Herrero et al 2009)

Farming system	Agro-pastoral pastoral	Mixed extensive	Mixed intensifying	Others	Total
Bovines	4,353,250	2,291,670	344,621	1,899,710	8,889,251
Goats	2,911,600	1,730,230	775,076	2,920,870	8,337,776
Sheep	2,826,090	678,948	212,043	625,979	4,343,060
Pigs	985,813	835,169	358,327	2,728,110	4,907,419
People	8,888,550	7,730,480	10,530,100	31,979,900	59,129,030
Poor livestock keepers	3,657,390	2,660,500	2,891,810	9,223,170	18,432,870

Central and South Eastern Africa is characterised by:

- Poor livestock-keepers 31% of the population. Second highest after W Africa.Generally similar to W Africa in species, systems and zoonoses
- Goats the most numerous, followed by cattle then sheep.
- Pastoralism/agro-pastoralism the most important system. Mixed extensive, and mixed intensifying both important.
- Pigs important, especially in Congo DR
- Central African rain forests a hot-spot for bio-diversity, human incursion, game meat utilisation and disease emergence
- Insecurity problems persisting in Congo DR

South Central Asia Region
Countries: Iran, Afghanistan, Pakistan, Nepal, India, Bhutan, Bangladesh (our review of endemic zoonoses included Sri Lanka)

Fig 5.7: South Central Asia region: Farming systems (Herrero et al 2009)

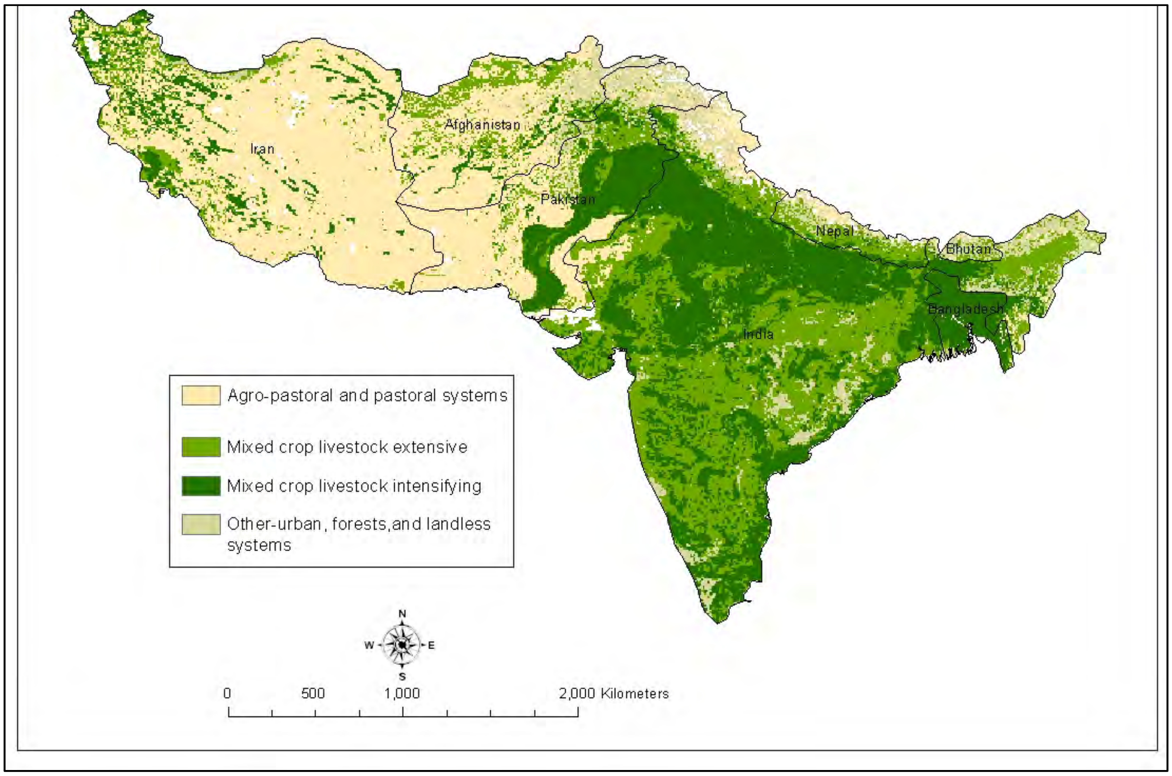


Table 5.6: Species population by farming system in SC Asia (Herrero et al 2009)

Farming system	Agro-pastoral pastoral	Mixed extensive	Mixed intensifying	Others	Total
Bovines	10,545,400	125,910,000	204,813,000	16,553,900	357,822,300
Goats	29,862,700	66,316,600	95,724,300	9,702,000	201,605,600
Sheep	37,978,700	40,641,100	39,511,400	5,621,940	123,753,140
Pigs	185,107	4,873,080	6,977,520	1,212,390	13,248,097
People	51,652,300	281,271,000	630,135,000	44,731,600	1,007,789,900
Poor livestock keepers	11,086,000	54,073,900	57,803,200	5,890,470	128,853,570

South Central Asia is characterised by:

- Poor livestock-keepers 13% of the population. A relatively low proportion compared to West and East Africa but in absolute numbers about the same.
- Mixed intensifying systems most important followed by mixed extensive
- Cattle are the most important followed by goats and then sheep.
- Important dairy (mainly from buffalo) and draft sectors but production low. Milk-borne zoonoses very important but transmission more from contact than consumption.
- Pigs are localised mainly in the North East of India but here they are very important.
- Relatively stronger government services than much of SSA
- Insecurity problems persisting in Iran, Afghanistan, and Pakistan

South East Asia region

Countries: Myanamar, Thailand, Laos, Vietnam, Cambodia, Malaysia, Indonesia, Brunei, Philippines, Papua New Guinea

Fig 5.8: South East Asia Region: Farming systems (Herrero et al 2009)

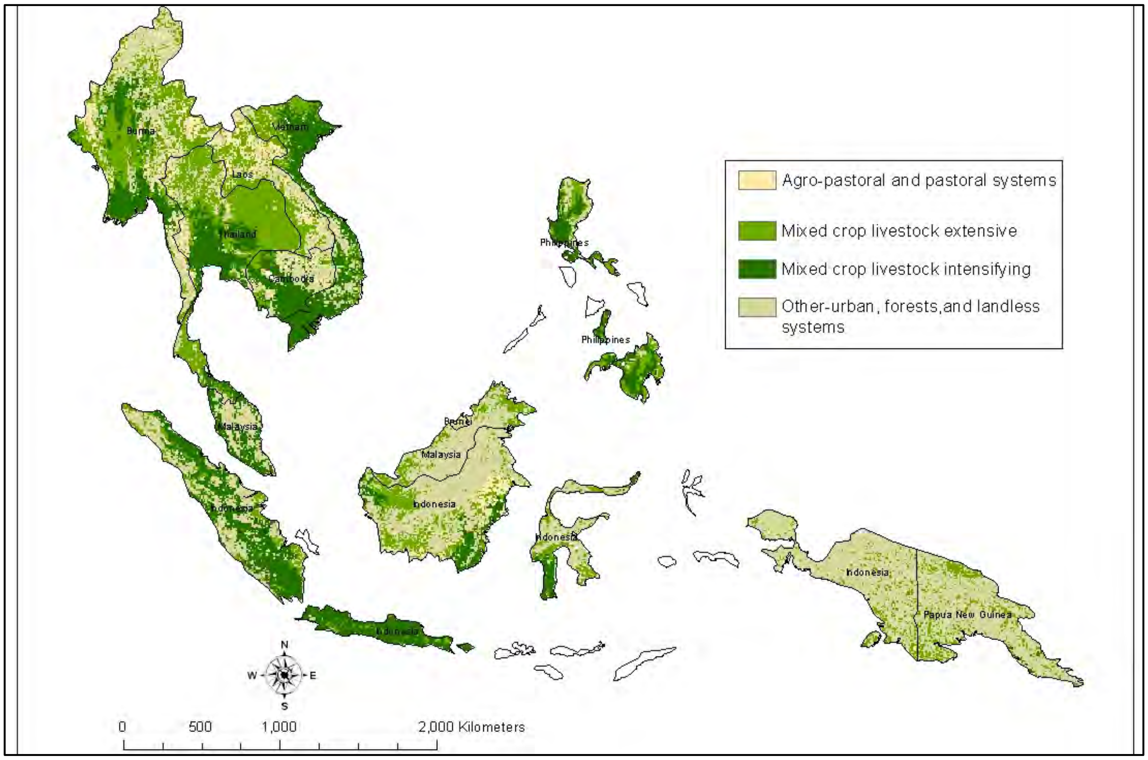


Table 5.7: Species population by farming system (Herrero et al 2009)

Farming system	Agro-pastoral pastoral	Mixed extensive	Mixed intensifying	Others	Total
Goats	209,463	2,658,470	9,412,130	2,107,110	14,387,173
Sheep	675	616,862	6,016,720	226,156	6,860,413
Pigs	584,026	4,160,260	10,307,800	3,275,040	18,327,126
People	1,678,350	11,542,900	28,397,400	9,013,500	50,632,150
Poor livestock keepers	654,932	7,726,660	11,278,000	4,160,070	23,819,662

South East Asia is characterised by:

- Poor livestock-keepers 47% of the population but concentrated in Indonesia, Vietnam and the Philippines. China has high numbers but poverty decreasing rapidly (not included in this map).
- Mixed intensifying systems most important followed by mixed extensive
- High urbanisation, high demand for animal source foods, stabilising populations.
- Pockets of deprivation and high vulnerability to zoonoses: hill tribes in Thailand and Vietnam, Papua New Guinea and Timor Leste.
- Pigs are the most important followed by goats then sheep. Only region where pigs predominate. Cattle are few in number but growing rapidly in some countries (especially Muslim).
- High zoonoses burden in Viet Nam, Myanamar, Philippines and Indonesia
- Very high density of monogastrics, poor biosecurity, wildlife interfaces, backyard close to intensive systems all favour disease emergence and persistence

Chapter 5: Conclusions

This final short chapter pulls together some of the more important points and conclusions around zoonoses, poverty, poor livestock keepers, emerging markets and livestock system changes.

Objectives of controlling zoonoses

The review makes a distinction between different categories of zoonoses and suggests that endemic zoonoses are of most concern where the objective is lowering the burden of human disease and increasing the productivity and profitability of livestock for poor people. Among the most important and most neglected of endemic zoonoses are food-borne zoonoses. Outbreak zoonoses are of concern when there is an objective of reducing vulnerability of neglected populations. Emerging zoonoses are of concern when the object is foresight, and understanding disease emergence in order to try and avert pandemics of major impact. Because a small number of zoonoses are responsible for the majority of human and animal burden, targeting these zoonoses is likely to be an effective use of scarce resources.

Lack of evidence

The report draws attention to the lack of evidence. There are obviously major problems around disease reporting systems in developing countries, despite considerable support at the time of the avian influenza pandemic. A question is whether to invest more in existing systems or to explore alternative ways to generate evidence about disease? We suggest the latter. Our report revealed showed literature is one of the best ways of understanding what diseases are present and their impact. Moreover, valuable information exists in the grey literature, which is not currently easily available. However, more and better information is needed which can only be obtained through field surveys. Recent advances in technology (bio-repositories, genomics, e-technologies, etc) offer opportunities for radically improving our understanding of zoonoses epidemiology and control.

Hotspots of zoonoses, poverty and emerging markets

An underlying hypothesis of the report was that hot spots for zoonoses and poverty exist, and that targeting these hotspots has good prospects for alleviating health burdens while improving livelihoods. The study confirmed that a relatively small number of countries have a disproportionate share of poor livestock keepers and zoonoses burden (notably India, Ethiopia, and Nigeria). However, the association between zoonoses as a barrier to emerging markets for smallholders was less obvious (because countries with rapidly evolving markets tend to have fewer poor livestock keepers and better control of human disease). The relation between poverty and livestock keeping with emerging zoonotic events was not obvious, possibly because of the unpredictable nature of disease emergence, relatively poor detection and a possible relation between emergence and intensive livestock-keeping (associated with rich countries). We conclude, controlling zoonoses could substantially reduce the human disease burden and support the livelihoods of poor farmers, but the links to emerging markets require further research.

Opportunities

We identified gaps and opportunities for research to reduce the burden of disease for the zoonoses and regions in the report. These include: better understanding implications for intensification and emerging markets on zoonoses; models for zoonoses control in emerging markets; ecosystem models for management of zoonoses with a wildlife interface; improvement of surveillance for existing and new diseases; understanding the impacts multiple burdens of zoonoses in order to better allocate resources; technologies and innovation for detection, diagnosis, prevention, treatment and response.

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ANNEX ONE – PRIORITSATION OF ZOONOSES

Disease	Expert opinion	Deaths - annual	Affected	Impact livestock	Farm intervention	other	Score
Cysticercosis	OIE, Perry	50000	50000000	High	1		5
Gastrointestinal (zoonotic)	GBD, Rosetta	1466666.667	2333333333	High	1		5
Leptospirosis	OIE, Perry	123000	1700000	High	1		5
Hepatitis E		300000	14000000	Low	1		4
Tuberculosis (zoonotic)	GBD, OIE, Perry	100000	554500	High	1		4
Rabies	OIE, Perry	55000	70000	Medium	1	1	4
Leishmaniasis	OIE, GBD, Rosetta	47000	2000000	Low	1		4
Brucellosis	OIE, Perry	25000	500000	High	1		4
Echinococcosis	OIE	18000	300000	High	1		4
Toxoplasmosis		10000	2000000	High	1		4
Q fever	OIE	3000	3500000	Medium	1		4
Trypanosomosis (zoonotic)	GBD, OIE, Rosetta, Perry	2500	15000	High	1		4
Anthrax	OIE, Perry	1250	11000	High	1		4
Chagas	GBD, Rosetta	10000	8000000	Low			3
Chickungunya		12500	500000	Low		1	3
Clostridium difficile		3000	300000	Low		1	3
Dengue	GBD	20000	50000000	Negligible			3
Ebola		500	800	Negligible		1	3
Hanta virus		1750	175000	Low		1	3
Avian influenza virus	OIE	77	145	High	1	1	3
BSE	OIE	182	188	High	1	1	3
Buffalo pox	Perry	negligible	common?	High	1		3
Chlamydophila psittaci	OIE	2250	22000	Medium	1		3
Japanese encephalitis	OIE, GBD, Perry	11000		Low	1		3
Rift valley fever	OIE, Perry	45	150	Medium	1	1	3
Mange	Perry	negligible	common?	High	1		2
Lassa fever		5000	500000	Low			2
Lyme		2000	100000	Medium			2
Pneumonia zoontoic	GBD	300000		Medium			2
Shistosomiais (zoonotic)	GBD, Perry	4000		Low			2
Tetanus	GBD, Rosetta	160000		Low			2
Trichinellosis	OIE, Perry	2000	10000	Low			2
Brucella melitensis	OIE, Perry	..	..	High	1		2
Brucella suis	OIE, Perry	..	..	High	1		2
Enzootic abortion of ewes (ovine chlamydiosis)	OIE	negligible	rare	High	1		2
Foot and mouth disease	OIE	negligible	low	High	1		2
Nipah		100	300	Medium	1	1	2
Orf	Perry	negligible	common?	Medium	1		2
Paratuberculosis	OIE	Unknown		Medium	1	1	2

Toxocara vitulorum	Perry	unknown	unknown	High	1		2
Vesicular stomatitis	OIE	0	rare	High	1		2
Bovine babesiosis	OIE		16	High			1
Crimean Congo haemorrhagic fever	OIE	165	5000	Low		1	1
Kyasanur forrest		20	500	Low		1	1
Marburg virus		9	11	Low		1	1
Pasteurella multocida	OIE	100		High			1
West Nile fever	OIE	100	100000	Low		1	1
Equine encephalomyelitis (Eastern)	OIE	2	6	Low	1		1
Equine encephalomyelitis (Western)	OIE	low		Low	1		1
Newcastle disease	OIE	Negligible	low	Medium	1		1
Burkholderia mallei	OIE	negligible	low	Medium			0
Clostridium botulinum	Perry	100	1000	Low			0
New world screwworm (Cochliomyia hominivorax)	OIE	negligible	low	Medium			0
Old world screwworm (Chrysomya bezziana)	OIE	negligible	low	Medium			0
Tick borne encephalities		300	15000	Medium			0
Tularaemia	OIE	1000	50000	Low			0

ANNEX 2 SYSTEMATIC LITERATURE REVEW REFERENCES (SOME INCOMPLETE)

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ANNEX 4 Summary details of the 30 new zoonotic EID events collected that were mapped (greater spatial resolution than country-level) with major references.

Pathogen	Type	Location	Year	Refs
unnamed *Brucella* spp.	bacteria	Lima, Peru	1985	[1]
Ngari virus	virus	Kassala, Sudan	1988	[2,3]
Baboon cytomegalovirus	virus	Pittsburgh, Pennsylvania, USA	1992	[4,5]
Castelo dos Sonhos virus	virus	Castelo dos Sonhos, Brazil	1995	[6]
Araraquara virus	virus	Araraquara, Brazil	1996	[6,7]
Babesia venatorum	protozoa	Romagna, Italy	1998	[8,9]
Iquitos virus	virus	Iquitos, Peru	1999	[10]
Bartonella tamiae	bacteria	Khon Kaen province, Thailand	2000	[11]
Anajatuba virus	virus	Anajatuba, Brazil	2000	[12,13]
Clostridium difficile 027/BI/NAP (gatifloxacin & moxiflacin resistant)	bacteria	Pennsylvania state, USA	2001	[14]
Rickettsia parkeri	bacteria	Tidewater, Virginia, USA	2002	[15,16]
Nam Dinh virus	virus	Nam Dinh province, Vietnam	2003	[17,18]
Chapare virus	virus	near Cochamba, Bolivia	2003	[19]
Juquitiba virus	virus	Juquitiba, Brazil	2003	[20,21]
Campylobacter jejuni SA clone (tetracycline resistant)	bacteria	Vermont state, USA	2003	[22]
Bartonella melophagi	bacteria	Ohio state, USA	2004	[23]
Brucella inopinata	bacteria	Portland, Oregon, USA	2005	[24]
Bartonella alsatica	bacteria	Alsace region, France	2005	[25]
Human T-cell lymphotropic virus 3	virus	Southern Cameroon	2005	[26]
Human T-cell lymphotropic virus 4	virus	Southern Cameroon	2005	[26]
Melaka virus	virus	Melaka, Malaysia	2006	[27]
Kampar virus	virus	Kampar, Malaysia	2006	[28]
Severe fever with thrombocytopenia syndrome bunyavirus	virus	Dingyuan county, China	2006	[29,30]
Neoehrlichia mikurensis	bacteria	Middle Franconia, Germany	2007	[31,32]
Plasmodium falciparum (artemisinin resistant)	protozoa	Pailin, Cambodia	2007	[33,34]
Dandenong virus	virus	Dandenong, Australia	2007	[35,36]
Crimean-Congo Hemorrhagic Fever virus AP92 (newly virulent)	virus	Istanbul, Turkey	2007	[37]
Bundibugyo ebolavirus	virus	Bundibugyo, Uganda	2007	[38,39]
Lujo virus	virus	Lusaka, Zambia	2008	[40,41]
Titi monkey adenovirus	virus	Davis, California, USA	2009	[42]

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Figure 2. Global maps of zoonotic EID events at a one decimal-degree level, where size of circles denotes number of events in grid cell. Maps depict a) labelled new events collected in this update (n = 30), b) all combined events from Jones et al. 2008 and this update (n = 202), and stratified maps of only those events with c) wildlife hosts (n = 121), and d) non-wildlife hosts (n = 91). Events with both host types are included in both c) and d), and events with unknown hosts are included in neither.

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