Surveillance for Diseases of Poultry
with Specific Reference to Avian Influenza

A dissertation presented
in partial fulfilment of the requirements
for the degree of Doctor of Philosophy
at Massey University

Caryl Yolanda Lockhart
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— Abstract —

This thesis addresses issues related to surveillance for disease in commercial and non-commercial poultry populations. The motivation for this work has largely arisen from the unprecedented outbreaks of highly pathogenic avian influenza (HPAI) H5N1 that have occurred in 52 countries in Asia, Africa and Europe since 2003. A series of studies are presented using data derived from two countries, Vietnam and New Zealand. The two Vietnamese studies provide in-depth epidemiological analyses of the outbreak of HPAI H5N1 from December 2003 to March 2004. The three New Zealand studies deal with issues related to the development of effective surveillance strategies for HPAI — informed both directly and indirectly by the findings from the Vietnamese studies. This approach provides an example of how 'lessons' learnt from countries that have experienced large scale infectious disease epidemics can be used to assist in the design of surveillance activities in (as yet) unaffected countries.

The descriptive analyses of the 2003 – 2004 outbreak of HPAI H5N1 in Vietnam indicate that the epidemic was seeded simultaneously in the north and south of the country in the later part of 2003 with 87% of provinces affected by February 2004. HPAI risk was concentrated around the Mekong and Red River Deltas. The broad scale spatial distribution of disease is likely to have been associated with regional differences in the poultry farming, trade in poultry, and environmental conditions such as the presence of bodies of water which would support reservoir species for the virus. A Bayesian zero-inflated Poisson regression model was used to quantify the influence of environmental and demographic factors on the spatial distribution of HPAI positive communes. In areas where disease was reported, our results show that HPAI risk was positively associated with the presence of irrigation and negatively associated with elevation. After controlling for these fixed effects, a single large area of elevated risk in the Red River Delta area was identified, presumably arising from similarities in the likelihood of reporting disease or the presence of factors increasing disease transmission and spread. Further investigations to elucidate likely transmission mechanisms, targeting this area of the country, would be a profitable area of future research.

The second part of this thesis presents three studies that address issues related to the development of effective surveillance strategies for HPAI in New Zealand. The first was a cross-sectional study to enumerate the prevalence of backyard poultry ownership in two areas (one urban and the other rural) close to a large provincial city in the North Island of New Zealand. The prevalence of poultry ownership was 2% (95% CI 1% – 4%) in the urban area and 19% (95% CI 12% – 30%) in the rural area. The relatively low numbers of land parcels where poultry are present indicates that these areas, in the event of an infectious disease incursion, would be unlikely to pose a risk for spread of infectious agent.

A cross-sectional survey of all members of the Poultry Industry Association of New Zealand was conducted in the later half of 2007. Respondents were asked to document contacts made with other enterprises related to feed, live birds and hatching eggs, table eggs and poultry product, and waste litter and manure. Patterns of contact were analysed using social network analyses. Each of the four networks had scale-free properties, meaning that for each movement type there were small numbers of enterprises that had contacts with large numbers of enterprises (potential 'super-spreaders' of disease). The presence of an undetected infectious disease in enterprises with super-spreader characteristics increases the likelihood that an epidemic will propagate rapidly through the population, assuming there is a directly proportional relationship between the number of contacts an enterprise makes and the probability that disease will be transferred from one location to another. While the finding that feed suppliers had large numbers of poultry farm contacts in the feed network came as no surprise, what was of greater interest was that there were small numbers of poultry farms that reported off-farm movements of feed. This should serve as an important reminder for disease control authorities: movement (and other) restrictions applied during the course of an animal health emergency should be applied across a range of industry sectors, recognising that some industry participants may practice activities that are not entirely typical for their enterprise type (e.g. poultry farms on-selling feed to other farms). In the absence of perfect and up-to-date network data, knowledge of the characteristics of individual enterprises that render them more likely to be atypical (e.g. size, type, and geographic location) would be of value, since this information could be used to inform a risk based approach to disease surveillance and control.

A scenario tree model was developed as an approach for evaluating the effectiveness of New Zealand's passive surveillance system for HPAI. The model was developed in two stages. In the first, factors thought to influence the geographic distribution of NAI risk of introduction and spread (and therefore surveillance strategy) were combined to create a spatial risk surface. In the second stage, a scenario tree model of the passive surveillance system for NAI was developed using the spatial risk surface and the HPAI surveillance

strategy prescribed by Biosecurity New Zealand. The model was most sensitive to farmers reporting the presence of suspected cases of disease. This implies that the sensitivity of the system as a whole stands to increase if the importance of reporting suspicious clinical signs is reiterated to poultry producers.

The studies presented in this thesis have presented a range of techniques and methodological approaches that are sufficiently generic to be used in any country to inform the design of surveillance strategies for a variety of animal diseases, not just those of poultry. Although epidemiology, as a discipline, is endoured with a vast range of analytical techniques that can be used to enhance the understanding of factors influencing the spread of disease among animal populations, the quality of data used to support these techniques is often lacking. The challenge in the years ahead, for both developed and developing countries, is to set in place the appropriate infrastructures to collect details of animal populations consistent in quality over time and space.

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Nomenclature

AC-EIA	Antigen-capture enzyme immunosorbent assays
AGID	Agar gel immunodiffusion
AHSM	Animal Health and Surveillance Management system
AIDS	Acquired immune deficiency syndrome
AMLS	Animal Movement Licensing System
ASF	African swine fever
BOSSS	The Bovine Syndromic Surveillance System
BSE	Bovine spongiform encephalopathy
CIRAD	The French Agricultural Research Centre for International Development
CSF	Classical swine fever
CTS	Cattle Tracing System
DAH	Department of Animal Health (Vietnam)
DCS	Disease Control System
Defra	Department for Environment Food and Rural Affairs (United Kingdom)
DIVA	Differentiating Infected from Vaccinated Animals
DP-DCS	The Diseases of Poultry Disease Control System
DSM-4	The Diagnostic and Statistical Manual of Mental Disorders
ELISA	Enzyme linked immunoabsorbent assay
EMPRES	Emergency Prevention System for Transboundary Animal and Plant Pests and Diseases
EU	European Union
FAO	Food and Agriculture Organization of the United Nations
FMD	Foot-and-mouth disease
GLEWS	The Global Early Warning and Response System
GPHIN	The Global Public Health Intelligence Network
GOARN	The Global Outbreak Alert and Response Network
HA	Haemmaglutinin

HI	Haemmaglutinin inhibition test
HPAI	Highly pathogenic avian influenza
ICAHMS	Computerised Animal Health Monitoring System (Israel)
INRA	The National Institute for Agriculture Research (France)
LAMP	Loop mediated isothermal amplification
LPAI	Low pathogenic avian influenza
MAF	Ministry of Agriculture and Forestry
NA	Neuraminidase
NASBA	Nucleic acid sequence-based amplification
NAHIS	National Animal Health Information System (Australia)
NAI	Notifiable avian influenza
ND	Newcastle disease
NI	Neuraminidase inhibition test
NLIS	National Livestock Identification System for Cattle
OIE	World Organization for Animal Health
OR	Odds ratio
POC	Point-of-care
RADAR	Rapid Analysis & Detection of Animal-Related Risks
R_0	Basic reproductive ratio
RRT-PCR	Real-time polymerase chain reaction
RT-PCR	Reverse transcriptase polymerase chain reaction
RSVP-A	The Rapid Syndrome Validation Project – Animal
SARS	Severe acute respiratory syndrome
SGS	El Sistema de Gestin Sanitaria
Sisbov	The Bovine Identification and Certification System (Brazil)
SND	Scrapie Notification Database
SNIG	El Sistema Nacional de Información Ganadera (Uruguay)
SPS	Sanitary and phytosanitary measures
TVD	The National Movement Database Tierverkehrsdatenbank (Switzerland)
vCJD	variant Creutzfeldt-Jakob disease
VetPAD	The Veterinary Practitioner Aided Disease system
WAHID	World Animal Health Information Database

WHO   World Health Organization

WNV   West Nile virus

WTO   World Trade Organization

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List of Publications

Lockhart CY, Stevenson MA, Hoang Van Nam, Lai Thi Kim Lan, Jackson R, Morris R, French NP (2006) Descriptive epidemiology of the outbreak of highly pathogenic avian influenza in Vietnam, December 2003 to February 2004. In: *Proceedings of the 14th FAVA Congress and the Food Safety & Biosecurity, and Epidemiology & Animal Health Management Branches of the New Zealand Veterinary Association*, Foundation for Continuing Education Publication Number 253, VetLearn Foundation, Palmerston North, New Zealand, 179 – 192.

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Introduction

The recent unprecedented spread of highly pathogenic avian influenza (HPAI) H5N1 across three continents as well as the emergence and spread of diseases such as foot-and-mouth disease (FMD), bovine spongiform encephalopathy (BSE), rabies, severe acute respiratory syndrome (SARS), monkey pox, and Nipah virus has caused concern for animal health authorities throughout the world. A response to these concerns has been acknowledgement of the need for effective surveillance strategies to allow incursions of known and emerging disease syndromes to be detected and managed promptly. Effective surveillance should reduce production losses associated with disease outbreaks and, in the case of zoonotic diseases, limit threats to human health.

This thesis presents an approach for designing effective surveillance strategies for animal diseases taking as example insights gained from an outbreak of highly pathogenic avian influenza (HPAI) in Vietnam to inform surveillance requirements in New Zealand, a country that is currently free of the disease. The Vietnamese outbreaks of HPAI in early 2004 is representative of the situation in which lack of knowledge of the distribution of disease risk factors together with inadequate surveillance infrastructure can result in undetected entry and uncontrolled spread of disease impeding proper management. It is also representative of the constant threat of spread presented by the Southeast Asian region to New Zealand, therefore an understanding of the disease epidemiology in the region is important. Lessons learnt from such an outbreak gives insight into risk factors that a country like New Zealand needs to focus on in order to prevent entry and subsequent spread of disease. Given knowledge of the factors involved in the epidemiology of the disease in Vietnam, animal health authorities in New Zealand can then focus on information that is lacking (e.g. location of the population at risk) and what needs to be done to ensure early

detection of the disease or in the case of entry, to rapidly curtail spread. In the various chapters presented in this thesis a number of methods have been used towards this end and will focus primarily on highly pathogenic avian influenza due to H5/H7 subtypes.

This thesis is presented as a series of papers prepared for publication. Each chapter represents the stage of preparation each paper has reached at the date of thesis submission. Chapter 2 provides a review of avian influenza in terms of its epidemiology, pathogenesis, clinical findings, diagnostic features, and control and prevention. Chapter 3 reviews current concepts relating to surveillance for animal diseases. Particular emphasis is given to electronic surveillance tools which are a cost-effective (if not overly sensitive) means for monitoring official and unofficial sources of disease outbreak information. The reviews presented are not intended to be exhaustive, rather to provide a context and background for the research chapters that follow.

Building on the concepts and issues raised in each of the reviews Chapter 4 provides a descriptive analysis of the epidemic of HPAI H5N1 that occurred in Vietnam from December 2003 to March 2004. The data for these analyses were derived from a survey conducted by the Vietnamese Department of Animal Health in May 2004. A feature of this data set is that outbreak details are missing for 3 of the 57 provinces that were surveyed. Attempts were made to account for this using a Bayesian imputation approach informed by spatial autocorrelation. In Chapter 5 regression analyses are applied to the same data set to quantify the effect of factors influencing the spatial distribution of HPAI-positive communes during the 2003 – 2004 outbreak. A regular grid was applied across the teritorial boundaries of Vietnam and the outcome variable expressed as the number of HPAI-positive communes within each cell of the grid divided by the total number of communes present in each cell. Due to the relatively large number of grid cells that contained communes where HPAI was not reported, regression coefficients were estimated using a Bayesian zero-inflated Poisson model accounting for spatial autocorrelation. Chapter 5 provides useful information in terms of understanding factors influencing the spatial distribution of HPAI. Firstly, it allows the effect of risk factors for HPAI to be quantified. Secondly, it allows areas of the country where HPAI risk is elevated to be identified, controlling for the fixed effects included in the model. This implies that additional (as yet unidentified) effects are at work in these areas, resulting in the observed disease risk in these areas being greater than that estimated from the modeled fixed effects alone. This

information is of use for Vietnamese animal health authorities — investigative effort can be applied to these elevated risk areas to elucidate additional component causes of disease. For countries which are HPAI free, knowledge of factors causally or non-causally associated with the presence of disease are of use in terms of facilitating an evidence-based approach to the design of surveillance programs.

Chapters 6 to 8 present a series of studies that address issues related to the development of effective surveillance strategies for HPAI in New Zealand, which, at the time of writing, is free of disease. At this point it should be pointed out that the spectrum of issues addressed in the second part of the thesis have been directly or indirectly informed by the findings presented in Chapters 4 and 5. This provides an example of how the 'lessons' learned from countries that have experienced epidemics can be used to assist in the design of surveillance activities in unaffected countries.

In Chapter 6 a methodological approach for addressing an important issue for effective HPAI surveillance is presented: enumerating the spatial distribution of the non-commercial poultry population at risk. Two areas close to a large provincial city in the North Island of New Zealand were selected. The first in an area classified as urban and the second in an area classified as rural. A cross-sectional study was conducted to determine the proportion of land parcels where domestic poultry are kept. For those land parcels where birds were kept, details of the numbers of individual birds present and how they were managed were solicited from survey respondents.

In Chapter 7 a cross-sectional survey was conducted to identify patterns of movement within the commercial sector of the New Zealand poultry industry. The motivation for this work was a need to enhance understanding of how infection (not necessarily HPAI) might move from one enterprise to another via the movement of feed, poultry (or poultry product), and/or waste. Social network analyses were applied to these data, allowing individual poultry enterprises within the network to be ranked in terms of their 'connectedness', that is, their ability to facilitate infection spread throughout the network, if it was present.

Up to this point of the thesis emphasis has been placed on the analysis of accumulated data and how the results of these analyses may be used to inform particular components of a HPAI surveillance strategy. Chapter 8 represents a change in research direction where a methodology is developed to quantify the effectiveness of an existing surveillance sys-

tem, New Zealand's passive surveillance strategy for HPAI. The approach here follows the scenario tree approach described by Martin, Cameron & Greiner (2007) and Martin, Cameron, Barfod, Sergeant & Greiner (2007). A novel feature of Chapter 8 is that a geographical HPAI incursion and spread risk assessment has been conducted on the land area of New Zealand, allowing the country to be arbitrarily classified into low, medium, and high HPAI risk zones.

Chapter 9 draws all of the concepts identified in Chapters 2 to 8 together, in attempt to develop general conclusions regarding surveillance for animal disease and the infrastructure required by animal health authorities to conduct these activities in a cost effective and efficient manner.

CHAPTER **2**

Literature review: avian influenza

2.1 Introduction

Avian influenza is an acute, highly contagious disease with a predilection for the respiratory, digestive and nervous systems of a variety of both domestic and wild bird species (Alexander 2000, Swayne & Suarez 2000). Over the last decade, avian influenza has emerged as an animal disease of concern for veterinary and human health organisations across the world (Jutzi 2005, World Health Organization 2006). This is primarily because of its ability to cause illness and death in poultry and humans, disrupt poultry trade, threaten the food security of resource-poor countries and the high costs associated with control measures (Horimoto & Kawaoka 2001, Campitelli et al. 2002, McLeod et al. 2004). The main epidemiological features of avian influenza that contribute to these concerns include the large number of possible virus strains, the presence of a wild bird virus reservoir which represents a constant, uncontrollable source of infection and, the inherent ability of the virus to convert to high virulent strains once it is transmitted to other species as a result of mutation or reassortment. Adding to these complexities, infection with avian influenza viruses produces variable clinical manifestations that are often indistinguishable from endemic poultry diseases (Swayne & Suarez 2000, Elbers et al. 2007). In domestic poultry, the disease presents in two clinical forms: low pathogenic avian influenza (LPAI) which is generally associated with recent introduction of viruses from a wild bird reservoir, and a more severe form, highly pathogenic avian influenza (HPAI), associated with viruses of the H5 and H7 subtypes that have acquired virulence as a result of adaptation (Swayne & Suarez 2000).

2.2   Aetiology

The viruses that cause avian influenza belong to the influenza A genus of the *Orthomyx-oviridae* family of viruses (Webster et al. 1992). This family contains five genera: Influenzavirus A, Influenzavirus B, Influenzavirus C, Thogotovirus (tick-borne viruses which may infect humans) and Isavirus, associated with infectious salmon anaemia (Anonymous 2006*c*). Influenza A is an enveloped virus comprised of eight segments of single stranded RNA molecules which are responsible for encoding the ten structural viral proteins. These include three surface proteins haemagglutinin (HA), neuraminidase (NA) and matrix protein (M2); the three transcriptases PB1, PB2, and PA proteins; one matrix protein M1; one nucleocapsid protein; and two non-structural proteins NS1 and NS2. Identification of avian influenza A is primarily based on identifying the matrix and nucleocapsid protein structures of the virus. Of these proteins, haemagglutinin is considered to be the major determinant of virulence (Senne et al. 1996, Perdue et al. 1997) and therefore the severity of clinical signs and immune response (Easterday et al. 1997).

2.2.1   Strain classification

Influenza A viruses are classified into subtypes based on the haemagglutinin and neuraminidase surface proteins present. Currently 16 HA subtype (H1 – H16) and nine NA subtypes (N1 – N9) have been documented, all obtained primarily from wild aquatic bird isolates (Hinshaw et al. 1982, Kawaoka & Webster 1985, Fouchier et al. 2003, Olsen et al. 2006). Influenza A viruses are further differentiated into high and low pathogenic types on the basis of the severity of disease in susceptible poultry and/or the presence of multiple basic amino acids at the precursor sites of the haemagglutinin protein of virus isolates. Routine tests conducted on virus isolates obtained from wild bird surveillance and outbreaks caused by avian influenza viruses indicate that low pathogenic viruses may include all possible combinations of the 16 haemagglutinin and 9 neuraminidase surface proteins, while HPAI has been associated solely with influenza A viruses containing the H5 and H7 antigens (Swayne & Suarez 2000).

Irrespective of pathogenicity, the accepted international nomenclature for influenza virus strains in animals include the type, the host, the geographic location, strain number, year and details of the haemagglutinin and neuraminidase antigens. For example, A/Chicken/Scotland/59

(H5N1) refers to a H5N1 influenza strain isolated from chicken isolates in Scotland in 1959.

2.2.2 Official classification

The OIE defines notifiable avian influenza (NAI) as any infection of poultry caused by influenza A viruses containing the haemagglutinin antigens H5 or H7, irrespective of pathogenicity (Anonymous 2007*a*). This definition was recently introduced to address concerns related to the ability of low pathogenic H5 and H7 strains to mutate to high pathogenic strains in domestic poultry (Capua & Alexander 2004). Thus, NAI includes both low pathogenic avian influenza and high pathogenic avian influenza. Specifically, NAI HPAI is defined as an infection caused by any influenza A virus meeting one of the following diagnostic criteria: (1) an isolate with an intravenous pathogenicity index of greater than 1.2 in 4 – 8 week old chickens, (2) an isolate that causes greater than 75% mortality or death within 10 days of inoculation in 4 – 8 week old chickens and/or, (3) an infection with influenza A viruses of H5 or H7 subtype for which nucleotide sequencing has demonstrated the presence of multiple basic amino acids at the cleavage site of the haemagglutinin. Similar definitions have been adopted by the European Union (Council of the European Communities 2005).

2.3 Epidemiology

The natural state of avian influenza viruses is the LPAI condition in wild reservoir hosts in which limited clinical disease occurs (Webster et al. 1992). Transmission of these viruses from their natural host to other species such as poultry is considered an important means through which virulence is acquired, though this does not always occur. The question of what mechanisms are involved in conversion to virulence has puzzled researchers, and the issue remains largely unresolved. Various hypotheses have been proposed. Conversion to virulence is considered to be a genetic trait of the virus, together with the presence of conditions that exert selective pressure for higher virulence (Garcia et al. 1996, Perdue et al. 1997). The most widely accepted view is that HPAI viruses emerge as the result of mutational changes that occur in LPAI viruses of the H5 and H7 subtypes that are in-

troduced to domestic poultry from their reservoir hosts as a means of adaptation to the new host (Garcia et al. 1996, 1997, Perdue et al. 1997). These changes may result from insertions or substitutions of nucleotides at the virus cleavage sites of the virus HA protein (point mutations or antigenic drift) or recombination (reassortment or antigenic shift) with other viruses (Perdue et al. 1997, Ito et al. 2001, Suarez et al. 2004). This theory is based on the fact that the introduction of LPAI viruses into domestic poultry from wild reservoir species increases the evolutional rate of these viruses with subsequent increase in virulence, pathogenicity and host adaptation (Garcia et al. 1997). Therefore, conditions that favour genetic changes in the virus via antigenic shift (mutation) and drift (reassortment) are most likely to favour the emergence of HPAI viruses. The natural tendency for influenza viruses to regularly undergo point mutations, an inherent characteristic of RNA viruses, means that new viruses are continually being produced, with differences in genetic fitness (Horimoto & Kawaoka 2001). Conditions that exert selective pressure on circulating viruses at both the host and population level act to increase the rate of mutation of viruses and therefore favour the appearance and establishment of dominant virus strains (Ferguson et al. 2003). Thus, intensive poultry production systems in which a continuous and easily accessible source of susceptible hosts are present are considered prime conditions under which pathogenicity may emerge. Other cited conditions have been the inadequate use of vaccinations or incomplete vaccination coverage that have allowed field strains to reassort with vaccinal strains (Escorcia et al. 2008). Examples of situations in which changes in virulence of been demonstrated include the outbreaks due to HPAI H7N3 in Canada (Pasick et al. 2005), HPAI H7N3 in Chile (Rojas et al. 2002, Suarez et al. 2004) and Italy (Capua & Marangon 2000, Capua, Marangon, dalla Pozza, Terregino & Cattoli 2003). The appearance of LPAI in domestic poultry does not always result in changes in pathogenicity. Examples of outbreaks in which LPAI H5 and H7 have occurred without any signs of conversion to virulence include outbreaks due to LPAI H7N3 in Oregon in 1971 (Beard & Helfer 1972), LPAI H5N2 in Japan from 2005 to 2006 (Okamatsu et al. 2007), LPAI H7N2 in Pennsylvania from 1996 – 1998 (Davison et al. 2003) and LPAI H5N2 in Taiwan (Capua & Alexander 2004). As a result of uncertainty around whether or not conversion to virulence conversion will occur, the decision to make all identified cases of avian influenza involving H5 and H7 reportable is well founded.

Although it is well accepted that the presence, or absence, of multiple basic amino acids at

the HA cleavage site is a key factor in determining virulence, it has been shown that other 7 genes are also important (see (Basler & Aguilar 2008) for a review). Recent studies have shown that the HPAI H5N1 viruses currently found circulating on three continents (from the goose Quandong lineage), carry only the HA gene from its H5N1 Gs/GD/1/96 lineage whilst the remaining 7 genes were acquired from other avian influenza viruses through genetic reassortment (Zhao et al. 2008). This implies that a number of different H5N1 virus strains/clades could potentially co-circulate in a region with possible emergence of new viruses with varying levels of virulence as have been shown in Vietnam (Wan et al. 2008) and Africa (Ducatez et al. 2007).

2.3.1 Host range

Wild birds, domestic birds and a number of mammalian species may be affected by avian influenza viruses. Natural infection with LPAI viruses have been reported in wild birds from the Anseriform (water fowls, ducks, swans) and Charadriform (shore birds and gulls) genus (Webster et al. 1992, Olsen et al. 2006) which have resulted in these species generally being regarded as reservoir hosts. This is because most viral subtypes have been repeatedly isolated in these birds (Webster et al. 1992, Fouchier et al. 2003) without clinical disease (Horimoto & Kawaoka 2001).

Surveillance and experimental studies provide evidence for the varying susceptibility of a wide range of domestic and captive birds to influenza viruses. A review undertaken by Alexander (2000) cite the range of susceptible species. These include wild birds, caged pets, domestic poultry, commercial ducks, geese, quail, turkeys and guinea fowls. Other birds from which viruses have been isolated include pheasants, mynah birds, passerines, partridges and psittacines (parrots, parakeets and budgerigars). Amongst the domestic avian species, turkeys have been the species most frequently affected by avian influenza outbreaks. The higher incidence of outbreaks among turkeys has been attributed to periodic introductions from migrating birds and the fact that most turkey farms are operated under open range systems. Prior to 2000, very few reports of HPAI in wild birds were reported. Since 2000 outbreaks involving H5N1 virus in 126 wild bird species from 15 orders have been reported. A list of wild birds affected by the H5N1 HPAI is provided by

the United States Geological Survey.[1]

Mammals are regarded as aberrant hosts for avian influenza. A number of species may be infected including horses, pigs, whales and seals. Current thinking indicates that this host range is expanding to include cats, leopards, civets, and dogs (Keawcharoen et al. 2004, Thanawongnuwech et al. 2005, Amonsin et al. 2006, Songserm et al. 2006, Yingst et al. 2006, Amonsin et al. 2007). Natural infections of H5N1 have occurred in humans in Hong Kong in 1997 (Claas et al. 1998, Yuen et al. 1998), Southeast Asia between 2003 and 2007 (Chen et al. 2007), and Egypt from 2006 to 2008 (reviewed in Uyeki, 2008). At the time of writing the WHO estimates the total number of human cases of the H5N1 to be 385 in 15 countries (World Health Organization 2008).

2.3.2   Geographic distribution

Since 1959 outbreaks of disease due to NAI viruses in domestic poultry have occurred in most regions of the world, with higher reporting frequencies in Europe, North America and, more recently, Asia. Table 2.1 provides details of NAI outbreaks reported since 1959. The spatial distribution of these outbreaks have coincided with the distribution of highly dense poultry growing areas (Capua, Marangon, dalla Pozza, Terregino & Cattoli 2003, Power 2005), live bird marketing systems (in the USA, Hong Kong, and Southeast Asia, Senne et al., 2003, Sims et al. 2003), duck rearing systems integrated within rice growing agricultural systems (e.g. Southeast Asia, Tiensin et al. 2005), large unregulated backyard bird populations (Egypt and Turkey, Alexander 2007, Meleigy 2007), and in countries along wild bird migratory pathways (e.g. Russia and the Ukraine, Anonymous 2008*e*). Of the major poultry producing countries throughout the world, Brazil is the only country to date that has not reported an outbreak of NAI.

On the American continent, outbreaks have occurred in Canada, the USA, Mexico, Guatemala, Nicaragua, Chile, Haiti and the Dominican Republic. Viruses reported in the Central American countries included LPAI H5N2, largely thought to have originated from Mexico and a HPAI variant of H5N2 that occurred in Mexico between 1994 and 1995 (Table 2.1). In Chile, a LPAI H7N3 virus mutated to the HPAI form in 2002 (Suarez et al. 2004). Birds were culled and, at the time or writing, there have been no further outbreaks re-

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[1] http://edc.usgs.gov/products/elevation/gtopo30

ported. In the Caribbean, LPAI H5N2 viruses have occurred in the Dominican Republic and Haiti in 2007 and 2008, respectively. The outbreaks in Haiti occurred in three geographically distinct areas in fighting cocks, thought to be associated with illegal trade ProMED-mail (2008). In Canada both HPAI and LPAI viruses have been reported in chickens and turkeys and have included a variety of virus subtypes, namely: HPAI H5N9 in 1966, LPAI and HPAI H7N3 in 2004 and HPAI H7N3 in 2007. In the USA outbreaks due to NAI have been reported sporadically between 1984 and 2004. Reports of subtypes causing outbreaks include LPAI H5N2 from 1983 to 1985, and LPAI H7N2 in Pennsylvania, Virginia, Connecticut, Delaware and Maryland from 1996 to 2003 (Senne 2007). The last reported outbreak in the USA was in 2004. It was caused by a HPAI H5N2 subtype in broilers in Texas (Lee, Swayne, Linares, Senne & Suarez 2005, Pelzel et al. 2006). Avian influenza outbreaks in the USA have been attributed to contact with wild birds and live bird markets (Panigrahy et al. 2002, Senn et al. 2005, Garber et al. 2007). The sole report of the H5N1 subtype in the USA was a LPAI virus detected in serum samples obtained from a turkey flock at slaughter in 2002 (Senne 2007). To date there have been no reports of infection due to H5N1 in domestic poultry on the American continent.

In Europe subtypes involved in HPAI outbreaks included H5N2 in Italy and Belgium in 1997, H7N7 in Ireland in 1998, H5N9 in Italy in 1998, and H7N3 in Italy in 2003 (Table 2.1). Outbreaks in Italy have mostly occurred in poultry dense areas (Capua & Marangon 2000, Marangon et al. 2003).

In Asia, although numerous incursions of HPAI H5N1 occurred between 1996 and 2008 (Table 2.1), other virus subtypes have caused significant outbreaks including H7N3 in Pakistan in 1995, H5N2 in Pakistan, Taiwan, South Africa and Japan in 2001, 2001, 2004, and 2005, respectively. HPAI H5N1 virus was first isolated from outbreaks of avian influenza in Hong Kong in 1996 in which both poultry and humans were affected (Claas et al. 1998). Genetically similar viruses were associated with outbreaks that occurred in eight Southeast Asian countries between 2003 and 2004 (Chen et al. 2006, Wang et al. 2008). Since then, H5N1 has become endemic in the region, occurring between the months of December and March in most countries. This subtype has become notable on account of its ability to infect wild aquatic birds and humans (Ellis et al. 2004, Li et al. 2004).

Australia, New Zealand, and the Pacific Islands have been least affected by avian influenza

viruses. In Australia outbreaks of H7N7 occurred in 1976 and 1986, H7N3 in 1992, and H7N4 in 1997 (Capua & Alexander 2004). New Zealand, in contrast, has never reported outbreaks due to avian influenza, but have isolated 2 LPAI H5N2 viruses in 2001 (Stanislawek et al. 2002), and one H7 subtypes between 2004 and 2006 (Tana et al. 2007) in wild ducks. The low incidence of avian influenza in Asia-pacific region compared to other areas may be reflective of the geographic isolation that limits the migration of wild birds or the biosecurity strategies (including surveillance) adopted. Few wild birds (especially water fowls), likely to spread disease migrate annually to the region, limiting the possibility of spread of avian influenza viruses such as H5N1 into the region. New Zealand and Australia are known to have well established border security and animal surveillance systems that are likely than not to detect the presence of avian influenza if it was present.

A number of factors may limit the ability to extrapolate assumptions about the epidemiology of avian influenza, particulary the H5N1 virus subtype, from one country to another. The occurrence of multiple H5N1 subtype clades circulating on three continents around the world (Anonymous 2008*d*), differences in diagnostic capacity and reporting rates between and within countries are three such factors. Previous studies have shown that H5N1 clades appear to be spatially and temporally distributed with certain clades remaining localised (in space and time), whilst others are more widely distributed, reflecting the possible modes of virus spread (movement of viruses via wild birds and poultry trade). For example, Wan et al. (2008) found that certain clades were predominant in the north, compared to the south of Vietnam, potentially associated with co-circulation of particular groups of viruses, whilst certain clades remained localised to Southeast Asian countries like Vietnam, Laos, Cambodia, Thailand, China until 2005 (Smith et al. 2006) and other clades which emerged in China after 2005 spread via wild birds to over 30 countries in Asia, Africa and Europe (Salzberg et al. 2007). These studies have also shown that clades behave in different ways in different areas and that one strain of the virus may not demonstrate the same rate of spread or the same degree of virulence in poultry or wild birds. Kim et al. (2008) showed that although four dominant clades from Asia isolated between 2004 and 2006 caused highly pathogenic influenza signs in ducks, there were differences in mortality and the degree of extent of clinical signs observed. The lack of ability to confirm the cause of disease(s) in poultry (common in rural areas of developing coun-

tries) as well as differences in reporting rates between areas (i.e. countries or regions) are important limiting factors. It is necessary that a clear distinction is made between virus isolation from birds (wild or domestic) which may or may not cause clinical disease and, confirmed clinical cases of avian influenza that may result from notifiable highly pathogenic strains or strains that are not notifiable (e.g. H9, H1) but cause disease (that may mimic clinical signs of pathogenic strains) in the presence of concurrent bacterial infections and environmental stress. Differences in reporting of outbreaks between H5N1 countries affected countries have been cited (Morris & Jackson 2005) which makes it difficult to obtain details on the epidemiological picture in certain countries.
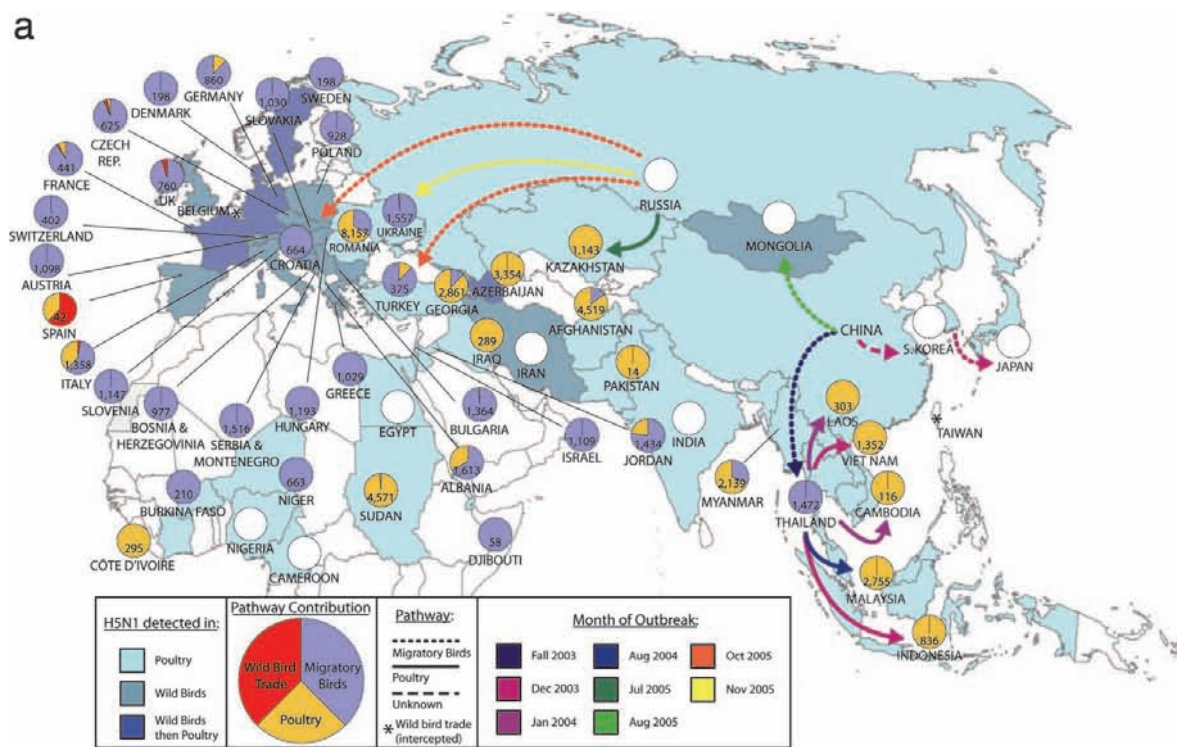
Figure 2.1: Spread of HPAI H5N1 in Asia, Europe and Africa 2003 – 2005. Reproduced from Kilpatrick et al. (2006).

Table 2.1: Details of outbreaks of notifiable avian influenza between 1959 and 2009. Adapted from Capua & Alexander (2004), Alexander (2007) and Anonymous (2008*e*).

Year	Country	Subtype	Species affected
1959	Scotland	H5N1	Chickens
1963	England	H7N3	Turkeys
1966	Canada	H5N9	Turkeys
1976	Australia	H7N7	Chickens, ducks
1979	Germany	H7N7	Chickens, geese
1979	England	H7N7	Turkeys
1983 – 1985	USA	H5N2	Various
1983	Ireland	H5N8	Turkeys
1985	Australia	H7N7	Chickens
1991	England	H5N1	Turkeys
1992	Australia	H7N3	Chickens, ducks
1994 – 1995	Mexico	H5N2	Chickens
1995	Australia	H7N3	Chickens
1995	Pakistan	H7N3	Chickens
1997	Hong Kong	H5N1	Poultry and waterfowls
1997	Australia	H7N4	Chickens, emus
1997	Italy, Belgium	H5N2	Poultry
1998	Ireland	H5N7	Poultry
1998	Italy	H5N9	Poultry
1999 – 2000	Italy	H5N2	Chickens
2001 – 2004	Pakistan	H5N2	Poultry
2002	Chile	H7N3	
2003	Netherlands	H7N7	Chickens
2003	Italy	H7N3	Poultry
2004	Canada	H7N3	Chickens
2004	USA	H5N2	Chickens
2004	Taiwan	H5N2	Poultry
2004	South Africa	H5N2	Ratites, chickens
2004 – 2007	China	H5N1	Chickens, ducks

Table 2.1 (continued)

Year	Country	Subtype	Species affected
2004 – 2007	Hong Kong	H5N1	Wild birds
2004	Cambodia, Thailand	H5N1	Poultry
2004 – 2006	Indonesia	H5N1	Poultry
2005	Zimbabwe	H5N2	Ostriches
2005	Japan	H5N2	Poultry
2005 – 2006	Croatia	H5N1	Swans
2006	Niger, Sudan	H5N1	Poultry
2006 – 2008	Nigeria	H5N1	Poultry, ostriches
2006	Denmark	H5N1	Swans, buzzards
2006 – 2007	Ivory Coast, Djibouti	H5N1	Backyard poultry
2006	Egypt	H5N1	Chickens
2006	Greece	H5N1	Wild birds
2006 – 2007	France, Germany	H5N1	Wild ducks, wild birds
2006 – 2007	Czech Republic, Hungary, India	H5N1	Chickens
2007	Turkey	H5N1	Chickens, ducks, turkeys, pigeons
2007	United Kingdom	H5N1	Turkeys
2007	Korea, Laos, Thailand, Vietnam	H5N1	Ducks
2007	Kuwait, Saudi Arabia	H5N1	Ostrich
2007	Middle East, Southeast Asia	H5N1	Chickens
2007	Japan	H5N1	Wild birds
2007	Hungary	H5N1	Geese
2007	Canada	H7N3	Backyard poultry
2007	Ghana	H5N1	Poultry
2008	Korea	H5N1	Poultry
2008	India, Iran	H5N1	Backyard poultry
2008	Israel	H5N1	Chickens, ducks, pigeons
2008	Laos, Korea, Thailand, Togo	H5N1	Poultry
2008	Switzerland	H5N1	Wild birds
2008	Ukraine	H5N1	Wild birds
2008	Hong Kong, Japan	H5N1	Wild birds

Table 2.1 (continued)

Year	Country	Subtype	Species affected
2008	Thailand, Turkey	H5N1	Poultry , backyard poultry
2008	Turkey	H5N1	Backyard poultry
2008	United Kingdom	H5N1	Wild birds
2008	Vietnam	H5N1	Civets

2.3.3 Virus survival in the environment

Successful transmission of virus from infected to susceptible hosts is determined in part by persistence of the virus in the environment. Knowledge of virus persistence forms the basis of biosecurity measures aimed at preventing or eliminating disease transmission. Influenza viruses are generally unstable in conditions of extreme pH and heat but are able to survive for long periods in cold or moist conditions.

The persistence of the virus in water (an important environment of the natural host) is considered critical for virus transmission within wild water bird populations (Webster et al. 1978, Hinshaw et al. 1980, Stallknecht, Kearney, Shane & Zwank 1990) and has been shown to vary with temperature, pH and salinity (Stallknecht, Shane, Kearney & Zwank 1990, Brown et al. 2007). Under field conditions virus has been shown to survive in river water at 4° Celsius for 32 days and at 22° Celsius for 4 days (Webster et al. 1978). Stallknecht, Shane, Kearney & Zwank (1990) showed that virus could survive for 102 days in distilled water at 28° Celsius.

Avian influenza viruses have been shown to survive on a number of fomites and objects associated with poultry farming. Tiwari et al. (2006) investigated the survival times of avian influenza viruses on a number of materials and objects routinely found on poultry farms (Table 2.2). These authors showed that virus could survive for up to 6 days in latex and feathers. A study by Brown et al. (2007) demonstrated virus survival for up to 35 days in faeces at 4° Celsius and 6 days at 37° Celsius. The same study demonstrated virus survival for up to 105 days in liquid manure.

Under field conditions, nasal secretions and faecal material protect avian influenza viruses, increasing their resistance to chemical and physical deactivation. In the absence of organic matter they are readily deactivated by oxidising agents, dilute acids, hydroxylamine

and quaternary ammonium disinfectants. In the presence of organic matter they are deactivated by compounds such as formaldehyde and beta-propiolactone. Avian influenza viruses are easily inactivated at temperatures of $56°$ Celsius for three hours or $60°$ Celsius for 30 minutes. A study by Lu et al. (2003) showed that virus in manure was inactivated in less than 7 days under ambient temperatures of $15 - 20°$ Celsius. Under conditions of pH 2 and $56°$ Celsius virus was destroyed within 30 minutes.

Table 2.2: Survival times of avian influenza viruses on different fomites. Adapted from Tiwari et al. (2006).

Material	Survival
Steel	72 hours
Latex	6 days
Wood	48 hours
Tire	72 hours
Egg trays	0 hours
Egg shell	0 hours
Feathers	6 hours
Cotton fabric	24 hours
Polyester fabric	0 hours

2.3.4   Occurrence of virus in infected tissues

The presence, duration and concentration of virus in excretions, secretions and tissues of infected birds determines the role of each as a means by which virus can be transmitted from one host to another. These features depend on the type of virus, its preferred replication site and the host species involved. LPAI viruses replicate preferentially in the epithelial tissue of the respiratory and gastrointestinal tracts causing localised infections in these organs, with little or no evidence of viraemia or lesions in other tissues (Swayne & Beck 2005*a*). Thus, LPAI viruses are primarily concentrated in faeces and secretions from the upper and lower respiratory tracts of infected birds. In contrast, HPAI viruses begin initial replication in these organs and spread systemically to replicate in a number of organs including the brain, skin, and kidneys (Mo et al. 1997, Perkins & Swayne 2001, Swayne & Beck 2005*a*, Antarasena et al. 2006). In its natural host, the wild duck, infection with LPAI influenza viruses results in large amounts of virus excreted in the faeces for periods of up to 3 to 4 weeks, often accompanied by little or no clinical signs. The

quantities of virus released via this route can be as much as 10^{10} 50% egg infectious dose (EID_{50}) within the first 24 hours of infection (Webster et al. 1978). Tissue tropism of the LPAI virus in domestic poultry may vary, with some viruses preferring the respiratory over the intestinal tract or *vice versa* (Swayne & Beck 2005*a*). Observed replication periods range from 1 to 7 days with peak viral replication occurring on day 3 associated with viral titres of $10^{4.2}$ to $10^{5.5}$ EID_{50} per millilitre in respiratory samples (tracheal and oropharyngeal swabs). Because infection tends to be localised, LPAI viruses are usually not able to be isolated from muscle tissue (Swayne & Beck 2005*a*). HPAI virus appears in tissues anywhere from a few hours to 7 days post infection depending on the species of bird infected (Perkins & Swayne 2001). Virus has been isolated from muscle tissue (breast and thigh) from artificially infected birds (Mo et al. 1997, Perkins & Swayne 2001, Tumpey et al. 2003). In experimentally infected birds virus has been isolated between 1 to 5 days post infection with concentrations ranging from $10^{2.7}$ to $10^{3.2}$ EID_{50} per millilitre of blood (Swayne & Beck 2005*a*). Virus particles have also been shown to replicate in feather follicles of infected birds, implying that waste feathers are a possible route of infection (Yamamoto et al. 2008).

2.3.5 Between country spread

It is acknowledged that between country spread of influenza viruses may occur via trade in poultry and poultry product, movement of wild migratory birds, and trade in wild captive bird species (Olsen et al. 2006, Feare 2007). The relative importance of each of these routes has, and continues to be, a source of debate (Sturm-Ramirez et al. 2005, Butler 2006b, Normile 2006, Feare 2007). Moreover, in countries that experience influenza outbreaks, it is unlikely that the exact route of introduction and spread will be definitively identified due to scarcity of information relating to illegal movement of birds, limited capacity to investigate incursions, and delays in reporting disease incursions. Few studies have examined the role of each of these routes in the spread of avian influenza to unaffected countries. Thus, elucidation of the source and route of introduction of influenza viruses causing outbreaks around the world is increasingly reliant on the use of molecular techniques (Pillai et al. 2008, Wang et al. 2008) and remotely sensed data and spatial analyses to support anecdotal evidence arising from from outbreak investigations.

Of the outbreaks of avian influenza that have occurred, there are few examples of instances in which international or transboundary spread of virus has taken place. Of those reported in the literature, four outbreaks stand out: the H5N2 outbreaks in Central America in 1994 and 1995, the outbreaks of H7N7 that involved three countries in Europe, namely Belgium, The Netherlands and Germany in 2003 (Capua & Alexander 2004), the outbreaks of H5N1 in Southeast Asia from 2004, and the outbreak of H5N1 in the United Kingdom in 2006 (Defra 2007). Information regarding the sources of incursion for the outbreaks in El Salvador and Guatemala in Central America is lacking, but anecdotal evidence have implicated trade in poultry (Senne et al. 2003, Irvine et al. 2007) and wild birds (Anonymous 2008*b*) as the likely source.

Most data for quantifying the relative role of each route in the spread of Avian influenza comes from outbreaks that have occurred since 1996. Increasing access to data on poultry trade and the use of phylogenetic analysis of virus isolates has aided this process. Kilpatrick et al. (2006) attempted to put into perspective the relative contribution of each of the three routes to the spread of H5N1 influenza viruses around the world. These authors used data on country-to-country imports and exports of live poultry, trade in wild birds and data on migratory patterns and cold weather movements of wild Anatidae to determine the most likely pathway for H5N1 incursion into 52 countries in Asia, Africa and Europe. The response evaluated was the estimated risk associated with each of three pathways: wild birds, trade in poultry and trade in wild birds. The risk associated with each pathway was an estimate of the number of infectious bird days defined in terms of the product of the number of birds entering the country, the prevalence of H5N1 in each country and the number of days birds are likely to shed the virus. From these analyses (summarised in Figure 2.1) it was estimated that incursion of the H5N1 influenza virus to countries in Asia was most likely to have occurred through trade in poultry (9 of 21 incursions) and secondly by wild migratory birds (3 of 21 incursions). In Europe wild birds were most likely to have seeded infections (20 of 23 incursions) and in Africa both poultry and wild birds were equally likely to have seeded infection (2 of 8 and 3 of 8 incursions, respectively). Although the study of Kilpatrick et al. (2006) provides useful insight into the possible routes of entry, variations in the quality of the data used to inform this study means that the results are inherently prone to bias, the magnitude and direction of which is difficult to quantify.

Wild birds

The evidence to support the role of wild birds in primary disease incursion has been summarised by Alexander (2007) into four key areas: (1) higher prevalence of infection in poultry units located along migratory pathways of wild water fowls, particularly in turkey and chicken growing areas, (2) a higher level of infection in poultry kept under free range conditions, compared with those reared indoors, (3) similar virus subtypes causing infection in domestic poultry and wild water fowls in an outbreak area, and (4) seasonality in the occurrence of LPAI outbreaks associated with migration patterns of wild birds.

Keawcharoen et al. (2008) tested the ability of six species of wild ducks to act as long distance carriers of virus on the basis of an experimental inoculation study. The species included in this study included tufted ducks (*A. fuligula*), Eurasian pochards (*A. ferina*), mallards (*A. platyrynchos*), common teals (*A. crecca*), Eurasian wigeons (*A. penelopes*) and gadwalls (*A. strepera*). Inclusion criteria were based on bird abundance, preference for fresh water habitats and migratory patterns that spanned Asia, Europe and Africa. The hypothesis tested was that birds that became infected and excreted high levels of virus could act as long distance virus vectors. Birds 8 – 11 months of age were artificially infected with H5N1 virus isolates from an outbreak in Turkey in 2005. The authors observed high rates of infection (93%) amongst inoculated birds but only observed clinical signs in two species (tufted ducks and Eurasian pochards). Of the two clinically affected species, signs were more severe in the tufted ducks and appeared 3 to 4 days post inoculation. The clinical signs observed included laboured breathing, recumbency and neurologic signs. Severely affected birds died. Those with mild clinical signs recovered 6 to 7 days post inoculation. The dominant mode of excretion was via the pharynx (*cf* the cloaca) but this varied among and between species. Ducks were divided into high excretion (mallards, tufted ducks, pochards) and low excretion groups (teals, wigeons and gadwalls). Species with the highest excretion rates were those showing the more severe clinical signs of disease. Keawcharoen et al. (2008) concluded that mallards were the prime candidates for long distance spread of disease because they were the only species that excreted large amounts of virus without clinical or pathologic evidence of disease. Pochards, on the other hand, were considered sentinel species because, when infected, they developed obvious clinical signs. Observations that have supported these conclusions include outbreaks of HPAI in Europe involving tufted ducks and pochards (Anonymous 2008*b*). Keawcharoen

et al. (2008) concluded that active surveillance for HPAI should be focused on mallard ducks, while passive surveillance of dead and diseased birds should focus on tufted ducks and pochards.

By far the most widely used method to determine the role of wild birds in the spread of avian influenza has been anecdotal evidence and phylogenetic analysis of isolates from wild and domestic bird species. Before the outbreaks of H5N1 in Southeast Asia in 2003, wild birds were considered to have little or no role in the introduction and spread of HPAI viruses to domestic poultry and those found positive for such viruses were regarded as sentinels for outbreaks in domestic poultry units (Swayne & Halvorson 2003). The rapid and simultaneous spread of H5N1 from Southeast Asia to Central Asia and Africa from 2004 to 2006 (Anonymous 2008*e*) has lead many to question what role wilds could have played in disease incursion to these countries and whether they were acting as disease sentinels or reservoir species. Outbreaks of H5N1 in wild birds were reported in China and Mongolia between April and August 2005 followed by reports of infected whooper swans in Croatia in October of the same year (Anonymous 2008*e*). Along with the spread of H5N1 in wild birds, primary incursions into domestic poultry were reported in six countries in Central Asia between July and December of 2005, namely Russia, Kazakhstan, Romania, Turkey, Ukraine and Iraq (Anonymous 2008*e*). Retrospective analysis of virus isolates from the poultry outbreaks in countries in Southeast Asia were linked genetically to the earlier Chinese wild bird isolates (Wang et al. 2008). In early 2006 H5N1 virus spread to a number of countries in Central Asia and 20 countries in Europe affecting a number of wild bird species (Alexander 2007, Anonymous 2008*e*). H5N1 infections have since been reported in wild birds in Germany, France, the Czech Republic, and Hungary in 2007 and the United Kingdom in 2006 (Anonymous 2008*e*).

Trade in live birds and poultry product

Introduction of influenza virus into countries by means of trade in live birds and poultry product is believed to occur often but reports of spread to susceptible poultry populations following incursion are limited. Recent examples this transmission mechanism include the introduction of the H9N2 influenza virus to Japan in 2007 (Mase et al. 2007), the identification of H5N1 virus in chicken meat imported into Japan from China (Mase et al. 2005), and H5N1 found in eagles smuggled into Belgium from Thailand in 2004 (van Borm et al. 2005, Steensels et al. 2007). In 2005 H5N1 was introduced into quaran-

tine facilities in the United Kingdom via birds imported from Taiwan (Defra 2005). In both cases, spread did not occur from the site of incursion to domestic poultry populations. The outbreak of H5N1 in a large commercial turkey farm in the United Kingdom in February 2007 was linked to outbreaks of H5N1 in Hungary (Defra 2007, Irvine et al. 2007). The farm on which the outbreaks occurred was adjacent to a slaughter plant owned and operated by the same company. Phylogenetic analyses of the nucleotide sequence of virus isolated from this outbreak and of farmed geese that were concurrently affected in Hungary indicated that they were of similar origin. This evidence, together with regular transport of poultry meat from Hungary to the processing plant, lead investigators to hypothesise that virus may have been transported to the United Kingdom from Hungary and lapses in biosecurity may have allowed virus to enter the farm to infect birds.

Between-farm spread

Once virus has been introduced into a country, spread between farms occurs through direct or indirect contact between infected and susceptible poultry. Knowledge of factors facilitating the introduction and spread of the disease is critical for effective disease control measures. Transmission occurs mainly through the movement of infected birds and the mechanical transfer of infected faecal material on inanimate and animate vectors (Halvorson et al. 1980, Webster et al. 1992). Vectors include humans (farm personnel, veterinarians), vehicles used to transport poultry, and equipment used on poultry farms. Other suggested routes of secondary spread include animals such as rodents, flies (Sawabe et al. 2006, Sievert et al. 2006) and mosquitos (Barbazan et al. 2008). In 2005 blood engorged mosquitoes collected at poultry farms during an outbreak of H5N1 in Thailand were positive for the H5N1 influenza virus in the reverse-transcription polymerase chain reaction (RT-PCR) test. To date, there is no evidence that between-farm spread of virus can occur via this route (Barbazan et al. 2008).

Local or contiguous transmission refers to the transmission of infection between farms over short distances by unknown or poorly understood routes (Henzler et al. 2003, Thomas et al. 2005) often as the result of aerosol dissemination of viruses downwind from infected farms (Capua & Marangon 2006). Between-farm spread mediated by humans appears to play a key role in virus dissemination between farms based on evidence from outbreak investigations. A case-control study to identify potential sources of virus introduction into poultry farms during the 2003 outbreak of HPAI H7N3 in The Netherlands found that

infection was positively associated with layer-finisher type poultry units (OR 1.65, 95% CI 1.06 – 2.56), thought to be a proxy for farms with large numbers of human contacts made by egg transporters (Thomas et al. 2005). Factors thought to influence the extent and speed of spread between farms include, distance between farms (Boender et al. 2007), the density of farms and the density of poultry (Elbers et al. 2004, Stegeman et al. 2004, Garske et al. 2007).

Within-farm spread

Within-farm morbidity and mortality varies with virus, bird type, age of bird, environment and the presence of secondary infections (Easterday et al. 1997, Swayne & Suarez 2000). LPAI viruses are characterised by high morbidity and low mortality (Easterday et al. 1997). In HPAI outbreaks morbidity and mortality rates range from 50% to 100% (Easterday et al. 1997, Swayne & Suarez 2000). In the 2007 outbreak of HPAI H5N1 in Great Britain, mortality rates of 38% were observed in seven to eight week old turkeys. Morbidity rates in this outbreaks were as high as 90% (Defra 2007, Irvine et al. 2007). In the outbreak of H7N4 that occurred in Australia in 1997 mortality rates in broiler breeder birds ranged from 13% to 92% (Selleck et al. 2003)

Within-farm transmission of virus occurs by direct and indirect contact with infected birds. It is well accepted that the main route of infection for both domestic and wild birds is faecal-oral, though evidence from experimental studies of HPAI H5N1 in a number of domestic species, particularly ducks, have identified the respiratory route as being important (Perkins & Swayne 2001, Sturm-Ramirez et al. 2004, 2005, Antarasena et al. 2006). High concentrations of virus are generally isolated from respiratory secretions or tissues. In tissues isolated from naturally infected ducks and quails with the H5N1 in Thailand from 2004 to 2005, recovery of virus was greater from respiratory tissues compared with intestinal tissues (30% *vs* 10%) leading researchers to conclude the respiratory route was the main route of transmission for ducks. In chickens inoculated via the nasal route with HPAI, recovery of virus was greatest in secretions obtained from the oropharynx compared with those obtained from cloacal swabs (Perkins & Swayne 2001). The quantities of virus recovered were $10^{4.2} - 10^{7.7}$ EID$_{50}$ per millilitre and $10^{2.5} - 10^{4.5}$ EID$_{50}$ per gram for respiratory secretions and faecal material, respectively. There are observed differences in transmission between virus types, with regards to the level of shedding and shedding period. In a comparison of LPAI and HPAI viruses that caused outbreaks in

Pennsylvania (1983 - 1984), Mexico (1994 - 1995), and Italy (1999 - 2000), van der Goot et al. (2003) showed that, compared with LPAI viruses, infectious periods for HPAI were longer and the basic reproductive number, R_0, was greater. They also observed that prior infection with LPAI reduced disease transmission when birds were subsequently infected with HPAI strains.

2.4 Pathogenesis

Lesions associated with HPAI infections are variable and, due to the peracute course of disease, may not be present at the time of death. In chickens haemorrhage and oedema are usually observed. Severe congestion of the musculature, conjunctivae, kidneys and haemorrhage in the ovaries and sternum has been cited as a common *post mortem* finding (Easterday et al. 1997, Swayne & Suarez 2000). Lesions in turkeys are similar to those observed in chickens but may not be as severe. The commonly identified lesions include multifocal lymphoid necrosis, pancreatic necrosis, myocarditis, and lesions in the skeleton muscle, brain and comb. Clinical and macroscopic manifestation of avian influenza in domestic birds are variable and are generally indistinguishable from Newcastle disease, avian pneumovirus, other paramyxoviruses, infectious laryngotracheitis, infectious bronchitis, and chlamydial and/or mycoplasma infections.

2.5 Clinical findings

The incubation period for avian influenza is highly variable, ranging between 3 and 5 days. Extremes ranging from a few hours to 14 days have been reported for HPAI infections with or without the appearance of clinical signs (Swayne & Halvorson 2003). Mortality and morbidity rates are variable and depend on environmental conditions (hygiene, ventilation, and ambient temperature), the type and age of birds and the presence of concurrent infection with other pathogens (Easterday et al. 1997). The presence of infection with LPAI viruses in wild water fowls generally progresses with limited or no clinical signs of disease (Swayne & Halvorson 2003). LPAI infections in domestic poultry may be asymptomatic or cause a wide range of clinical signs involving the respiratory, urogenital, and/or gastrointestinal tracts (Easterday et al. 1997, Swayne & Suarez 2000).

A range of non specific clinical signs are observed. This can include depression, apathy, absence of sounds in poultry houses, decreased feed and water intake, and reduction in egg production within days of infection.

Infection in turkeys is more severe in younger birds; older birds able to recover from disease within a week of infection (Mutinelli et al. 2003*a*). Signs in turkey flocks include respiratory distress associated with swelling of the infraorbital sinuses, loss of appetite, fever and depression. Mortality rates range from 5% to 97%. In breeder flocks egg production may drop by anywhere between 30% to 80% during the acute phase of disease with an associated decrease in egg quality. Clinical signs in broilers are variable. In breeder flocks, egg production may drop by 5% to 20% accompanied by loss of appetite and cyanosis. Morbidity rates be as high as 100% with mortality rates anywhere between 3% to 8%.

The clinical manifestations of HPAI infection are equally variable but clinical signs, when they are present, are more severe than LPAI. There may be differences in the speed with which disease moves through a flock which will vary according to the type of housing. For birds reared on litter, mortality rates may be as high as 100% within 24 to 72 hours. In domestic poultry clinical signs reflect the damage done by viral replication in the visceral organs, cardiovascular and nervous systems and vary according to the extent of damage. In most situations turkeys and chickens die within 1 − 3 days of becoming infected with little or no clinical signs (Perkins & Swayne 2001). Respiratory signs include sneezing, rales and coughing whilst nervous signs include paresis and paralysis. The appearance of clinical signs and occurrence of death is variable. Under experimental conditions death can occur anywhere between 1 and 6 days following infection (Perkins & Swayne 2001). In ducks HPAI generally produces limited or no clinical sign of disease (Swayne & Suarez 2000). A few exceptions have been reported however, associated with the recent outbreaks of HPAI H5N1 in Asia and Europe (Ellis et al. 2004). An important aspect of avian influenza is that clinical signs observed may be modified by concurrent bacterial or viral diseases or the presence of environmental stressors which can lead to misdiagnosis (Swayne & Suarez 2000).

2.6 Immunology

Knowledge of host immunological responses to avian influenza viruses is important for planning diagnostic as well as vaccination strategies. The response to natural infections and vaccination is mediated via humoral or cell based immunity, though the role of the latter is not well understood (Suarez & Schultz-Cherry 2000). Humoral immunity is responsible for stimulating the production of systemic immunoglobulins (IgM, IgY) and mucosal antibodies (IgA). Following infection circulating systemic IgM immunoglobulins develop within 5 days followed by IgY. Though antibodies are produced against all 10 virus proteins, variability exists in terms of the type and level of antibody response as well as differences in species. These differences have implications for the appropriateness of diagnostic tests and vaccination. Neutralising antibodies are produced against all three surface proteins (HA, NA, M1), but HA antigen are considered to be the most important determinant for host protection against avian influenza infection though antibodies against NA may also play a role. Protection is therefore HA or NA specific and cross protection does not occur. Vaccination is therefore primarily targeted at the HA protein though NA have also been the target as in the case with the DIVA (Differentiating Infected from Vaccinated Animals) strategy practiced in Italy (Suarez 2005). The extent of humoral response to infection or vaccination varies with host species. Studies of immune responses in a number of species have been reviewed by Higgins (1996). These indicate that chickens produce the largest antibody response, followed by pheasants, turkey, quail and ducks. Experimental and field evidence shows that the the antibody response to the HA antigen in ducks is poor (Kida et al. 1980, Toth & Norcross 1981). In the case of HPAI viruses, immune response may not occur due to rapid death.

2.7 Diagnosis

There are three methods by which avian influenza may be diagnosed: (1) clinical signs, (2) direct detection of virus, and (3) serological methods. Due to the highly variable clinical picture associated with avian influenza infections, clinical signs are only used as an indicator of the presence of disease. Confirmatory diagnosis by means of direct virus detection or serology is required (Swayne & Suarez 2000). The relative usefulness

of diagnostic tests for avian influenza will vary with the type of virus and the specific objective of testing. Serological methods are primarily used for testing historical exposure to LPAI infections for providing evidence of disease freedom. Virus detection methods are the preferred method for HPAI detection in outbreak situations. In outbreak situations, diagnostic tests need to be rapid and reliable, allowing prompt identification of affected flocks and the implementation of effective control measures. Diagnostic tests for avian influenza should therefore be: (1) able to rapidly detect the presence or absence of disease with high accuracy, (2) simple and easy to use and, (3) affordable (Perdue 2003, Chua et al. 2007, Suarez & Das 2007). The OIE considers virus detection as the only certain method for identifying influenza infected birds (Anonymous 2008*b*). Procedures suitable for virus detection include virus isolation, antigen capture immunoassays and molecular diagnostic techniques and pathogenicity testing.

2.7.1   Virus isolation

Although virus isolation is considered the gold standard for determining the presence of disease (Anonymous 2008*e*) it is a technique that is costly, requires special laboratory facilities and is time consuming (taking up to three weeks to obtain a definitive result). The method involves inoculation of clinical material into allantoic fluid of 10 – 11 day old pathogen free embryonated chicken eggs or eggs from flocks free of antibodies to avian influenza viruses and incubating the eggs for a period of up to 5 days. Allantoic fluid from dead eggs or eggs with dead embryos are then collected and checked for the presence of any haemagglutinating agents (presence of avian influenza viruses or an avian paramyxovirus type 1) by the haemagglutination test (HA), and if negative, passed at least one more time through fresh eggs. Recommended methods to confirm the presence of avian influenza viruses after virus isolation include agar gel immunodiffusion (AGID), ELISA and, RT-PCR directed at avian influenza nucleoproteins or matrix protein (Anonymous 2008*e*). Where an influenza virus is identified, haemagglutination inhibition (HI) and neuraminidase inhibition (NI) tests are used to subtype the haemagglutinin and neuraminidase proteins, respectively.

Samples submitted for virus isolation may come from live or dead birds. From dead birds, pooled or separate samples of organs including those from the respiratory tract, intestines,

brain, liver and heart are suitable as well as faecal material and swabs from the cloaca and trachea. From live birds tracheal and cloacal swabs are recommended.

Given the time taken to obtain test results and extensive laboratory infrastructure required, other rapid tests that either detect viral nucleic acids or viral antigens have been developed to supplement virus isolation to facilitate more rapid diagnosis particularly during outbreaks.

2.7.2 Antigen detection tests

Rapid antigen assays developed for use in humans and other animal species may be used as screening tests for avian influenza infection during outbreaks. These tests have been designed to detect avian influenza A nucleoproteins, antigens that are common to all type A influenza viruses (Bai et al. 2006) and, H5 (He et al. 2006, Tsuda et al. 2007) or H7 (Manzoor et al. 2008) subtypes. Available tests fall into two categories: rapid chromatographic immunoassays and enzyme linked immunosorbent assays (ELISAs) (Cattoli et al. 2004).

Several antigen-capture enzyme immunosorbent assays (AC-EIA) kits have been developed including Directigen Flu A (Becton Dickinson), Flu OIA (Biostar Inc), Flu Detect (Synbiotics) and Anigen A (South Korea), QuickVue Influenza Test Kit (Quidel), and Zstat Flu (ZymeTX, Inc). These tests are generally easy to use, requiring little or no laboratory facilities and have a turn around time of around 15 – 20 minutes (Cattoli et al. 2004, Chua et al. 2007). Their main disadvantage is that they are generally less sensitive and specific than virus isolation or polymerase chain reaction (PCR) tests, and they have not been validated in a number of species, particularly wild birds.

Because antigen detection tests have been developed to measure viral antigen, the diagnostic sensitivities of these tests will depend on the concentration of virus present in samples and the minimum antigen titre the test can detect. Comparative studies to assess test characteristics of the antigen-capture enzyme immunosorbent assays (AC-EIA) have shown that these tests have relatively low sensitivity compared with virus isolation and molecular typing and sensitivities vary with the sample type, the level of testing (individual *vs* pooled) and type of bird. They also show variable test characteristics when compared to other AC-EIA tests. Davison et al. (1998) found that the Directigen Flu A

test, when used on pooled swabs from field and surveillance samples, had a 77% sensitivity and 100% specificity for detecting H7N2 subtypes. Woodcock & Cardona (2005) evaluated commercially available tests on field samples: a summary of their findings is provided in Table 2.3. Chua et al. (2007) evaluated the characteristics of four rapid detection tests on H5N1 positive surveillance samples obtained during the 2001 to 2003 H5N1 outbreaks in Hong Kong. Samples were comprised of cloacal and faecal swabs or tissues from infected chickens, ducks, geese and wild birds. Five diagnostic tests were evaluated. Two were commercially available rapid chromatographic immunoassays: Rockby Avian Influenza Virus Antigen Kit (Rockby) and Flu Detect Influenza A Immunoassay (Synbiotics). Three were antigen detection ELISAs developed for use in China and Australia: an H5 hemagglutinin antigen detection ELISA (NIDVD), an influenza A antigen detection ELISA (CSIRO), and an H5-specific dot ELISA (dNIDVD). Results from each of the tests were compared with the result obtained from virus culture confirmed by PCR methods and nucleic acid sequencing. Comparatively, the test sensitivities were highly variable and could only detect between 36% and 51% of the truly positive specimens. All tests showed similar sensitivities for cloacal samples, pooled cloacal and tracheal swabs obtained from sick and dead chickens.

Table 2.3: Estimates of test sensitivity and specificity of commercially available rapid antigen tests tests for highly pathogenic avian influenza.

Test	Virus	Sample	Sensitivity[e] (%)	Specificity[e] (%)	Source
Directigen	H5N2	Swabs	0.77	1.00	Davison et al. (1998)
			0.44 (0.19 – 0.73)	1.00	Woodcock & Cardona (2005)
Quickvue (Quidel)	–		0.66 (0.35 – 0.88)	1.00	Woodcock & Cardona (2005)
Flu OIA (Biostar Inc)	–		0.44 (0.19 – 0.73)	1.00	Woodcock & Cardona (2005)
Directigen	H5N1		0.50 (0.38 – 0.61)	–	Chua et al. (2007)
Rockby [a]	–		0.43 (0.37 – 0.49)	–	Chua et al. (2007)
Direct Flu [a]	–		0.44 (0.39 – 0.50)	–	Chua et al. (2007)
NIDVD [b]	–		0.51 (0.45 – 0.57)	–	Chua et al. (2007)
CSIRO [c]	–		0.36 (0.31 – 0.42)	–	Chua et al. (2007)
NIDVD [d]	–		0.38 (0.32 – 0.45)	–	Chua et al. (2007)

[a] Chromatographic immunassay.

[b] H5 specific ELISA assay. Developed by the National Institute of Diagnostics and Vaccine Development, China.

[c] Influenza A ELISA. Developed by the Commonwealth Scientific and Industrial Research Organisation, Australia.

[d] dot ELISA. Developed by the National Institute of Diagnostics and Vaccine Development, China.

[e] Test sensitivity and specificity will depend on the antigen strain used (i.e. H5N2 *vs* H5N1). It has been observed that the N1 component prepared from the H5N1 virus may be very immunogenic and therefore cause cross reactions with antibodies from other virus subtypes, thereby reducing test specificity. The test is therefore run using two H5 antigens.

2.7.3 Molecular diagnosis

Molecular techniques in avian influenza diagnosis can be used for any of three purposes: (1) screening for the influenza A matrix gene, (2) determination of HA and NA subtypes and, (3) determination of the pathogenicity of the virus through molecular sequencing of the virus cleavage site. Available techniques include reverse transcription polymerase chain reaction (RT-PCR), RT-PCR with enzyme linked immunosorbent assay (ELISA), real-time reverse transcription polymerase chain reaction (RRT-PCR), nucleic acid sequence-based amplification (NASBA), and loop mediated isothermal amplification (LAMP). See (Pasick 2005) and (Alexander 2008) for reviews.

Molecular diagnosis based on polymerase chain reaction (PCR) involves the direct detection of nucleic acids of viral genomic RNA. This procedure requires that the viral RNA be extracted from samples and converted to complementary deoxyribonucleic acid (cDNA) which is subsequently amplified via RT-PCR. Two types of PCR assays exist, the standard conventional reverse-transcription polymerase chain reaction (RT-PCR) and real-time reverse-transcription polymerase chain reaction (RRT-PCR). Several PCR assays have been developed for identification of influenza A viruses and for virus subtyping. RT-PCR methods for identification of influenza A viruses use nucleoprotein-specific or matrix-specific conserved primers whereas those for subtyping of H5 and H7 viruses use H5- or H7-specific primers (Munch et al. 2001, Spackman et al. 2002, 2003a,b, Ng et al. 2006). These methods have an advantage over virus isolation in that live virus is not essential so there is no need to inoculate embryonated eggs which may be costly and dependent on the availability of sufficient numbers of pathogen free eggs. Results may be obtained within 24 hours. Compared with virus isolation PCR techniques have higher test sensitivities and lower test specificities: usually greater than 90% (Dybkaer et al. 2003, Cattoli et al. 2004), but this is not always the case. Sensitivity of PCR may be affected by the amount of viral material present, the timing of sample collection post exposure and the quality of the sample. In situations where the amount of viral material is limited, virus isolation can facilitate virus amplification via multiple passages in embryonated eggs. False positive results may occur as a result of contamination.

2.7.4   Serology

Serological assays for avian influenza either detect antibodies against any influenza type A (type specific: M1, NP) or antibodies against the surface proteins (subtype specific, e.g. HA or NA). Serology is often used as a screening test to determine the presence of historical exposure to low pathogenicity viruses in domestic poultry and wild birds and to identify seroconversion post vaccination (Cattoli & Terregino 2008). Three serological tests are used: (1) agar gel immunodiffusion (AGID), (2) haemagglutination inhibition (HI), and (3) enzyme linked immunosorbant assays (ELISAs).

AGID is considered by the OIE to be the gold standard serological test for screening domestic poultry sera for avian influenza viruses. The test measures antibody responses to the nucleoproteins of influenza A viruses. Antigen preparations from the chorioallantoic membranes of embryonated eggs, preparations of suspect test sera and preparations of positive control sera are placed side by side in wells dug into agar gel and examined for the presence of precipitation lines. If influenza A virus is present then the precipitation line between the known positive control wells will be continuous with the line between the antigen and test wells. Results are obtained within 1 to 2 days. The AGID is inexpensive, simple and highly specific but suffers from low sensitivity when compared with the ELISA (Beard 1970). Moreover, it cannot be used in species that do not produce precipitating antibodies post infection such as in the case of waterfowls (Higgins 1989)

HI is the most commonly used serologic method for detecting antibodies to the HA antigen of influenza A viruses It is regarded as a standard reference method by the OIE. The test is an indirect antibody test that measures the ability of test serum to inhibit the haemagglutination of a constant amount of virus. The test requires antigen for each of the 15 haemagglutinin virus subtypes, but in most cases two antigens for H5 and H7 are used. Finding an HI titre in suspect sera may indicate one of two things: indication of historical exposure to a virus of the same subtype and, protection from vaccine challenge of the same subtype. The advantages of HI are its cost, rapid turn around time, and that it provides a quantitative indication of virus titre.

Several ELISA tests have been developed to detect antibodies to influenza A nucleoproteins (Shafer et al. 1998, Zhou et al. 1998, Sala et al. 2003). Indirect ELISAs are species specific tests meaning that they have been developed for use in particular animal species

because they employ anti-chicken or anti-turkey secondary antibodies. Examples of indirect ELISAs include those described by Wu et al. (2007). Competition ELISAs (cELISA), on the other hand, are used to test serum from a wider range of animal species (e.g. mammals and birds). These employ a mouse clonal antibody to compete with the test serum for binding to the nucleoprotein of the virus. These tests are highly sensitive but have low specificity and require more complex laboratory facilities than the AGID tests. Seropositive results to either of the screening tests are usually subjected to subtype-specific tests such as the HI and NA inhibition test. Shafer et al. (1998), Sala et al. (2003) and Yamamoto et al. (2007) provide estimates of serological test characteristics (Table 2.4).

Table 2.4: Estimates of test sensitivity and specificity of three serological tests for highly pathogenic avian influenza.

Test	Virus	Sensitivity (%)	Specificity (%)	Source
AGID	H5N2	0.67 (0.57 – 0.77)	0.96 (0.81 – 1.00)	Yamamoto et al. (2007)
AGID	H5N9	0.96	0.99	Shafer et al. (1998)
HI	H5N2	0.99 (0.97 – 1.00)	0.90 (0.59 – 1.00)	Yamamoto et al. (2007)
ELISA	H7N3	0.98	1.00	Sala et al. (2003)

2.8 Control and prevention

Studies and field experience show that movement of birds, the presence of wild birds, legal and illegal trade in live birds and bird products, the density of farms and live bird markets are factors influencing risk of avian influenza introduction into a country and subsequent spread (Capua & Marangon 2000, Elbers et al. 2004, Thomas et al. 2005, Kaoud 2007, Kung et al. 2007).

A case-control study to identify risk factors for the spread of LPAI H7N2 virus between poultry farms in West Virginia, USA showed that disposal of dead birds by rendering, having birds greater than 10 or 20 weeks of age, use of non-family caretakers and the presence of mammalian wildlife on farm increased the risk of disease spread (McQuiston et al. 2005). A study conducted in The Netherlands to identify factors associated with the introduction of HPAI H7N7 in poultry farms found that layer-finisher flocks were at an increased risk of infection (Thomas et al. 2005). In Italy, Mannelli et al. (2006) found

that being within 1 kilometre of an infected premise and being a turkey farm increased the flock-level risk of HPAI. In Hong Kong, outbreaks due to the HPAI H5N1 were associated with contact with markets, among other factors (Kung et al. 2007). Similar findings were observed during the outbreak of LPAI in West Virginia in 2004 (Pelzel et al. 2006). The outbreaks of HPAI H5N1 in many Southeast Asian countries since 2003 have been associated with free grazing ducks (Gilbert et al. 2006, Pfeiffer et al. 2007). Outbreaks in Egypt were significantly associated with wild birds and poultry transportation (Kaoud 2007).

Reducing the losses associated with avian influenza in poultry populations is centred around two main objectives: preventing the entry of the disease into poultry populations when it is absent, and minimising the economic impact of the disease or total eradication when it is present (Swayne & Halvorson 2003). These objectives are achieved through a combination of strategies including biosecurity, surveillance, elimination of infected birds, reduction of host susceptibility to infection (e.g. vaccination) and education.

2.8.1 Control

Measures implemented to control avian influenza infection are based on achieving early disease control to reduce virus transmission with the final goal of eradication using the following methods based on controlled marketing, slaughter of infected poultry, movement controls, vaccination, compartmentalisation, and compensation (Halvorson 2002, Capua & Marangon 2006). Control strategies for HPAI H5N1 influenza are described by Anonymous (2005*a*).

Controlled marketing

Controlled marketing of infected flocks is applied as a means to reduce bird density in an area in order to limit disease transmission while at the same time ensuring that producers have a means for disposing of affected birds. This approach has been practiced for turkey flocks that have recovered from LPAI infections in the USA (Halvorson 2002). There is no reported use of controlled marketing of HPAI infected flocks.

Slaughter

Slaughter and disposal is the preferred method by which NAI infected birds are eliminated. Various terms have been applied including stamping out, depopulation, culling and

pre-emptive slaughter. Culling refers to the process of humanely killing animals, while stamping out refers to the slaughter of infected and in-contact birds.

Movement controls

The idea behind movement control is to reduce the probability that disease will be transferred from one area to another via the act of movement of poultry, equipment used with poultry, or poultry product. The success of this method of disease control is dependent on early identification of the index flock as well as the ability to trace all movements off infected farms. Movement controls are generally implemented on suspicion of the presence of both HPAI and LPAI virus infections in order to reduce spread of disease from infected to susceptible farms.

Vaccination

Vaccination reduces the susceptibility of the population in order to limit or prevent disease spread (Marangon et al. 2008). Experimental and field experience show that vaccination can increase resistance to field challenge, reduce shedding of virus and reduce rates of disease transmission (van der Goot et al. 2005). Emergency vaccination can be used as an alternative to culling, the success of which is dependent on bird density, biosecurity, virus strain, and the availability of vaccine and personnel to administer it. Prophylactic vaccination is an appropriate means for augmenting biosecurity during high risk situations.

Most countries in which outbreaks of avian influenza have occurred have been hesitant to use vaccination as a means for control for a number of reasons. The first reason is related to the difficulty associated with disease freedom declarations and re-establishment of trade. The second is related to the fact that the currently available vaccines, although able to protect birds from infection, may not stop virus replication and shedding causing the phenomenon of silent spread. The third reason is associated with the difficulty differentiating vaccinated birds from naturally infected birds thereby interfering with serological surveillance. Differentiating vaccinated animals from naturally affected animals (DIVA) strategies (Marangon et al. 2008) have been proposed as an alternative to facilitate vaccination, but problems remain with its implementation. A number of DIVA methods are available and serological or virological testing of unvaccinated birds (sentinel birds) placed within vaccinated flocks is the most widely method used (see Berg et al. 2008 for a review of other methods). Use of sentinel birds requires birds to be marked in order to

Table 2.5: Use of vaccination to control LPAI and HPAI outbreaks due to H5 and H7 subtype viruses. Adapted from Marangon et al. (2008).

Country	Year	Virus	Vaccine type	Species
Mexico	1995 – 2001	HPAI H5N1	Inactivated H5N2	Broilers, layers, breeders
Mexico	1998 – 2001	HPAI H5N1	Recombinant fowlpox H5	Broilers, breeders
Utah USA	1995	LPAI H7N3	Inactivated H7N3	Turkeys
Connecticut USA	2003	LPAI H7N2	Inactivated H7N3 H7N2	Layers
Egypt	2006	HPAI H5N1	Inactivated H5N2	Backyard poultry
Italy	2003 – 2006	LPAI H7N3	Inactivated H7N1 H5/H7 H5N9	Turkeys, layers, cockerels
		LPAI H5N2		
Pakistan	1995	LPAI H7N3	Inactivated H7N3	Breeders
Pakistan	2006 – 2007	HPAI H5N1	Inactivated H5N2	Breeders
Hong Kong	2002 - 2003	HPAI H5N1	Inactivated H5N2	Broilers
China	2003 - 2006	HPAI H5N1	Inactivated H5N2, H5N1	Ducks, chickens
Vietnam	2005 - 2006	HPAI H5N1	Inactivated H5N2, H5N1	Ducks, geese, chickens
Afghanistan	2007	HPAI H5N1	-	Broilers, layers, breeders
Russia	2006 – 2007	HPAI H5N1	Inactivated H7N1	Backyard poultry
Siberia	2006	HPAI H5N1	Inactivated H7N1	Broilers, layers, breeders
Ivory coast	2006 - 2007	HPAI H5N1	Inactivated H5N9	Backyard, commercial poultry

be easily recognised. In addition, vaccinated birds produce low levels of antibodies to circulating field strains, requiring diagnostic tests of high sensitivity in order to avoid false negative results. On the positive side, a DIVA strategy may allow countries to resume or continue trading as they are able to provide sufficient evidence of the absence of disease in vaccinated flocks. Italy used a H7N3 heterologous vaccine against outbreaks caused by LPAI H7N1 virus strain in 2001 and was able to differentiate infected animals from those that were vaccinated and were therefore able to continue trading poultry products (Capua, Terregino, Mutinelli, Terregino & Rodriguez 2003). A DIVA strategy was cited as an acceptable alternative to mass culling of birds as occurred in Chile in 2002, The Netherlands in 2003 and Canada in 2004 (Capua & Alexander 2004). Table 2.5 provides details of outbreaks of LPAI and HPAI where vaccination has been used as part of control efforts.

Compartmentalisation

Zoning and compartmentalisation are two processes to facilitate implementation of control measures and maintain trade (Zepeda & Salman 2007). Zoning is the process of declaring defined geographical areas as infected, to facilitate the implementation of control measures (Anonymous 2007*c*). Compartmentalisation is a procedure implemented to

define and manage poultry populations under a common biosecurity management system in order to facilitate international trade. Within the compartment are subpopulations of animals with similar health status that are subjected to a common intensity of surveillance, control and biosecurity measures. Compartments could refer to live bird marketing systems or integrated domestic poultry companies as described by Myers et al. (2003). Given the tendency of the avian influenza virus to persist in the environment in combination with movement of wild birds, it is not likely that zoning as a single control measure would be acceptable to trading partners.

Compensation

Compensation refers to the process of reimbursing poultry producers for losses incurred during a NAI outbreak (Anonymous 2006*a*). It has been used as an incentive to encourage early reporting of disease by owners and as a way of encouraging owners to comply with culling programmes (Anonymous 2006*a*). Compensation has been used in a number of infectious disease outbreaks including FMD and CSF. The expected benefits from compensation include a reduction in the time between incursion and implementation of control measures, which in turn reduces the likelihood of virus mutation. Potential negatives are that this may encourage producers to neglect basic biosecurity measures aimed at preventing disease entry and other factors related to the design and implementation of the compensation scheme. A successful compensation programme to enhance avian influenza control must have the following features: (1) a clear definition of who will be compensated and who will be responsible for funding the compensation programme, (2) the types of losses to be compensated, (3) a clear understanding by all parties (particulary producers) of what is required in terms of reporting, (4) an organised structure for payments, and (5) availability of funds. Avian influenza compensation schemes have been implemented in The Netherlands, Canada, Vietnam and Thailand (Anonymous 2006*a*).

2.8.2 Prevention

Biosecurity encompasses the use of management strategies at the national and farm level to reduce the likelihood of virus entry into a naïve population or once infection is present, to reduce the likelihood of spread to other areas. This strategy is thought to be the most important approach for preventing disease incursion (Halvorson 2002, Capua & Marangon

2006, Marangon et al. 2008). Biosecurity at the farm level focuses on movement restriction, preventing exposure to wild birds, and reduction of contamination by disinfection and cleaning, practice of all-in-all out production systems amongst other measures. At the national level, biosecurity measures may include quarantine regulations restricting the importation of live birds and bird products into a country and the implementation of government policies restricting bird rearing to indoor facilities during high risk periods. The success of biosecurity measures implemented at the farm level to prevent disease incursion will depend on the type of production system and country. A recent survey conducted in Australia to examine the rate of adoption of biosecurity measures by poultry farms showed differences between independently owned commercial farms that were part of the turkey and duck sectors compared with farms operated by integrated companies (East 2007). An assessment of village poultry systems in Vietnam acknowledged limitations associated with implementation of these measures in some areas (Cristalli & Capua 2007).

Surveillance

In disease free countries, the major objectives of avian influenza surveillance are to detect incursions of disease as early as possible and demonstrate disease freedom to trading partners. In countries that are infected, surveillance objectives include: (1) description of the spatial and temporal distribution of disease, with a view to informing control measures, (2) assessment of the efficacy of vaccination campaigns and other control programmes, and (3) monitoring of antigenic drift. The Terrestrial Animal Health Code provides specific guidelines for appropriate level of avian influenza surveillance (Anonymous 2007*f*). These guidelines relate to possible strategies for countries seeking recognition of disease free status at the country-, zone- or compartment-level when disease has historically been absent or after an outbreak. The requirements for a well functioning surveillance program for avian influenza are discussed in detail in Chapter 3.

The exact conduct of surveillance strategies for avian influenza varies from country to country, but generally include activities to monitor wild and domestic bird populations using a combination of passive and active approaches. In the United Kingdom, the avian influenza surveillance strategy involves surveys of wild birds, surveys of domestic poultry populations for H5 and H7 viruses, investigation of mortality reports in domestic poultry populations and investigations of unusual mortality reports in wild bird populations. Wild

bird surveillance is based on three components: (1) targeted sampling of defined wild bird species during the autumn and winter to detect the presence of H5N1 viruses, (2) survey of hunter killed birds to identify the presence of avian influenza virus, and (3) targeted screening of wild birds found dead in designated surveillance areas. Wild bird surveillance is used as an early warning system to identify the likelihood of entry into domestic poultry populations. It is therefore focused on species considered by experts to have a high likelihood of spreading virus in areas where domestic poultry are at risk. Surveillance for NAI in domestic poultry is based on passive reporting of clinical signs as well as an annual surveys of domestic populations. An example of this type of system is the The National Avian Influenza Plan in the USA.[2] In this plan are described data collection methods, populations under surveillance, database systems, and scenario tree analyses of surveillance system sensitivity. Given the possible risk that wild migratory birds (waders and shore birds) might play in the introduction and spread of avian influenza viruses in New Zealand, surveillance in wild birds is focused on migratory species arriving in large numbers during spring (between September and November) and waterfowls, which are sampled during the summer months (Fraser et al. 2008). Sampling during the summer months is targeted at juvenile wild ducks as these are known to shed more virus than older birds. Sampling of juvenile birds increases the number of viruses isolated (Stanislawek et al. 2002).

Risk analysis of potential routes of entry and spread

The basic framework for conducting a risk analysis of NAI incursion and spread is that described by Murray (2004). Modifications to this approach are described by Zepeda & Salman (2007) and Goutard et al. (2007). The framework proposed by Goutard et al. (2007) defines the various steps involved in the risk assessment process for avian influenza using a quantitative approach. These include: (1) risk release through migratory birds and/or poultry-product marketing chains, (2) risk exposure by means of studying interfaces among imported and exposed poultry, and (3) risk consequences for establishing the probability of AI spreading within the poultry population and the probability of it escaping detection.

Many countries have used qualitative risk analyses to evaluate the likelihood of disease

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[2]http://www.usda.gov/wps/portal/usdahome?navtype=SU&navid=avian_influenza

incursion via the importation of poultry product, live birds, wild birds and pets. This has been assisted by data from outbreaks monitored by electronic sources as ProMED. For example, the United Kingdom periodically assesses the risk of HPAI H5N1 incursion via wild birds and trade in poultry and poultry product (Sabirovic et al. 2007). Quantitative risk analyses are an alternative approach, as described by Zepeda & Salman (2007). This approach involves development of a model to assess the likelihood of importation of HPAI into a country, taking into account the surveillance activities carried out by the importing country. Risk assessments have also been applied to identify high risk wild bird species likely to carry the disease into new areas (Crick et al. 2006, Williams et al. 2004).

Another approach includes risk assessment to identify areas at risk of incursion either based on knowledge of seasonal migratory patterns of wild birds, likely areas of incursion based on data from wild bird surveillance and banding surveys as well as data on distribution of poultry units. Peterson et al. (2007) examined the relative distribution of 137 migratory bird species based on seasonal movements of their geographic behaviour during breeding and wintering on the American, African and Asian continent in order to inform likely areas for targeted surveillance. Under the assumption that HPAI H5N1 would be likely to enter via migratory wild birds from Asia and Africa, the authors selected birds (both land based and water birds) that were seasonally distributed in both the Palearctic (i.e. Eurasian) and the Nearctic (North American) regions. To identify the likely areas of incursion of HPAI into the North America the authors divided the selected species into four groups based on similar seasonal migratory patterns: (1) breeding in North America and Eurasia and wintering in southern Eurasia or Africa, (2) breeding in North America and Eurasia and wintering in the Americas, (3) breeding in North America and Eurasia and wintering pelagically, and (4) holarctic, with breeding and wintering grounds in both hemispheres but no clear intercontinental movements. The seasonal ranges of the selected species were mapped and formed the basis for identifying areas at risk of incursion. The results indicated that although the second group of birds species were likely to be distributed throughout Alaska (an area currently targeted for surveillance) the distribution of many species with trans-continental movement had a larger distribution range, extending as far as South America, and in areas not currently under surveillance. The authors concluded the need for surveillance decisions to be made on detailed scientific analyses that use the best data available as opposed to traditionally held views.

Other approaches include the identification of high risk areas based on poultry husbandry systems and proximity to staging and mixing points for wild migratory waterfowls proceeding from areas with disease presence in poultry or wild birds as advocated by the European Union (Pittman & Laddomada 2008). Various examples of the implementation of this concept exist as in the methods described by Snow et al. (2007) in the United Kingdom, Goutard et al. (2007) in Ethiopia and East et al. (2007) in Australia.

Examples of consequence assessment to examine the likelihood of spread include the models developed by Truscott et al. (2007) and Sharkey et al. (2008). Few examples exist of the scenario tree model for assessing avian influenza surveillance sensitivity. The USDA describes a scenario-tree model to evaluate the sensitivity of the surveillance systems for various sub-components for avian influenza surveillance (Anonymous 2007*g*).

CHAPTER **3**

Literature Review: Surveillance

Veterinary surveillance has been defined as the on-going systematic collection, collation and interpretation of accurate information about a defined animal population with respect to disease and/or infection, closely integrated with timely dissemination of that information to those responsible for control and prevention measures (Meah & Lewis 2000). The Terrestrial Animal Health Code of the OIE defines surveillance as the investigation of a given population or subpopulation to detect the presence of a pathogenic agent or disease; the frequency and type of surveillance will be determined by the epidemiology of the pathogenic agent or disease, and the desired outputs (Anonymous 2007*b*). Surveillance is a tool for monitoring changes in health related events in a defined animal population with specific goals relating to: (1) the detection of disease incursions, both new and emerging, (2) the assessment of progress in terms of control or eradication of selected diseases and pathogens, (3) demonstration of disease freedom for trading partners, and (4) identification of hazards or risk factors for disease outbreaks.

The activities required to achieve each of these objectives include voluntary and mandatory notifications to animal health authorities, outbreak investigations, monitoring of sentinel species, surveys and attempts at completely enumerating animal populations via censuses. Each of these techniques have advantages and disadvantages, as summarised in Table 3.1.

Table 3.1: Veterinary surveillance methodologies as adapted from Scudamore (2002).

Method	Description	Form	Advantages	Disadvantages	Examples
Voluntary notifications	Farmers report unusual events	Scanning/passive	Cost effective method for detecting new diseases	Highly dependent on awareness and motivation, prone to under reporting	Farmer reports of high mortality events in poultry
Mandatory notifications	Reporting of diseases mandated by law	Scanning/passive	Possible to capture all cases	Success will depend on actions taken as the result of reporting (i.e. compensation or slaughter)	CSF and avian influenza in the UK
Sentinel field surveillance	Important sites are selected for prospective examination of specific diseases over time	Scanning active or targeted	Allows for changes in disease status to be monitored	Difficult to recruit participants and expensive to maintain	Sentinel surveillance for bluetongue in The Netherlands
Sentinel laboratory surveillance	Laboratories report submission data and results of investigation	Scanning/passive	Highly specific, opportunity to detect rare events, microbial resistance, veterinary drug residues	Prone to underreporting as dependent on farmer reporting to veterinarian	
Sentinel practitioner surveillance	Veterinary practices selected for regular reports of health events	Scanning/passive	Monitor trends in disease occurrence, level of disease in the population	May not identify rare events	NADIS[a] in the UK
Structured surveys	A sample of the population of interest is examined for the evidence of disease	Targeted, active	Precise population estimates can be obtained, repeated surveys provide assessment of trends	Only collects data relevant to the studied disease, costly, time consuming and reliant on participation	
Census	All members of a population are measured for evidence of disease		True estimates of disease frequencies obtained	Costly and requires a sample frame of all members of the population, expensive	Meat inspections of all animals slaughtered for human consumption
Veterinary investigations	Veterinarians recruited to investigate outbreaks of unusual syndromes	Scanning/passive	Important for identifying new diseases	Reliant on clear definition of an outbreak and defined level for intervention	Potential triggers for investigation include mortality events from farms or carcase disposal systems, public health information, lesions observed during meat inspections

[a] NADIS: National Animal Disease Information Service.

3.1   Types of surveillance

3.1.1   Passive *vs* active surveillance

Passive surveillance refers to the reporting of clinical suspect cases to authorities (Lilienfeld & Stolley 1994). In this case the information obtained on disease occurrence is not the result of dedicated actions by the authorities but the result of initiatives of veterinarians, farmers or members of the public. Active surveillance refers to data collection specifically for surveillance purposes and is usually conducted to answer a particular question using structured survey techniques (Scudamore 2002). Examples of active surveillance include serological surveys of poultry flocks to determine exposure to avian influenza viruses, surveillance to confirm that a country is free of bovine spongiform encephalopathy (BSE) and cross-sectional surveys to determine the distribution of bluetongue virus.

3.1.2   Scanning *vs* targeted surveillance

Due to the confusing interpretations associated with the terms active and passive surveillance Morris (cited in Scudamore 2002) introduced the terms *scanning* and *targeted* to refer to the types of veterinary surveillance conducted in Great Britain. Scanning surveillance is defined as a general process whereby the entire animal population is continuously monitored for unexplained changes in the endemic disease situation. It does not target a specific disease but focuses on disease syndromes. For example, the occurrence of an increased number of cases of unexplained mortalities in poultry might provide the first indication that highly pathogenic avian influenza is present in a country. Scanning surveillance forms an important part of an early warning system and may be informed by both active and passively collected data.

Targeted surveillance, on the other hand, refers to the use of statistically structured surveys to collect specific information about a defined disease or condition so that its level of occurrence in a defined population can be measured, or its absence confirmed (Scudamore 2002). An example of targeted surveillance would be the use of surveys to determine the prevalence of *Varroa destructor* infestation among honey bee apiaries in the Auckland region of New Zealand after the disease was first detected in April 2000 (Benard &

Thornton 2000). Targeted surveillance may also refer to the sampling of high risk populations to detect the presence of disease (Salman 2003). An example of this would include the testing of fallen cattle stock for the presence of BSE (Doherr et al. 2001). Examples of targeted surveillance for avian influenza would be the wild bird surveillance program in Great Britain, in which wild birds (Anonymous 2008*a*) and hunter-caught birds (Ferro et al. 2008) are sampled and tested.

3.1.3   Sentinel surveillance

Sentinel surveillance refers to the monitoring of a group of animals or farms, geographic areas or laboratories for changes in disease frequency (McCluskey 2003, Racloz et al. 2007). Sentinel surveillance is a form of targeted surveillance in which selected populations are periodically monitored. Well known examples include the use of sentinel chicken flocks to detect or monitor diseases caused by arboviruses such as St Louis encephalitides and West Nile virus in the USA (Day 1989, Patiris et al. 2008), the use of sentinel chickens in poultry flocks to detect subclinical infections with low pathogenicity viruses (Marcus et al. 2007), The National Sentinel Hive Program to detect incursions of exotic bees or bee parasites into Australia and the use of sentinel cattle herds to monitor vesicular stomatitis in Colorado (McCluskey et al. 2000) and El Salvador (McCluskey et al. 2003).

3.1.4   Risk based surveillance

Stärk et al. (2006) proposed the following definition for risk based surveillance: *A surveillance programme in which exposure and risk assessment methods have been applied together with traditional design approaches to ensure appropriate and cost-effective data collection*. The impetus for the development of risk based surveillance approaches was the appearance and spread of diseases such as foot-and-mouth disease (FMD) and bovine spongiform encephalopathy in Europe. This situation caused veterinary surveillance agencies to come to a number of realisations. The first was that it is economically impossible to maintain surveillance for all diseases because of the limited funds available to support state veterinary services. The second was that a structured process is required to prioritise disease surveillance which considers the availability of finite resources.

3.1.5 Syndromic surveillance

According to the Centers for Disease Control and Prevention in the USA syndromic surveillance refers to the use of health-related data to signal the probability of a case or an outbreak prior to a formal diagnosis being made to warrant further public health response (Centers for Disease Control and Prevention 2006). Another more intuitive definition refers to syndromic surveillance as an investigational approach where health department staff, assisted by automated data acquisition and generation of statistical alerts, monitor disease indicators in real-time or near real-time to detect outbreaks of disease earlier than would otherwise be possible with traditional public health methods (Henning 2004). For example, public health departments might monitor over-the-counter drug sales as a means for detecting flu epidemics or foodborne illness such as salmonellosis. This approach relies on the use of traditional surveillance methods augmented by automated methods of data collection, analysis and reporting in real-time.

3.1.6 Rumour surveillance

Rumour surveillance is defined as the process whereby disease outbreaks are identified on the basis of reports from unofficial sources such as the media, professional groups and the general public (Grein et al. 2000). This type of surveillance has been important in the recognition of the occurrence of disease outbreaks such as Ebola in Uganda (Okware et al. 2002), severe acute respiratory syndrome (SARS) in China in 2003 (Crampton 2003) and avian influenza due to the H5N1 virus in Western Pacific countries (Samaan et al. 2005). SARS was initially brought to the attention of the World Health Organization (WHO) via anonymous email messages describing the occurrence of a mysterious pneumonia affecting patients in southern China (Crampton 2003).

Rumour surveillance is routinely carried out by a number of national and international organisations involved in the monitoring of human and animal health. These include the WHO, the Food and Agriculture Organization of the United Nations (FAO), and the World Organization for Animal Health (OIE). The main information sources for rumours of disease events include informal sources such as the electronic media (e.g. news, the Internet) and electronic discussion groups such as ProMED-Mail.

3.2   Requirements of a surveillance system

The OIE describes a surveillance system as a method that includes one or more component activities that generates information on the health, disease or zoonotic status of animal populations (Anonymous 2007*d*). A successful surveillance system is comprised of the following components (Zepeda & Salman 2003, Dufour et al. 2006):

- clear objectives (i.e. what diseases are to be targeted);

- definition of what indicators will be monitored (numbers of cases, species, the population at risk, type of production system etc);

- case definitions;

- a method for data collection;

- a legal framework to support surveillance activities;

- an appropriate infrastructure to support data management; and

- a procedure for evaluating the system's effectiveness.

Other key requirements include:

- adequate resources (laboratories, buildings, vehicles, diagnostic materials);

- sufficient numbers of trained personnel (pathologists, field officers, epidemiologists); and

- an adequate operating budget.

Avian influenza surveillance in European Union member states is comprised of three components: (1) surveillance in wild birds, (2) surveillance in domestic poultry, and (3) surveillance of dead birds (Pittman & Laddomada 2008). Each of these populations are examined for the presence of avian influenza virus itself or antibodies to the virus. The system is supported by legal directives of the European Union Council Directive 2005/94/EC (Council of the European Communities 2005). An early warning system based at the farm level has also been implemented, to encourage reporting of unusual increases in mortality (Pittman & Laddomada 2008).

3.3 Rare disease surveillance

For the purpose of this review a rare disease is defined as any disease present in a population at a prevalence below 5%. When a disease has historically been absent from a country, the objectives of rare disease surveillance are two-fold: (1) to maintain a constant watch over the population to ensure rapid detection of disease incursions if (and when) they occur, and (2) to obtain accurate data on the health of the national livestock population in order to provide evidence of disease freedom for international trade purposes (Dufour et al. 2001). Ideally, such a surveillance system should provide (Anonymous 2007*d*):

- a representative coverage of the target animal populations by field veterinary services;

- the ability to undertake effective disease investigation and reporting;

- access to laboratories capable of diagnosing and differentiating relevant diseases;

- a training programme for veterinarians, veterinary para-professionals and others involved in handling animals for detecting and reporting unusual animal health incidents;

- a definition of the legal obligations of private veterinarians in relation to the state veterinary service;

- a timely reporting of events to the state veterinary service; and

- details of a national chain of command.

A recent initiative by the OIE and the FAO EMPRES group resulted in the production of a comprehensive set of training materials detailing practices essential for early disease detection.[1] When a disease is at the point of eradication and prevalence approaches zero or because by nature it is rare, the objectives of surveillance are to detect disease. When an emerging disease newly enters a country the objectives are to rapidly detect disease by identifying potential areas at risk of incursion and spread.

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[1] http://www.fao.org/ag/againfo/programmes/en/empres/gemp.html

3.3.1   Detection of emerging diseases

The term emerging disease may be applied to any of the following situations (Brown 2004): (1) where a known agent appears in a new geographic area, (2) where a known agent or its close relative occurs in a new animal species, and (3) where a previously unknown agent is detected for the first time. The National Institute for Agriculture Research (INRA) takes a more quantitative approach to defining an emerging disease. Specifically, an emerging disease is a disease whose incidence (percentage of cases in a population per unit time) has significantly increased in the last 20 years, or which might increase in the near future. The emerging disease can be linked to one or more new agents (infectious or not), can be a known disease affecting a new host or transmitted by a new mechanism (new vector), or simply be a known disease whose incidence is significantly increasing (INRA 2006).

Table 3.2 provides a list of animal diseases that have emerged over the last 20 years. Examples of known diseases that have appeared in new areas include classical swine fever in The Netherlands (1997), *Varroa destructor* in New Zealand (2001), bluetongue in Europe (1997 – 2007), FMD in the United Kingdom, South America, Taiwan and The Republic of Korea (2000 – 2002), Newcastle disease in California (2002), equine influenza in Australia (2007), and African swine fever in the Caucuses (2006 – 2007). Examples of disease incursions that were truly novel include bovine spongiform encephalopathy (BSE) in the United Kingdom (1986), Hendra virus in Australia (1994) and Nipah virus in Malaysia (1998).

Concerns associated with the incursion of these diseases and others not mentioned can be categorised into three groups: zoonotic, wildlife, and, economic. Zoonotic concerns relate to the ability of animal diseases to affect humans. BSE, first recognised in cattle in the United Kingdom in 1986 (Wells et al. 1987), is an example of a novel disease transmissible to humans as variant Creutzfeldt-Jakob disease (Will et al. 1996). Nipah virus emerged in pigs in Malaysia to infect humans (Chua 2003) whilst the emergence of HPAI due to the H5N1 virus has affected humans in Asia and Africa (World Health Organization 2006). Many zoonotic diseases have been associated with wildlife reservoirs such as wild civets in the case of SARS (Wang & Eaton 2007), and wild birds in the case of avian influenza (Webster et al. 1992, Fouchier et al. 2003). The costs attributable to

Table 3.2: Examples of diseases of livestock that have emerged over the past twenty years.

Desease or agent	Type [a]	Area	Time period	Zoonotic	Factors involved
BSE	2	UK, Canada, USA	1986 – 2000	Yes	Contaminated feed
Bluetongue	1	Europe	1997 – 2007	Non	Arthropod-borne
HPAI-H5N1	1, 2	Southeast Asia	2003 – 2008	Yes	Unknown
FMD[b]	2	Argentina, UK, Taiwan	1993 – 2002	No	Trade
Nipah virus	2	Malaysia	1998	Yes	Wildlife
ND[c]	1	USA	2003	No	Wild birds
CSF[d]	1	The Netherlands	2000	No	Trade
ASF[e]	1	Caucuses	2007	No	Trade
SARS[f]	3	Hong Kong	2002	Yes	Wildlife
WNV[g]	1	USA, Canada	1999	Yes	Wild birds
Monkey Pox	1	USA	2003	Yes	Trade in wildlife
Varroa mites	1	New Zealand	2001	No	Importation
Hendra	3	Australia	1994	Yes	Wildlife
Equine influenza	1	Australia	2007	No	Trade

[a] Key: 1 = known agent appearing in a new geographic area, 2 = known agent in a new animal species,

3 = known agent or its close relative occurring in a new animal species.

[b] FMD: foot-and-mouth disease.

[c] ND: Newcastle disease.

[d] CSF: classical swine fever.

[e] ASF: African swine fever.

[f] WNV: West Nile virus.

[g] SARS: severe acute respiratory syndrome.

control measures and loss in trade due to these diseases has been substantial (Webster et al. 2006).

3.3.2   Outbreak detection

By passive surveillance

Passive surveillance based on reports from individuals in direct contact with animal populations (e.g. farmers, veterinarians and abattoir inspectors) constitute the main means by which new disease incursions have been detected. The dependence on passive surveillance for incursion detection has been viewed by some as the most cost-effective option for monitoring the health of animal populations (Doherr et al. 2001). There are many examples of situations where passive surveillance has been instrumental in outbreak detection. A review of 24 epidemics of FMD that occurred between 1992 and 2003 in

countries around the world found that of the 15 epidemics for which data were available, the index cases were detected passively by farmers (8 of 15) or by meat inspectors at the time of slaughter (2 of 15) (McLaws & Ribble 2007).

Despite the benefits derived from wide coverage of animal populations under farmer and veterinary care, passive surveillance systems may fail to rapidly detect disease incursions causing delays in the implementation of control measures. The main reason for this failure is associated with case underreporting. A number of factors contribute to this problem. The is related to awareness on the part of the farmer and veterinarian. A review of the 2001 epidemics of FMD in the United Kingdom and Taiwan found that the delay between incursion and detection was approximately 3 and 6 weeks, respectively (Gibbens et al. 2001, Bates et al. 2003). The fact that the last major FMD epidemic in the United Kingdom had occurred in 1967 – 1968 may have contributed to lack of awareness. Similarly, in Taiwan the last outbreak of FMD had occurred in 1929. Secondly, clinical manifestation of disease has been cited as a factor that limits detection. Disease may manifest itself either as a new clinical manifestation of a known disease in a known host or as a clinical manifestation that is similar to an endemic disease. This was apparent in the detection of FMD in Taiwan in 2001, the outbreaks of HPAI H5N1 that have occurred in Southeast Asia from 2003 – 2008 (Sims et al. 2005), and the epidemic of classical swine fever in The Netherlands in 2000. In the case of Taiwan, swine vesicular disease (SVD) is endemic and is difficult to differentiate from FMD clinically. Similarly, the presence of endemic Newcastle disease in some countries in Southeast Asia was believed to have confused avian influenza reporting (Sims et al. 2005). The outbreak of classical swine fever in The Netherlands in 2000 initially presented in pigs with clinical signs that were not typical of the disease. It is estimated that the delay between incursion and detection in this outbreak was approximately 5 – 7 weeks (Stegeman et al. 2000). The third factor influencing the interval to detection relates to the nature of the disease. Diseases like BSE with long latency periods that occur at low frequencies in animal populations pose a particular challenge for detection (Doherr et al. 2001).

Factors related to the structure and function of a country's veterinary infrastructure may also limit detection. Within this category are issues around incentives for reporting, the existence of established reporting systems, veterinary coverage of the animal population at risk and the response capacity of the system. The lack of sufficient incentives to en-

able farmer reporting is often cited as the major hurdle facing animal disease surveillance authorities, particularly in developed countries that use surveillance to maintain their disease freedom claims. This is because reporting adverse events generally results in a loss to the farmer, either through quarantine, investigation and trade restrictions and very little reward in the event that disease status is cleared. The lack of a functional passive surveillance system has been cited as a reason for detection delays in the outbreaks of HPAI H5N1 that occurred in Southeast Asia in 2003 – 2004 (Morris & Jackson 2005, Sims et al. 2005).

By active surveillance

Theoretically, an active surveillance programme in which all susceptible animals in a population are routinely examined for the presence of disease, represents the ideal method for detecting new disease incursions. This is valid under conditions where the epidemiology of the disease in question is known, diagnostic tests are available and unlimited resources are available to undertake surveillance activities. Active surveillance as an incursion detection tool has been associated with either targeted surveillance programmes (e.g. routine import or export testing, sentinel surveillance) or after identification of the index case by passive surveillance.

The level of dependence on active surveillance for disease detection depends on the disease, the perceived risk posed to animal and human populations and availability of resources to conduct surveillance activities. In order to establish an active surveillance system a disease has to be first identified as a problem. The problem with this approach is that new diseases may bypass detection. The BSE and SARS epidemics are good examples of these. Prior to identification in 1986 and 2003 (respectively), BSE and SARS were unknown diseases making it impossible to plan surveillance activities to detect them. Another issue is the time needed to make a diagnosis. The time period between incursion, sampling and diagnosis may be long (Thurmond 2003) resulting in delays in the implementation of control measures and therefore uncontrolled spread of disease.

Recent outbreaks and factors influencing the speed of detection

A brief review of the major animal disease epidemics that have occurred between 1995 and 2008 is presented in order to illustrate some of the problems associated with early disease detection. Over the last few years, incursions of FMD, BSE, HPAI H5N1, and equine influenza have made their presence felt in both developed and developing countries. In 1997 an outbreak of classical swine fever occurred in 429 pig herds in The Netherlands after an absence of five years (Hennecken et al. 2000). The outbreak was first diagnosed on 15 February 1997 in an area of high pig density. Interview of the manager of the index case herd indicated that he had observed clinical signs one month before confirmation and he had a *post mortem* done which diagnosed torsion of the bowel as the cause of death in the affected pig. It is estimated that disease detection was delayed by 5 – 7 weeks, which caused the disease to spread widely before control strategies could be implemented. The change in clinical manifestation of CSF was identified as one of the main reasons for the delay in detection (Hennecken et al. 2000).

The incursion of the FMD virus into the United Kingdom in 2001 was detected on 20 February, approximately three weeks after the disease was estimated to have entered the country. This delay in the detection resulted in widespread dissemination of the disease (Gibbens et al. 2001).

HPAI H5N1 outbreaks occurred in eight countries in Southeast Asia between 2003 and 2004. The disease spread widely through infected countries before it was officially recognised. In many cases the presence of disease in humans were the main indicators that an outbreak of avian influenza was occurring (Sims 2007). In many countries Newcastle disease was endemic, with clinical signs indistinguishable from avian influenza, particularly related to mortality. This is a situation where the reporting of all high mortality events by farmers could have provided evidence of an emerging disease. Additionally, disease appeared at the time of the Tet Festival in Vietnam, a period traditionally associated with increases in bird movements (Morris & Jackson 2005, Sims et al. 2005). Moreover, illegal movement of sick birds across borders may have contributed to the problem (Sims et al. 2005).

3.3.3 Establishing disease freedom

Another important objective of rare disease surveillance is to provide evidence that a country is free of prescribed diseases at the herd, zone or national level (Cannon 2001*a*, Dufour et al. 2001). The drivers for disease freedom include international-level trade requirements as defined by the World Trade Organization (WTO) agreements on the application of sanitary and phytosanitary measures (SPS Agreement).[2] This specifies the need for science-based evidence of disease freedom. As a result, the OIE has developed international guidelines for official procedures for the recognition of disease freedom with or without vaccination for four diseases of international concern (Anonymous 2007*b*): FMD, rinderpest, contagious bovine pleuropneumonia and bovine spongiform encephalopathy (BSE). Surveillance activities for proving disease freedom is generally based on the following strategies: (1) survey-based approaches that examine animals or samples from susceptible populations in order to detect clinical signs or other indications of the occurrence of disease or transmission of infection, and (2) routine reports from farmers, veterinarians, abattoirs and laboratories. One of the problems associated with proving disease freedom is that it is impossible to determine with absolute certainty that a disease is actually absent.

The objective of a survey-based approach to establishing disease freedom is to estimate, on the basis of negative survey results, the probability that the level of disease in a country is below a specified design prevalence (Cannon 2001*a*). To achieve this objective, surveys are typically conducted using a two-staged cluster design where farms are sampled at the first stage and animals from within selected farms are sampled at the second stage (Cameron & Baldock 1998). When designing a survey to demonstrate disease freedom, the required number of farms and animals within farms is determined on the basis of a number factors including the size of the population at risk, the design prevalence, the level of confidence required and issues related to test performance (diagnostic sensitivity and specificity) (Cannon 2001*a*).

The level of confidence in the test results is often quoted as the 95% confidence that the disease does not occur above the stated between-farm and within-farm design prevalence. The choice of prevalence values will depend on the characteristic of the disease. For a

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[2]`http:www.worldtradelaw.net/uragreements/spsagreement.pdf`

highly contagious disease, within-farm prevalence will be high. Test characteristics are measured in terms of the probability that a test result is positive given the tested animal is truly disease positive (sensitivity) and the probability that a test result is negative given that the tested animal is truly disease negative (specificity).

The problems associated with surveys for estimating freedom from disease are numerous. The effect of testing a population, in which the prevalence of disease is close to zero, using imperfect tests, while at the same time wanting a high level of confidence in the results, means that a large number of animals will need to be sampled and tested (Cannon 2001*b*). Because the diagnostic tests that are used may be imperfect, the number of false positive reactors (requiring further investigation) may be numerous, further adding to survey costs. For these reasons prevalence estimates from surveys to ascertain disease freedom may not provide absolute proof of the disease status of animal populations. Enhancements to survey based approaches include targeted surveys of high risk groups.

3.4   Surveillance system components

As a consequence of a number of key outbreaks around the world national animal health authorities and international organisations have examined ways to improve surveillance for emerging diseases within the limits of financial resources. In 2002, primarily in response to the 2001 epidemic of FMD, the Department for Environment, Food and Rural Affairs (Defra) in the United Kingdom published a document titled 'Priorities, Partnerships and Professionalism' (Scudamore 2002). In this document a strategy for surveillance for animal disease was outlined, based on five strategic goals: (1) to strengthen collaborations with surveillance providers, users and beneficiaries, (2) to develop a prioritisation process for disease surveillance, (3) to derive better value from surveillance information and activities, (4) to share information more widely, and (5) to enhance the quality assurance of the outputs. Within this document are detailed methods for improving the efficiency of the surveillance system for endemic and exotic animal diseases, antimicrobial resistance and animal welfare based on risk based and syndromic surveillance approaches. Since 2002 Defra have implemented a number of initiatives to enhance surveillance for both exotic and endemic diseases. One of the initiatives included the establishment of an integrated database system, Rapid Analysis and Detection of Animal-related Risks,

(RADAR)[3] to combine data on animal populations, cases of disease and risk factors in a central location. Another initiative included the use of a disease profiles to prioritise diseases for resource allocation and surveillance.

Similar documents have been produced by the three international agencies that deal with animal health issues, namely the FAO, OIE, and WHO (Anonymous 2004*b*). These have all pointed to the need to strengthen surveillance systems by enhanced passive and risk based active surveillance activities with particular focus on information gathering and collaboration (Anonymous 2006*b*). Recently the three agencies developed The Global Early Warning and Response System (GLEWS),[4] a jointly run global surveillance system for animal disease. The purpose of this system is to enhance global surveillance by sharing of information on outbreaks, improving data analysis and response efforts.

3.4.1 Sources of data

Investment in a well functioning veterinary information system that has the capacity to integrate multiple sources of data has been identified as an essential component of an effective surveillance system (Scudamore 2002). The RADAR system operated by Defra in the United Kingdom has been designed to capture information recorded at the farm level, individual animal movement data, disease event information, and details from diagnostic veterinary laboratories. Additional information recorded by the system includes climate and weather information, details relating to companion animals (primarily from pet travel schemes and horse registration details). Data sources for the system include government databases on livestock, agriculture holdings, private veterinarians, farmers, abattoirs and, veterinary diagnostic laboratories. Due to the enormous task of integrating existing data sources and establishing new sources (e.g. detailed information about the spatial distribution of domestic livestock species), the full implementation of the system is ongoing and is being undertaken in three phases between 2005 and 2013. The potential benefits to be derived from this system include:

- the ability to detect disease outbreaks promptly;

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[3] http://www.defra.gov.uk/animalh/diseases/vetsurveillance/radar/project.htm

[4] http://www.who.int/zoonoses/outbreaks/glews/en/index.html

- the ability to monitor multiple data sources (increasing the sensitivity of detection methods);

- a standardised system of data entry, which should minimise data entry errors and therefore improve data quality;

- the opportunity to apply more sophisticated analytical techniques (e.g. temporal, spatial, and spatio-temporal analyses) on accumulated data; and

- the ability to evaluate the efficacy of the data gathering process.

In the event of infectious disease outbreaks in animal populations, it is anticipated that these systems will allow the true extent of disease to be quickly and accurately reported, allowing animal health authorities to make appropriate decisions when and where they are required.

A key factor in determining the success or otherwise of a data system like RADAR will be its ability to combine disparate data sources into a useable centralised database in real-time (Shephard 2006). The lack of standards in the systems, formats and type of data captured in animal health is a major hurdle to data transfer, amalgamation, verification, updating and linking (Shephard et al. 2006). Additionally, given the number of organisations involved in data collection and the commercial aspects of the animal health sector, issues related to information sharing presents yet another hurdle. In order to address these limitations, the developers of RADAR have taken a phased approach to system implementation, including introduction to interested parties, development of data standards, determination of the legal basis for data sharing amongst others.[5]

3.4.2 Data components

Health events

An effective veterinary surveillance system should acquire health event data from a number of sources to allow true changes in a population's health profile to be identified. This can be achieved by monitoring data routinely recorded by veterinarians, animal health

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[5] `http://www.defra.gov.uk/animalh/diseases/vetsurveillance/bag/pdf/radar.pdf`

laboratories, abattoirs, outbreak investigations and sentinel surveillance systems (Thrusfield 2007). Event details from each of these sources should include the unique identifier of the farm or village affected, the date of onset of clinical signs, the number of animals affected and the species, age and sex of affected individuals. These data represent the numerator when estimates of disease prevalence or incidence are calculated.

Ideally, data from multiple sources should be monitored and aggregated by a centralised body (usually the state veterinary service) in real-time. In most countries, data is generally managed and stored by data providers in electronic databases, but reporting of health events to animal health authorities generally occurs manually, which limits the possibility of real-time surveillance.

Examples of animal health database systems that have been developed specifically to manage animal health event information include the TickINFO system for storing data on amblyomma tick surveillance in seven countries in the Caribbean (Pegram et al. 2007), the Animal Health and Surveillance Management system in the USA (AHSM) and the National Animal Health Information System in Australia (NAHIS).[6] The TickINFO database was the result of a regional collaborative effort between the US Department of Agriculture (USDA), the French Agricultural Research Centre for International Development (CIRAD) and the FAO. The database was developed using a relational database and recorded data in three tables: (1) village-level details, (2) farm-level details, and (3) details relating to individual visits made to farms. The village data table listed all the villages within each of the islands taking part in the programme, the farm table recorded data relating to individual farms including geographic location and the visit data table recorded details of visit dates, the number of animals present at each visit, the number of animals examined and the number of animals found to be carrying ticks. Surveillance data were periodically transferred to the programme's regional office via email for analysis or uploaded directly to the CaribVet website[7] for presentation in the form of risk maps. Although this system was simple and easy to use it had a number of limitations. Counts of animals on each farm were intermittently recorded at each visit and it was frequent that visit details were not entered into the system due to a shortage of trained data entry personnel. The former limited the ability to compare tick prevalence within and between

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[6]`http://www.animalhealthaustralia.com.au/aahc/programs/adsp/nahis/nahis_home.cfm`
[7]`http://www.caribvet.net/`

islands.

TADinfo[8] is a Java based information management system developed by the FAO. Its purpose is to assist developing countries with a ready to use system for recording and storing animal health event information. At the time of writing it is used in at least 20 countries throughout the world. The system has been structured in the form of modules designed to store and analyse data related to field observations, abattoir observations, active surveillance, livestock census details and vaccination campaigns. It also has Geographic Information System capabilities.

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[8]`http://www.tadinfo.org`

The population at risk

Access to details of the farm and/or animal population at risk is important for two reasons. Firstly, it allows standard measures of disease frequency to be calculated, expressed in terms of the number of cases of disease per head of population. This allows the burden of disease to be compared across time frames, geographical areas and by animal- or farm-level factors. Secondly, details of the animal and farm population at risk is of great value in the event of an outbreak of infectious disease in an animal population. Knowing exactly where animal populations are located allows disease control and prevention efforts to be appropriately prioritised. Population at risk data is routinely derived from purpose-built farm animal databases, animal censuses and surveys.

National farm databases attempt to provide an inventory of commercial and non-commercial farm enterprises within a country. Details recorded for each enterprise include a unique enterprise identifier, the enterprise type and location and counts of each animal species present. Location may be recorded in either point or polygon format. Point location details for farm enterprises can be collected quickly and easily using global positioning systems. Using this approach longitude and latitude coordinates are recorded for some pre-defined location, say the farm gate, the main farm building or farm yards. To record location details in polygon format the coordinates of the vertices of the farm boundaries need to be defined and stored. New Zealand (Sanson & Pearson 1997) and Uruguay (Ministry of Livestock, Agriculture and Fisheries, Uruguay 2008) are two countries where individual farm locations are recorded in polygon format.

The ability of farm databases to provide complete and accurate details of a farm population at risk is entirely dependent on sufficient resources being made available to ensure that they are kept up to date. The infrastructure and costs associated with the implementation of such systems are considerable. The British Poultry Register (Houston et al. 2006) was established in 2005 in response to the passing of European legislation requiring Member States to reduce the possibility of HPAI H5N1 transmission from wild birds to domestic poultry. To establish the registry, animal health authorities first determined that premises with greater than 50 birds would be required to register with the system. Data were gathered by various means: telephone, post, email, and direct processing of company data. The British Poultry Register is currently linked to the Diseases of Poultry Disease Control System (DP-DCS) and RADAR, the main animal surveillance database

in use in the United Kingdom. Data transfer between these systems occurs via dynamic links updated every 30 minutes. This system has been used to define high risk areas for HPAI H5N1 incursion into the United Kingdom (Figure 3.1).
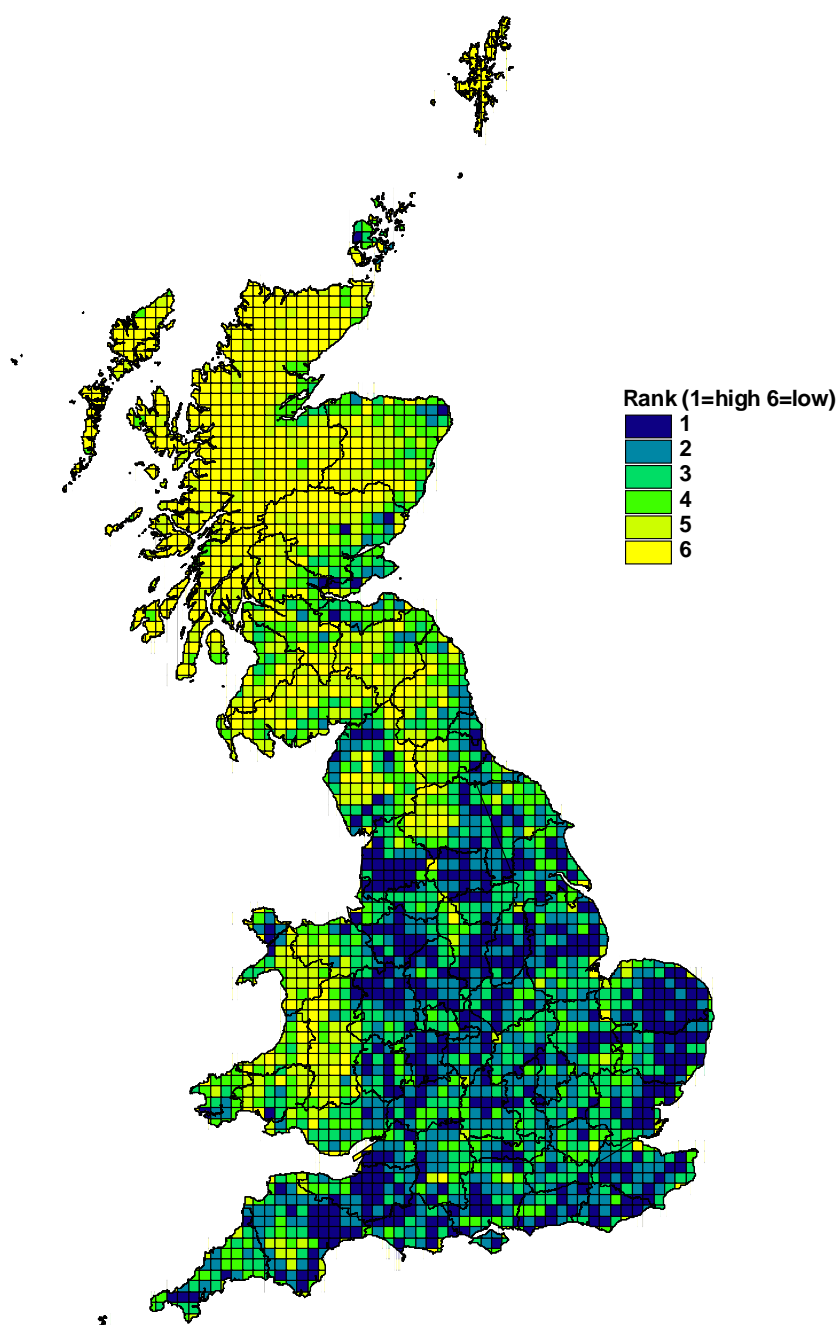
Figure 3.1: Combined poultry and wild bird scores to show areas of Great Britain where the probability of incursion of HPAI H5N1 is likely to be highest given knowledge of bird and poultry populations in those areas (ranked 1 – 6 in order of high to low priority/concern). Adapted from Crick et al. (2006).

In most countries information about the domestic animal populations at risk is derived from details recorded at a national agricultural census. Census data usually takes the form of a count of animals present at each farm location on the day of the census. For reporting counts are aggregated by administrative units such as village, regions or province. A major limitation of census data are that they are prone to under enumeration and inaccuracy. A study to examine differences in details recorded in Defra's Disease Control System (DCS) database and details collected from farms during the 2001 epidemic of FMD in the county of Cumbria in the United Kingdom showed that the DCS underestimated the number of premises with livestock by 16% (Honhold & Taylor 2006). Differences exist among countries in terms of how frequent animal censuses are conducted. For example census frequencies range from annually for the poultry data system in the United Kingdom to every 5 to 10 years for countries in the Caribbean. Despite the limitations of census data, it continues to provide a valuable estimate of the size of an animal population at risk for the conduct of veterinary surveillance activities. In the case that animal population numbers are required for periods between census years, various estimation approaches are possible. These approaches include population growth models (Baldock et al. 2003), capture-mark-recapture methods and interpolation.

Animal movement

Any early warning system requires information on the movement patterns of animal populations in order to assess the potential for disease spread arising from the movement of animals from one location to another. The 2001 outbreak of FMD in Great Britain highlighted the role that animal movements can play in dispersing disease among a naïve population (Kao 2002, Mansley et al. 2003, Mattion et al. 2004) through direct and indirect contact (Gibbens et al. 2001, Woolhouse et al. 2005). Moreover, knowledge of movement patterns and how they vary by season, area and enterprise type are useful in terms of identifying high risk periods and locations that are likely to disperse disease, in the event that it enters an animal population (Christley et al. 2005, Kiss et al. 2006, León et al. 2006). With knowledge of these risks, more focused and cost effective surveillance approaches can be applied. An example of this approach was that taken by New Zealand during the outbreak of equine influenza that occurred in the eastern states of Australia in August 2007. Acting on the reports of the occurrence of disease in two states of Australia on 25 August 2007, animal health authorities in New Zealand banned the importation of

live horses from Australia and used details of importation dates and the farm of origin of horses that were recently imported from Australia to determine the likelihood of an incursion of equine influenza into New Zealand (McFadden et al. 2007). The investigators stratified premises where horses were present into three risk categories in an effort to prioritise visits to be made to determine the clinical status of imported and in-contact horses. The three risk categories were: (1) high risk, classified as premises with horses showing clinical signs that were imported 10 days prior to notification of equine influenza in Australia (between 15 and 25 August 2007), (2) medium risk, classified as premises with healthy horses that were imported between 15 and 25 August 2007 and, (3) low risk, classified as premises with healthy horses imported from Australia between 1 and 14 August 2007. Although all premises identified as 'at risk' were visited, high and medium risk premises were visited by MAF personnel trained in biosecurity procedures whereas low risk properties were visited by private veterinarians. There were also differences in the tests applied to each risk group: high and medium risk premises were subject to both virus detection and serological testing whereas the low risk group received serological testing only. This example demonstrates how movement event details can be used to focus resources, in an effort to optimise the sensitivity of detection of disease. A limitation of this process was the use of serology to detect equine influenza in horses that are normally vaccinated against H3 subtypes (the OIE recommends vaccination against H3N8 strains from Europe and America). In this case a DIVA strategy might have been useful to differentiate between whether antibody titers in tested animals were due to vaccination or infection. Depending on the type of vaccine used (inactivated *vs* vectored) the ease with which a DIVA may be used will vary. For example, horses vaccinated with a vectored vaccine will be negative to a preliminary C-ELISA test, but positive to the HI test, whilst those that have been infected will be positive to both the C-ELISA and the HI test. In the case that inactivated vaccines are used, the C-ELISA is unable to differentiate between vaccinated and infected animals, making DIVA of little value.

As a consequence of widely publicised incidents of disease in humans arising from the consumption of food derived from animals, the need for food animal traceability systems has been stressed in recent times (Stevenson et al. 2007). Examples of food safety incidents include the link between BSE and vCJD (Will et al. 1996), the contamination of poultry feed with dioxin in Belgium in 1999 (van Larebeke et al. 2002), and *Escherichia*

coli O157:H7 contamination of beef in the USA (Rangel et al. 2005). Traceability is defined as the the ability to document all of the relevant elements – movements, processes, and controls – needed to document the location of an animal and the product derived from it throughout its life history (Caporale et al. 2001, Ammendrup & Barcos 2006). The term therefore encompasses two aspects, traceability of animals and traceability of animal product.

In addition to its obvious uses for maintaining food safety, traceability is also a useful biosecurity tool. Examples of animal registration systems used as tracing and surveillance tools for animal diseases include the pig traceability system in The Netherlands (Dagorn 2003) and the Israeli Computerised Animal Health Monitoring System (ICAHMS) (Van-Ham, 1996 cited by Caporale et al., 2001). In the Dutch system, all pigs destined for market are registered and identified, allowing stock to be traced back to the farm of origin if notifiable diseases are identified at the time of slaughter.

To enable complete tracing of animals within a country an ideal animal traceability system should have the following components (Caporale et al. 2001, Ammendrup & Barcos 2006):

- a system for uniquely identifying animals or groups of animals;

- a system for uniquely identifying farm premises;

- a system for recording movements of animals from one location to another throughout their lifetime;

- a system for recording interactions between premises; and

- clear rules and procedures for reporting, recording, updating, verifying, validating, processing and storing information to ensure integrity of the system.

A range of possibilities exist for defining farm and animal units and these will vary according to the animal species of interest and local conditions. Farms may be defined as any location where animals are kept for production and could refer to an area of pasture, land owned by an individual or a group of individuals, or a village. Within individual farm enterprises, animals may be identified individually or in groups or batches. Systems in
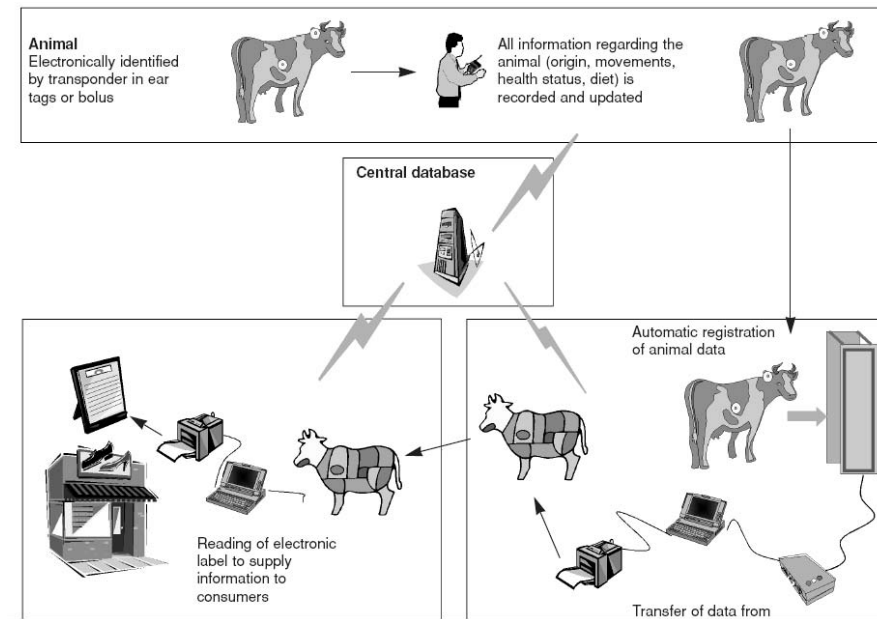
Figure 3.2: Example of a bovine traceability system using electronic transponders. Source: Caporale et al. (2001).

which animals are individually tagged are generally easier to track than systems where animals are identified at the group level. In certain production systems, for example broiler production and aquaculture, batch or group identification is the only feasible option.

The second component of a traceability system is the ability to trace animal product. Traceability of animals and animal product along the entire production chain is a major concern for consumers, and this has forced animal health authorities to make traceability a priority issue (Figure 3.2). An ideal animal product traceability system should have the following components:

- electronic identification of each animal;

- automatic registration of animal identification data at slaughterhouses and transfer of animal identity and animal-level details to the carcass and meat cuts using electronic labels; and

- a system for reading and printing tag data which can then be made available to the consumer, if required.

The benefits to be gained from complete food animal traceability include (Canadian Pork Council 2005):

- minimisation of the impacts of a foreign animal disease outbreaks by facilitating risk assessment of movement patterns, monitoring of animal movements during outbreaks, and improving outbreak response times;

- mitigation of the effects of food safety crises (through informed responses to animal disease outbreaks and food safety incidents);

- ensured continued access to domestic and export markets; and

- improved competitiveness of livestock industries.

A number of countries, particularly those with livestock industries involved in international trade, have implemented or improved existing traceability systems. Examples of implemented traceability systems include the National Livestock Identification System for Cattle (NLIS) in Australia (Meat and Livestock Australia 2008), the Sistema de Gestión Sanitaria (SGS) in Argentina (Ministry of Agriculture, Argentina 2008), the Sistema Nacional de Información Ganadera (SNIG) in Uruguay (Ministry of Livestock, Agriculture and Fisheries, Uruguay 2008), the Brazilian Identification and Certification System (Sisbov) (Ministry of Agriculture, Brazil 2008), the Livestock Ranch Official Certification Program in Chile (Ministry of Agriculture, Chile 2008), the Animal Movement Licensing System (AMLS) and Cattle Tracing System (CTS) in the United Kingdom (Mitchell et al. 2005), and the National Movement Database Tierverkehrsdatenbank (TVD) in Switzerland (Office Vétérinaire Fédéral 2008).

Ideally, all domestic animal species should be recorded within a system and the data captured should include: (1) a list of all animals and their unique identifiers, (2) a list of all farm enterprises and their unique identifiers, and (3) the dates and details of all movements of animals from one enterprise to another for the duration of each animal's lifetime. In reality, countries have taken various approaches when implementing animal traceability systems with the result that there are considerable differences between countries in terms of the number of components that have been implemented, the number of species and proportion of animals covered by each system and the methods of data capture (i.e. electronic *vs* paper based). In most cases implementation of a complete traceability system is

constrained by the costs associated with initial implementation and the resources required to maintain the system as well as the specific requirements of trading partners. Using the method proposed by Golan et al. (2004) the systems implemented in red meat producing countries throughout the world have been classified in terms of their breadth, depth and precision (Table 3.3). The breadth of a system refers to the amount of information recorded for the individual units, the depth of the system is the extent to which animals may be tracked forward or backwards. Precision is a measure of the extent to which a single modem can be traced within the system. Assessment by Stevenson et al. (2007) showed that, of the nine red-meat producing countries that were evaluated, the Australian National Livestock Identification system ranked highest in terms of depth, breadth, and precision.

Published studies describing animal movement patterns include those of cattle in the United Kingdom (Christley et al. 2005, Ortiz-Pelaez et al. 2006), cattle in Denmark (Bigras-Poulin et al. 2006), and cattle in Argentina (León et al. 2006). For countries without operational traceability systems, the only option for characterising animal movement patterns is by conducting appropriately designed randomised surveys of each industry of interest. Other options include using social network analyses using egocentric or snowball sampling. Egocentric sampling is the process whereby a select group of farms are contacted and asked to indicate who they have contact with (Andresen et al. 2004). These named contacts are then followed up and asked the same question. This process is repeated until there are no more contacts identified. Sanson (2005) provides an example of a cross-sectional survey of on- and off-farm movements of cattle and sheep in New Zealand, with the aim of determining the likely role of movement in the spread of an unrecognised outbreak of FMD.

3.4.3   Organising data

An important consideration in bringing together multiple data components in animal health, relates to how the data is aggregated in a centralised data system and what are the critical requirements for making such a system function. Stevenson et al. (2007), Fick & Doluschitz (2007) and Bellini et al. (2007) provide examples of how the various data components can be integrated to facilitate real-time surveillance at the national-level. Critical

requirements for a functional integrated animal health information system are provided by (Shephard et al. 2006).

A major hurdle in implementing effective surveillance systems relates to overcoming the logistics of retrieving data from those contributing to the system and then assimilating that data into a useable format. These factors are particularly a problem in animal health where there is no universal set of disease definitions, comparable with the International Classification of Diseases (Anonymous 1977) widely used in human medicine. Surveillance systems implemented in both human and animal health use a range of methods for data collection including both manual and automated data entry methods. Manual data entry is common when hand written reports from regional offices are sent to a central authority on a regular basis. The unavoidable delays in transferring hand written records into the system results in delayed reporting time, limiting the timeliness of the system as a whole. Electronic capture methods are those where data from contributors reach the central authority by electronic means (e.g. email, the Internet). An example of this approach is the Point-of-Care (POC) system that is commonplace in hospitals in the United Kingdom and the USA. POC is essentially a hospital-based information system where electronic devices (e.g. hand held computer devices) are used to record patient data (Shortliffe et al. 2001). This allows the hospitals to monitor in real time the medical record of each patient in a standardised format. In addition, summaries can be made of the patient record and transferred to the relevant authorities for biosurveillance. In addition to providing a means for real time monitoring, most POCs are designed as decision support tools for the clinician by providing lists of differential diagnoses, drug information (e.g. dose rates, contraindications, side effects) and diagnostic test information (e.g. test sensitivities and specificities) in a readily accessible format (Aryel 2006). The value of hand held computer devices is that recorded information can be validated at the time of data entry and, in the event of an error, the presence of the patient and the diagnostic or therapeutic procedure being carried out usually means that the error can be corrected quickly and easily.

Once data are collected it needs to be aggregated in a way that is useful for users of the surveillance system (Buehler et al. 2003). One particularly challenging issue is the process of standardising clinical observations and diagnoses into a common format. The approach used in human health surveillance systems is to classify events into syndromic or prodromic groupings (Reis & Mandl 2004). Systems in use in human medicine in-

clude the International Classification of Diseases (Anonymous 1977) and the Diagnostic and Statistical Manual of Mental Disorders (DSM-4).[9] The DSM-4 lists categories of psychiatric disorders and their associated diagnostic criteria, as defined by the American Psychiatric Association. It is used globally by clinicians and researchers as well as pharmaceutical companies and policy makers. An example of syndromic groupings used in a veterinary setting would be the disease classification system for dairy cattle used by Livestock Improvement Corporation (New Zealand, Livestock Improvement Corporation, 2008). Roberts et al. (2006) provide details of a system where equine diseases are classified by body system.

Data providers for veterinary surveillance systems should include farm managers, veterinarians, drug companies, abattoirs, and diagnostic laboratories. Each of these collect a range of information in a format which is often difficult (if not impossible) to be combined into a format that is able to be used for meaningful epidemiological analysis. I propose that a set of standards need to be devised for recording of health and production information in domestic animals. This would provide two benefits. Firstly, it would allow information from a range of different sources to be assimilated, enhancing the overall sensitivity of the system to detect outbreaks and emerging disease conditions. The second benefit is that, once developed, system components (e.g. animal-farm databases, animal movement databases) could be sold on to other countries. This would offset costs for the country developing the technology and dramatically reduce deployment costs for the country purchasing the technology, effectively eliminating the need to 'reinvent the wheel'.

3.5 Methods for incomplete data

An important aspect of veterinary surveillance is the provision of valid estimates of disease frequencies which may be used to inform policy decisions on control measures to be implemented. Valid estimates of disease frequency are possible when all case events have been captured by the system and updated data on the population at risk are available. The reality in animal health is that data obtained from the many sources may be subject to bias (selection and misclassification), which in turn decreases the validity of the correspond-

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[9]`http://psych.org/MainMenu/Research/DSMIV.aspx`

ing estimates of disease frequency. As a result, decisions informed by these estimates may be flawed. Sources of bias include underreporting and inconsistent reporting, which may vary with the source of the data and over space and time. Recognising that data gathered from surveillance systems generally reflect a proportion of the actual number of cases that occur (under ascertainment) a number of approaches, pioneered for AIDS surveillance and wildlife management, provide a means by which one can estimate the number of unrecognised cases. These methods include back-calculation or back extrapolation (Brookmeyer & Gail 1986, 1988), capture-mark-recapture approaches (Hook & Regal 1995), and epidemic transmission models (Wang & Ruan 2004).

Back-calculation methods were developed during the early years of the HIV/AIDS epidemic to estimate the incidence of infection on the basis of reported clinical cases and the distribution of incubation periods (Brookmeyer & Gail 1986, 1988). The method is based on the principle that the number of clinical cases of disease in a population will be dependent on the number of infected individuals present and the length of the incubation period (Donnelly et al. 2003, Brookmeyer 2004). This method has been used to estimate the incidence of BSE in the United Kingdom (Anderson et al. 1996, Donnelly et al. 2002, 2003) and France (Supervie & Costagliola 2004, 2007). Supervie & Costagliola (2004) used a modification of the back-calculation method to estimate the age and year-specific incidence risk of BSE in French cattle between 1990 and 2001 based on a previous study which showed that 20% of cases were identified by passive surveillance. These authors estimated that 301,200 (95% CI 27,600 – 837,600) cattle were infected with BSE during the study period, a number many times greater than the 103 cases that had been identified at the time by passive surveillance. This method is limited by its dependence on the observed number of cases which are themselves prone to underreporting. In addition, knowledge of the distributional form of the incubation period is critical. Reviews of these methods and their application to AIDS and BSE are provided by Donnelly et al. (2003) and Brookmeyer (2004).

Capture-mark-recapture methods have been developed to estimate the size of wild animal populations on the basis of capturing, marking, releasing and recapturing animals over a period of time (Seber 1982). These methods have since been used in a number of non-ecological settings, including studies to estimate the level of under-counting in a population census (Darroch et al. 1993) and to estimate the level of underreporting of

health events to provide adjusted estimates of disease frequency (Hook & Regal 1995, LaPorte et al. 1995). Examples of situations where capture-mark-recapture methods have been used in human epidemiology include the assessment of the most accurate data source for estimating the frequency of adolescent injuries (LaPorte et al. 1995), assessment of the surveillance sensitivity for sexually transmitted disease in The Netherlands (Reintjes et al. 1999), estimation of the prevalence of malaria in The Netherlands (Hest et al. 2002) and estimation of the incidence of stroke in the United Kingdom (Tilling et al. 2001). These examples are based on data aggregated over a single time period. Capture-mark-recapture methods use statistical models to aggregate data captured by multiple data sources (health registries, surveillance databases, birth or death registries) that contain incomplete and partially overlapping data as well as sources that may not be independent. The total number of cases of disease is then computed as the sum of the observed cases and the estimated number of unobserved cases from the capture-mark-recapture model. The use of these models rely on the following assumptions (Hook & Regal 1995):

- the population of interest should be constant or closed during the study period;

- information recorded on each unit of interest in the separate data sources must have a common, unique identifier to facilitate matching of information from different data sources;

- each unit of interest should have the same 'catchability' (that is, an equal probability of being monitored); and

- data sources must be independent (the probability of a unit being captured by one source does not depend on the remaining sources).

A number of models are available to conduct capture-mark-recapture analyses and their use will depend on whether the data sources are considered to be independent (two source models) or dependent (log-linear models) (International Working Group for Disease Monitoring and 1995). Examples of the use of capture-mark-recapture methods in veterinary science are rare. To the best of my knowledge, only two veterinary examples have been published: del Rio Vilas et al. (2005) and Böhning & del Rio Vilas (2008). In Great Britain del Rio Vilas et al. (2005) used capture-mark-recapture methods to estimate the number of holdings infected with scrapie as well as to estimate the sensitivity of three

scrapie surveillance systems. The authors used three capture-mark-recapture methods (two source models, log-linear models, and a sample coverage method) to aggregate data from three scrapie surveillance data sources: (1) statutory notifications of scrapie-positive holdings recorded within the Scrapie Notification Database (SND) ($n = 141$), (2) positive holdings ($n = 67$) from an abattoir survey (AS) of sheep greater than 18 months of age and, (3) scrapie-positive holdings ($n = 12$) from a fallen stock (FS) survey between January 2001 and April 2002. Using the two source model approach, the data sources were treated as independent and the estimated number of missing scrapie-positive holdings obtained from pairwise combinations of the data sets (i.e. SND-AS, SND-FS, and AS-FS), ignoring the third. The number of scrapie-positive holdings missed by each data source was 936 for the SND-AS comparison, 170 for the SND-FS comparison, and 336 for the AS-FS comparison. The estimated number of missed cases from the SND-AS comparison was 5.5 times greater than the number missed by the SND-FS comparison. This illustrates one of the major limitations of using capture-mark-recapture methods when data sources show some level of dependence. In the second approach, a series of log-linear models were fitted under various assumptions of independence or dependence between sources. The most significant model estimated a total of 1,653 (95% CI 354 – 6,434) missed scrapie-positive holdings under the assumption that data recorded in the SND and AS were related. The prevalence of scrapie-positive holdings in Great Britain was estimated to be 0.82%. The Rcapture package (Baillargeon & Rivest 2007) implemented in the statistical software package R (R Development Core Team 2008) provides a comprehensive and accessible set of tools for analysing capture-mark-recapture data.

3.6 Electronic surveillance

An obstacle to early disease detection in developing countries is the lack of a suitable infrastructure to support information flow (Butler 2006a, Johnson & Blazes 2007). This is a concern, as developing countries have been identified as the likely source of a number of emerging diseases (Butler 2006b). Recent examples of these include the recent spread of FMD to Europe from 1985 to 2006, thought to have originated in a number of countries in Asia and South America (Valarcher et al. 2008) and the outbreaks of HPAI H5N1 in Southeast Asia from 2003 (Sims 2006, 2007). The Internet provides a rich source of data

that can be used by developed and developing countries to increase situational awareness of infectious disease emergence (Grein et al. 2000, Hugh-Jones 2001, Heymann 2004). Ready access to the Internet and the presence of effective telecommunication networks in remote areas have increased the usage of electronic tools as ways to augment the effectiveness of traditional surveillance approaches. Recognising the need for consistent and timely reporting and dissemination of information about outbreaks, a number of initiatives have addressed early disease detection through electronic surveillance networks (Jebara & Shimshony 2006), many of them mediated though international organisations such as the FAO, OIE and WHO.

At the international level, electronic surveillance approaches have been used to monitor official and unofficial sources of disease information to alert participants of outbreaks of disease occurring in other countries and to raise awareness of emerging disease syndromes. This information can then be used by participating countries to modify import or export procedures on the basis of up-to-date risk assessments. Countries experiencing outbreaks of diseases of international concern in both animals and humans are mandated to report outbreaks to the respective international authorities (WHO, in the case of human diseases and the OIE in the case of animals). Although the official disease status of countries are available from these authorities, the degree of detail recorded in terms of the extent of outbreak areas tends to be limited, as does the speed with which disease status of countries is updated. The monitoring of unofficial sources such as Internet news groups and discussion sites provides a means for increasing the sensitivity of early outbreak detection. Examples of electronic surveillance systems include the Internet-based discussion group ProMED,[10] the Global Public health Intelligence Network (GPHIN) operated by the Canadian government, the World Animal Health Information Database (WAHID) operated by the OIE, the Emergency Prevention System for Transboundary Animal and Plant Pests and Diseases (EMPRES) operated by the FAO, and the Global Early Warning System (GLEWS) jointly operated by the OIE, FAO and WHO. Although these initiatives provide a useful starting point, they have been criticised for focusing on data reorganisation rather than data analysis (Brownstein et al. 2008).

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[10]http://www.promedmail.org

3.6.1 Data sources

ProMED

ProMED was established in 1994 as an Internet-based program to monitor emerging diseases (Madoff 2004). Its scope includes diseases of plants, animals and humans (Woodall 1997). Its role therefore is to serve as a global early warning and disease reporting system for emerging diseases. Information on disease outbreaks are received on a daily basis from subscribers from over 164 countries, and government and non-government agencies. These reports are verified by subject matter experts and posted to the ProMED website and emailed to the list with with comments and accompanying information regarding the disease of interest. ProMED is now a well recognised source of disease information for international agencies such as the WHO, OIE and FAO, government and non-government agencies (Jebara & Shimshony 2006).

Information gathered by the ProMED system has been used in several ways. In animal health it plays an important role in raising awareness of a potential disease threats in countries that trade with, or are neighbouring a reporting country (Hugh-Jones 2001). Examples include the equine encephalitis outbreak in Venezuela in 1999 (ProMED-mail 1999), the outbreaks of HPAI H5N1 in Indonesia in November 2003 (ProMED-mail 2003), and mortalities in pigs in China attributed to *Streptococcus suis* in 2003. Specific avian disease examples include the outbreaks of Newcastle disease in double-breasted Cormorants in Canada (ProMED-mail 1995*b*), and poultry in Sweden in 1995 (ProMED-mail 1995*a*), poultry deaths in Romania attributed to mouldy feed in 1998 (ProMED-mail 1998), and poultry products contaminated with dioxin in Belgium in 1999 (ProMED-mail 1999). In addition, ProMED have been instrumental in examining the spread of HPAI H5N1 (Kilpatrick et al. 2006).

Despite claims of its usefulness as a global early detection system, only one study has attempted to evaluate the quality of information reported by ProMED. Cowen et al. (2006) reviewed 10,490 disease reports from ProMED between January 1996 to December 2004. The authors found that reporting was dominated by the USA and Great Britain, followed by Canada, Australia, Russia, and China. For Africa, Asia and South America, reporting varied across and within continents. Rabies was the most frequently reported disease in 1997 and 1999, FMD in 2001 and avian influenza in 2003 and 2004.

The existence of ProMED has initiated a number of similar developments in both human public and animal health. Examples of early warning systems established in public health include the Global Public Health Intelligence Network (GPHIN), HEALTHMAP and the Global Outbreak Alert and Response Network (GOARN). Similar initiatives in animal health include the World Animal Health Information Database (WAHID) of the OIE and the EMPRES system of the FAO.

The Global Public Health Intelligence Network

The Global Public Health Intelligence Network (GPHIN)[11] is an electronic early warning system that provides data on outbreaks obtained from the news media, health and science web sites in a number of languages (Mykhalovskiy & Weir 2006). It is operated by the Public Health Agency of Canada on a continuous basis to provide information to a number of fee-paying subscribers such as the WHO and the FAO. Data gathered by this system are monitored by other global early warning systems such as EMPRES. GPHIN monitors disease outbreaks, infectious diseases, reports of food and water contamination, bioterrorism, exposure to chemical and radioactive agents, and natural disasters. Data are monitored by a combination of computer-based models and analysts for the presence of unusual events that would be of concern to public health.

World Animal Health Information Database

The World Animal Health Information Database (WAHID)[12] is operated by the OIE and stores reports of infectious disease outbreaks from member countries. It is intended to replace and extend the web interface system Handistatus II.[13] Three categories of information are provided to WAHID by OIE member countries: (1) notifications of animal disease emergencies, (2) endemic disease situation reports (submitted every six months), and (3) annual reports detailing a country's animal health situation, and capacity relating to diagnostic laboratories and other animal health affiliated facilities.

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[11]http://www.phac-aspc.gc.ca/media/nr-rp/2004/2004_gphin-rmispbk-eng.php

[12]http://www.oie.int/wahid-prod/public.php?page=home

[13]http://www.oie.int/hs2/report.asp

EMPRES

The Emergency Prevention System for Transboundary Animal and Plant Pests and Diseases (EMPRES)[14] was established by the FAO in 1994 to minimise the likelihood of transboundary diseases of plants and livestock causing major economic loss in developing countries. It was initially established as a means for facilitating the sharing of data between FAO staff at head office in Rome and field staff, as well as with other entities involved in disease outbreak management and response. The scope of EMPRES includes infectious diseases such as HPAI, FMD, Rift Valley fever, contagious bovine pleuropneumonia, African swine fever and rinderpest. Data sources monitored by the system include the official web sites of international health agencies (OIE, WHO), national animal health departments (such as the Ministry of Agriculture and Forestry in New Zealand and the Department of Agriculture, Fisheries and Forestry in Australia), and email list servers (e.g. ProMed, GPHIN, AI-watch). EMPRES provides the following information related to HPAI H5N1: (1) interactive maps showing the distribution of disease over space and time, (2) situation update reports three times per week, and (3) monthly reports of disease situation in a format suitable for the general public. The system is linked to a Geographic Information System and provides simple spatial analyses.

3.6.2   Examples of electronic surveillance systems

The Bovine Syndromic Surveillance System (BOSSS) is an Internet-based support tool for cattle producers in the Lower Gulf region of northern Australia. Veterinarians and herd managers enter clinical observations into the system and an expert system, driven by a set of Bayesian rules, is used to develop a set of differential diagnoses (Shephard 2006). BOSSS was developed in response to a need to enhance passive surveillance in Australia through improved reporting of disease event data, particularly from rural areas that lack adequate veterinary coverage (Clift et al. 2006). In order to meet its diagnostic goals, BOSSS contains a list of over 1,000 diseases with prior estimates of the prevalence of each derived from the literature and expert opinion. These details are used in conjunction with the observed data (entered by users of the system) to obtain a posterior probability that a given disease condition is present. BOSSS is also an interactive tool in

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[14]http://www.fao.org/EMPRES/default.htm

that it prompts users for additional clinical details (e.g. 'was salivation observed?'), encouraging a more systematic and thorough approach to observing and reporting clinical observations. The system is equipped with a Geographic Information System allowing the location of reported cases to be mapped, providing users with a broad-scale view of the current disease situation in their area. Data can be entered into the system via the Internet[15] and through hand held computer devices.

The Veterinary Practitioner Aided Disease (VetPAD) system (McIntyre et al. 2003a,b, 2006) is software for recording animal disease data using hand held computer devices. A novel feature of VetPAD is that it can be linked with a veterinary practice accounting system. In this way, it is anticipated that just as the billing of visits, procedures and drugs is carried out with a high level of accuracy, so too will be the recording of health event information. Aggregated summaries of details recorded by VetPAD can be sent to agencies responsible for managing animal health at the national level, providing real-time access to disease event information.

The Rapid Syndrome Validation Project – Animal (RSVP-A) is a US-based system focusing on the capture of farm attribute data and details of a specific number of disease syndromes of cattle (De Groot et al. 2006). This system has been modified for use in Minnesota, USA for monitoring swine populations (Davies et al. 2007). The system connects a network of veterinarians who connect to the system via the Internet using laptop computers or mobile phones. The system focuses on capturing details of atypical syndromes and specific diseases. In addition to disease presence it records disease absence.

Another useful source of animal health event information is data derived from veterinary diagnostic laboratories. Commercial laboratories typically have in-house database systems to record test results and the format of that data is generally standardised. Details of laboratory testing can be used to supplement knowledge of the true disease situation as well as for more focused uses such as detecting changes in antimicrobial resistance and the presence of chemical and biological contaminants in animals and animal product. The usefulness of laboratory data for surveillance purposes is dependent on the specific disease being monitored, the availability of appropriate tests and adequate coverage of the animal population by the diagnostic laboratories involved. One possible use of a laboratory-based surveillance system is that suggested by Bates et al. (2003). Where the

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[15]http://www.ausvet.com.au/bosss/

risk of an incursion of FMD is thought to be high, milk routinely tested for antimicrobial resistance can also be tested for FMD virus, since FMD virus appears in milk 1 to 4 days before the onset of clinical signs.

Examples of laboratory-based surveillance systems include the US National Animal Health Laboratory Network (NAHLN),[16] the Center for Disease Control and Prevention's Laboratory Response Network (LRN),[17] the US Food and Emergency Response Network (NPDN),[18] and activities of the Veterinary Laboratories Agency (VLA)[19] in the United Kingdom.

3.7   Conclusion

This review has outlined some of the major problems associated with early detection of emerging disease events. Strategies to enable more efficient and rapid detection of emerging disease syndromes have been discussed. Despite the numerous surveillance approaches available to animal health authorities, early disease detection have been hampered by a number of factors. These relate to: (1) difficulties associated with not knowing the location and distribution of at-risk populations, (2) lack of, or limited, information infrastructure to support data information flow, (3) inadequate awareness of diseases and their manifestations, and (4) general lack of preparedness for new disease incursions. Recognising these problems, this review has described and discussed the usefulness of a number of Internet-based tools that can be used to improve the quality of data gathered and to warn animal health authorities of emerging disease threats. This review has outlined the basic data needs as well as potential sources of data (official and unofficial) for an electronic surveillance system to enable early detection of diseases such avian influenza.

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[16]http://www.nahln.us
[17]http://www.bt.cdc.gov/lrn/
[18]http://www.fernlab.org/
[19]http://www.defra.gov.uk/vla/

Table 3.3: Depth, breadth, and precision scores on a scale of 1 to 5 for the traceability systems implemented in nine of the major meat producing countries throughout the world. Adapted from Stevenson et al. (2007).

System name Source	Country	Species	Type	Date	Farm identification[a]	Animal identification[b]	Data capture[c]	Depth[d]	Breadth[e]	Precision[f]	Total[g]
SGS	Argentina	Cattle	Mandatory	In force	1	2	2	3	2	3	8
NLIS	Australia	Cattle	Mandatory	In force	1	1	1,2[h]	5	4 – 5	3	12 – 13
Sisbov	Brazil	Cattle, bison, sheep	Voluntary[i]	In force	1	1	2	2	1	2	5
CLTS	Canada	Cattle, bison	Mandatory	In force	1	1	1	3 – 4	3	3	9 – 10
TrazaChile	Chile	Cattle	Voluntary	In force	1	-	2	2 – 3	2	3	7–8
CTS	Great Britain	Cattle	Mandatory	In force	1	-	2	3 – 4	2 – 3	2 – 3	7–10
NAIS	United States	Cattle	Voluntary	In force	1	-	2	3	2 – 3	3	8 – 9
SNIG	Uruguay	Cattle	Mandatory[j]	In force	1	1, 2	1	4 – 5	4 – 5	2 – 3	10 – 13
AHB	New Zealand	Cattle, deer	Mandatory	In force	1	1	2	3 – 4	2 – 3	3	8 – 9

[a] Identification of premises: 1 = actual farm location, 2 = enterprise or company.
[b] Identification of animal: 1 = individual, 2 = groups.
[c] Method of data submission by farms: 1 = electronic, 2 = paper, 3 = both.
[d] Depth: refers to how far back an animal or product can be traced. A system with depth allows for the tracing of animals or products from the end product on a supermarket shelf to the farm where the animal was born.
[e] Breadth: refers to the amount of information recorded for each unit within the system.
[f] Precision: refers to the ability to track individual transaction to a given day at a given place.
[g] Total = Depth + Breadth + Precision.
[h] 97% electronic entry for movements through feedlots, saleyards and agents and 3% paper based for farm-to-farm movements.
[i] Mandatory for export to the European Union.
[j] 17% of cattle of national stock registered, expected to be completed by 2011.

Descriptive epidemiology of the outbreak of highly pathogenic avian influenza in Vietnam, December 2003 to February 2004

4.1   Introduction

Avian influenza is an infectious disease of poultry caused by influenza A viruses of the *Orthomyxoviridae* family. Of the two categories of influenza infections that occur in birds, highly pathogenic avian influenza (HPAI) is the most virulent and is associated with viruses of the H5 and H7 subtype (Alexander 2000). The highly pathogenic H5N1 viruses responsible for avian influenza outbreaks in Asia, and more recently Europe and Africa, are considered mutants or re-assortments of the first Asian H5N1 virus (Goose/GD/96) that was isolated from sick geese in southern China in 1996 (Guan et al. 2002, Chen et al. 2004, Li et al. 2004). HPAI is a disease of global concern because of the threat posed to food security in regions that are dependent on poultry as a main source of protein and livelihood. An additional concern is that the H5N1 virus may mutate and cause a human influenza pandemic in which millions of human lives would be threatened (Zambon 1999, Barclay & Zambon 2004, Li et al. 2004, World Health Organization 2005).

The clinical signs of HPAI in poultry are variable and follow an incubation period lasting anywhere from between a few hours to up to three days (Easterday et al. 1997). Mortality rates vary between 50% and 100% (Mutinelli et al. 2003*b*). Clinical manifestations of disease involve the respiratory, enteric, reproductive and nervous systems though frequently the only sign observed is sudden death. Because infected birds shed virus from the

respiratory tract, conjunctiva and cloaca, transmission occurs by direct contact between infected and susceptible birds and indirect contact via aerosol or contaminated fomites (Easterday et al. 1997). The virus is spread to new areas by means of objects contaminated with faecal material, persons involved in shared production systems, transportation of live infected birds, or live bird markets (Alexander 2000). Other factors cited as important in the introduction and spread of the disease are wild, migratory birds (Webster et al. 1992, Campitelli et al. 2004, Gilchrist 2005), and illegal movement of birds across national borders (Sims et al. 2005, Witt & Malone 2005).

On 8 January 2004 the Vietnamese Department of Animal Health reported outbreaks of HPAI due to the H5N1 virus in the provinces of Long An and Tien Giang. In this outbreak 70,000 birds were either culled or died. Although the first date of infection was reported as 27 December 2003, unofficial reports indicate that HPAI was present in Vietnam as early as July 2003 (ProMED-mail 2004*a*,*b*,*c*). These outbreaks signalled the start of what is termed the first 'wave' of the H5N1 epidemic in Vietnam which coincided with a series of outbreaks in Southeast Asia involving nine countries from 2003 to 2004 (World Health Organization 2004). Official reports received by the World Organization for Animal Health (OIE) indicate that the 2003 – 2004 H5N1 epidemics in Asia began in South Korea in December 2003, followed by Vietnam, Thailand, Cambodia, Laos and Indonesia in February 2004 and Malaysia in August 2004. In January 2004, Japan confirmed the presence of H5N1 in a peregrine falcon.

During the first phase of the HPAI epidemic in Vietnam limited information was recorded in terms of the number and type of poultry affected. This was mostly due to the state veterinary service being overwhelmed by the scale and speed with which the outbreaks occurred. This situation was exacerbated by limited operational funds, the absence of regulations making HPAI a notifiable disease and the lack of a standardised disease investigation procedure. Once these deficiencies were acknowledged, retrospective surveys were conducted in March 2004 in collaboration with the Food and Agriculture Organization of the United Nations (FAO) to quantify the extent and spread of the disease throughout the country and to identify factors which may have precipitated outbreaks (Morris & Jackson 2005).

The objectives of this study were to describe the spatial and temporal features of the outbreaks of HPAI which occurred in Vietnam from December 2003 to February 2004.

4.2   Materials and methods

4.2.1   Study population

The study population was the 10,073 communes located within the 64 provinces (Figure 4.1) that comprise the Socialist Republic of Vietnam. Within Vietnam, the veterinary administrative structure is hierarchical and consists of provinces, districts, communes and villages. Each commune contains, on average, 10 villages and the mean area of each commune is 31 square kilometres.

Data pertaining to the outbreaks of HPAI caused by the H5N1 virus which occurred in Vietnam between 1 December 2003 and 1 March 2004 (inclusive) were retrieved from the Vietnamese Department of Animal Health (DAH) database. These data were obtained through a retrospective survey conducted in May 2004. In order to remedy the previous lack of uniformity in case reporting, the DAH, in conjunction with FAO, designed questionnaires which were sent to the 57 affected provinces. Each province supplied details relating to the names and unique identification code of all affected communes, dates on which the first cases of disease were detected, dates and details of investigations and laboratory procedures used to confirm the presence of disease, and numbers and types of poultry species affected. The data was gathered by the DAH in collaboration with Dr. Ron Jackson as part of an FAO funded project (Morris & Jackson 2005). Data analysis for this study was carried out be the first author, Caryl Lockhart.

4.2.2   Case definition

For the purpose of this study a commune was regarded as HPAI positive if at least one village within the commune had reported the presence of HPAI between 1 December 2003 and 31 March 2004. The HPAI status of the index village was determined on the basis of clinical signs reported in poultry flocks, *post mortem* examinations and/or laboratory confirmed clinical reports. Laboratory tests consisted of virus isolation and identification of the haemaglutinin surface protein (H5) using the Haemaglutinin Inhibition test (World Health Organization 2005). In this study the official case definition provided by OIE was extended to include cases diagnosed by clinical and *post mortem* examination as the large number of cases that were occurring at the time did not permit laboratory confirmation

for all reported cases. Clinical signs observed included depression, respiratory signs, congestion of wattles and combs and sudden death or high levels of mortality in flocks.

4.2.3 Statistical analyses

Fifty four of the 57 surveyed provinces provided sufficient details for analysis. The temporal evolution of the epidemic was described using epidemic curves. The spatial distribution of HPAI throughout Vietnam was described by plotting the province-level incidence risk of HPAI, expressed as the number of HPAI-positive communes within the province per 100 communes at risk.

Moran's I statistic (Moran 1950) was used to quantify the degree of spatial dependency (autocorrelation) in province-level HPAI incidence risk. We defined a 54×54 adjacency matrix to describe the spatial relationship between each province pair: provinces that shared a common border received a value of 1 and 0 otherwise. In the presence of positive spatial autocorrelation in HPAI incidence risk the computed Moran's I statistic will be close to 1 and in its absence its value will be close to zero. The statistical significance of the observed Moran's I statistic was assessed using a Monte Carlo permutation procedure where the 54 incidence risk estimates were randomly assigned to each province and Moran's I calculated on each occasion. The observed Moran's I statistic was then ranked among the simulated values. If the observed statistic ranked k^{th} among the 999 simulated values the one-sided significance level was k/999.

We use a Bayesian Poisson regression approach to impute the counts of HPAI positive communes in the 17 provinces with missing data. The count of HPAI-positive communes in each of the 64 provinces of Vietnam, O_i was modeled as a function of the expected number of counts and a spatially correlated heterogeneity term:

$$O_i = \text{Poisson}(\mu_i) \tag{4.1}$$

$$\log(\mu_i) = \log E_i + \beta_0 + S_i \tag{4.2}$$

In Equations 4.1 and 4.2 μ_i is the mean number of HPAI-positive communes in the ith province, E_i is the expected number of HPAI positive communes in the ith province,

β is an intercept term, and S_i is a spatially correlated heterogeneity term. The spatial heterogeneity term was parameterised using an intrinsic conditional autoregressive (CAR) prior (Besag 1989, Besag & Mollié 1989, Besag et al. 1991, Mollié 1996). Because the CAR prior requires the specification of a neighbourhood structure, the spatial proximity matrix specification used was the same as that used to compute Moran's I, described above ($w_{ij} = 1$ if areas i and j shared a common boundary and $w_{ij} = 0$ otherwise).

Markov chain Monte Carlo methods (MCMC) implemented in WinBUGS (Spiegelhalter et al. 2000) were used to impute the number of positive communes within provinces with missing data by repeatedly sampling from the predictive distribution of missing data given the observed data. We ran the Markov chain Monte Carlo algorithm for 40,000 iterations and discarded the first 1000 'burn-in' samples. Convergence was assessed using the Raftery and Lewis convergence diagnostic (Raftery & Lewis 1992a,b).

4.3 Results

Data were received from 57 provinces with outbreak details for 1,454 communes. After eliminating provinces for which the number of affected communes and the date of HPAI suspicion or confirmation was unknown, the data set was reduced to 54 provinces of which 47 (87%) were HPAI positive and the remainder HPAI negative. This was equivalent to 1,156 positive and 7,824 negative communes for which spatial and temporal data were available. The incidence risk of HPAI was 12 HPAI-positive communes per 100 communes at risk (95% CI 1 – 14 HPAI-positive communes per 100 communes at risk).

Of the positive communes, 113 (10%) were confirmed by laboratory diagnosis and 1022 (89%) by a combination of clinical and *post mortem* findings. The diagnosis of HPAI was inconclusive in 11 (0.95%) communes. The presence of HPAI in 38 of 54 provinces (72%) was confirmed by laboratory examination and the remaining 9 (17%) by means of a combination of clinical signs and *post mortem* examination.

The incidence risk of disease increased to 13 HPAI-positive communes per 100 communes (95% CI 13 – 14 HPAI-positive communes per 100 communes) when the counts for the seventeen provinces with either zero disease or null were imputed. This resulted in all provinces having at least two HPAI positive communes. The number of HPAI positive communes increased to 1,346 (190 more than that reported in the raw data).

The number of reported outbreaks rose throughout December 2003 to peak in January 2004 and decline in February 2004 (Figure 4.2). The first outbreak was detected on 12 December 2003 and the last on the 13 February 2004. The number of reported outbreaks varied between 3 and 18 case communes per week. By the second week of February the number of reported case communes had decreased markedly. Similar patterns of epidemic onset were observed for reported case communes located in the north, central and south of the country. The first reports of outbreaks were recorded simultaneously in the north and south of the country in late December 2003 with central communes reporting cases during the last week of January 2004 (Figure 4.2).

A choropleth map of province-level incidence risk of HPAI and a scatter plot showing northing coordinate of province centroids as a function of province-level incidence risk of HPAI for the imputed data set are shown in Figures 4.3a and b, respectively. Figure 4.3a shows a first order spatial trend in HPAI risk with the highest incidence of disease in provinces in the south and north and a comparatively lower risk in the central provinces. The results show that all provinces in Vietnam experienced cases of HPAI, irrespective of their reporting status. Figure 4.3b confirms the broad scale spatial pattern in risk of HPAI, with a U-shaped trend in which provinces in the north and south were at higher risk of reporting HPAI compared with provinces in the central parts of the country.

The Moran's I statistic for province-level incidence risk of HPAI was 0.29 ($P < 0.01$) indicative of moderate spatial autocorrelation in incidence risk of disease within the 54 provinces used for the initial analyses.
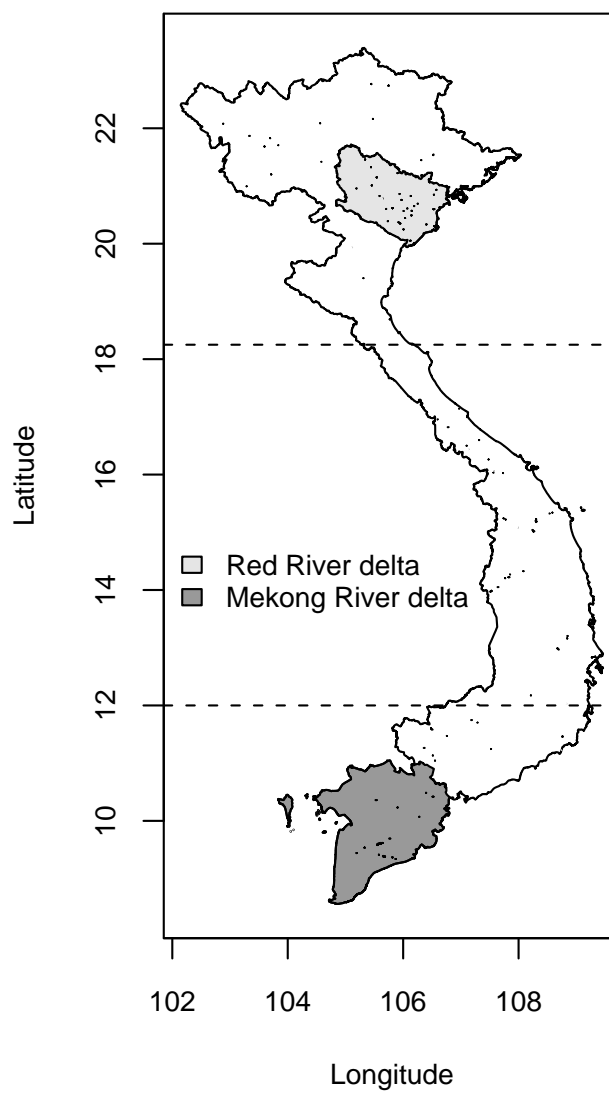
Figure 4.1: Map of the Socialist Republic of Vietnam. Dashed lines delineate the north, central, and southern regions described in the text.
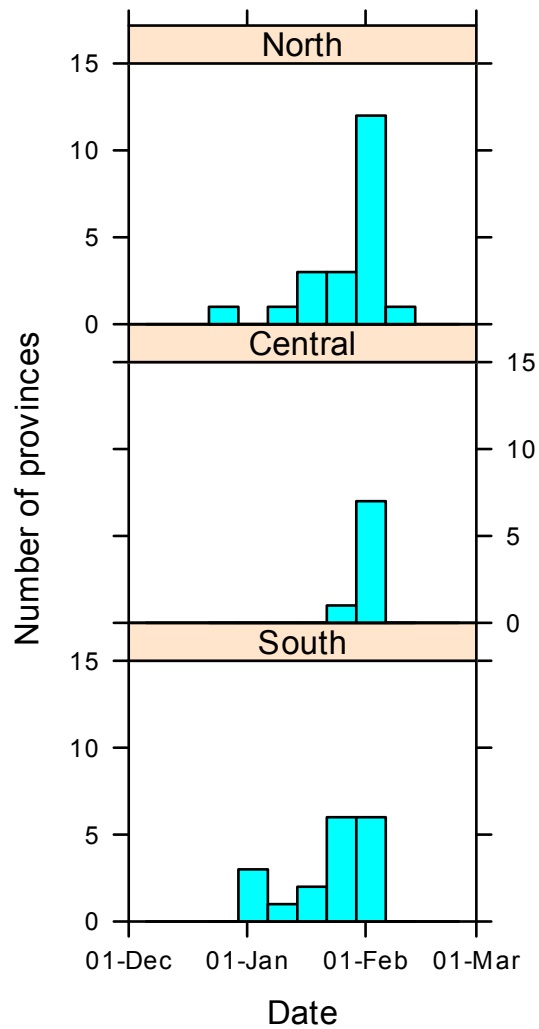
Figure 4.2: Highly pathogenic avian influenza (HPAI) in Vietnam, December 2003 to February 2004. Epidemic curves, showing the count of provinces experiencing an index case of HPAI as a function of calendar date, stratified by region (defined in Figure 4.1).
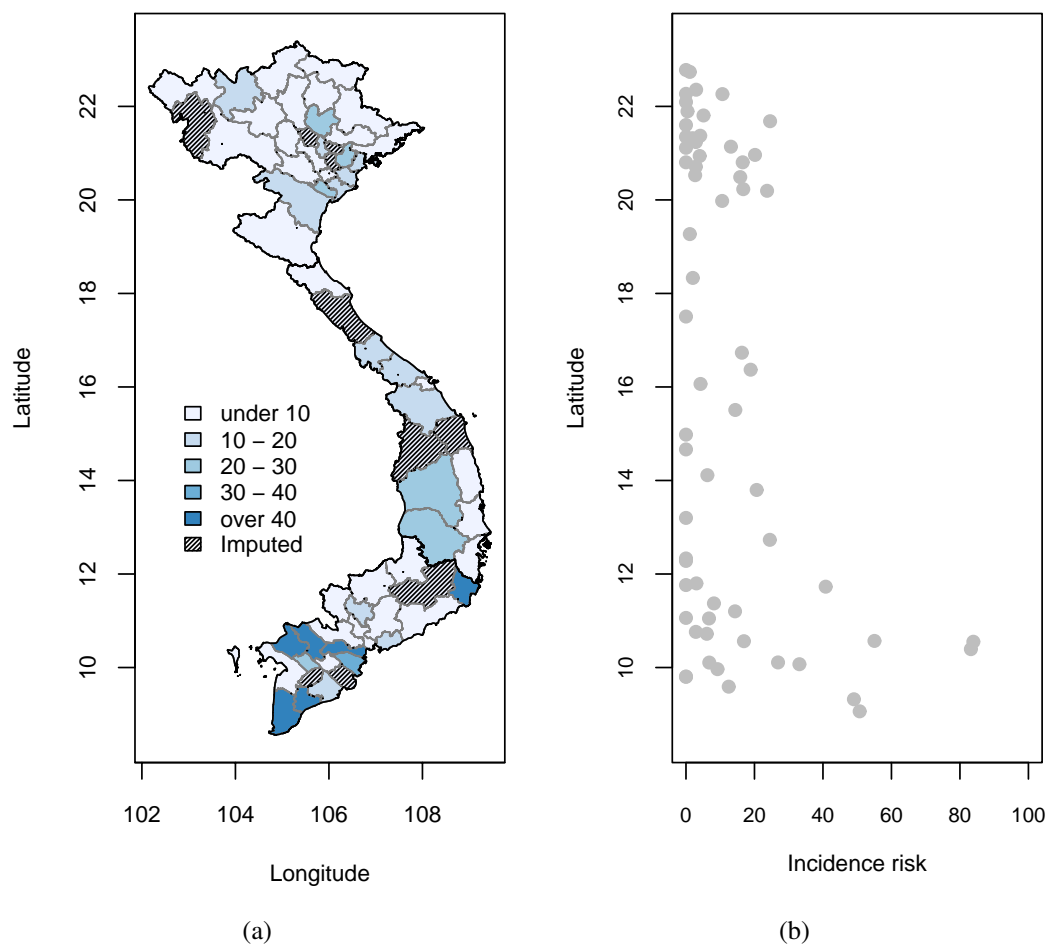
Figure 4.3: Highly pathogenic avian influenza (HPAI) in Vietnam, December 2003 to February 2004: (a) choropleth map showing the reported and imputed values of province-level incidence risk of HPAI (expressed as the number of HPAI-positive communes per 100 communes), and (b) scatter plot showing northing coordinate as a function of province-level HPAI incidence risk.

4.4   Discussion

This paper presents an overview of the epidemiological features of the first epidemic of highly pathogenic avian influenza in Vietnam. The report of HPAI due to the H5N1 virus in Vietnam was the first outbreak of its kind in this country and was accompanied by similar outbreaks in nine neighbouring countries.

Our results indicate that the epidemic was simultaneously seeded into the south and north of Vietnam in December 2003 but whether this was the result of single or multiple introductions is unknown. It is likely that the index case of H5N1 in Vietnam was not recorded since unofficial information sources reported the presence of the disease in the country well before official reports were made to the OIE on 8 January 2004. Our analyses show that cases of HPAI occurred as early as 12 December 2003 in the north, followed by the south on 24 December 2003 (Figure 4.2). HPAI could have been introduced into Vietnam by importation of infected live poultry, poultry products and/or pet birds from neighbouring countries, and/or by wild migratory birds. The borders between Vietnam and Thailand, China, Laos and Cambodia are porous and movement of birds across them are known to occur. The study by Chen et al. (2006) supports the assertion that convalescent migratory birds are able to transfer the H5N1 virus over long distances. The virus involved in the 2003 – 2004 outbreaks in Vietnam was the Z subtype, which was isolated in Thailand and Malaysia and considered to be a sublineage of the first H5N1 virus isolated in geese in China in 1996 (Li et al. 2004). This provides limited support to the hypothesis that the source of infection was birds originating from neighbouring countries.

The detection of HPAI in the outbreak described in this paper was primarily based on the identification of characteristic clinical signs and *post mortem* examination. It is likely that incident cases of HPAI were under reported and the possibility of reporting of diseases with similar clinical signs may represent a source of misclassification bias in these analyses. The clinical signs associated with HPAI are variable and are not specific to the disease and there could have been confusion with Newcastle disease. We acknowledge this weakness, but recognise that other diseases if present would need to have been highly prevalent to change the inferences drawn from these analyses. The OIE recommends laboratory confirmation by means of virus isolation and identification (Anonymous 2005*b*). Despite the clinical reports of HPAI in early December 2003, official laboratory confir-

mation did not occur until 6 January 2004. The delay between the appearance of clinical signs and official notification of disease by veterinary authorities may have been due to delays in farmers reporting the presence of disease and/or delays in outbreak response by the Department of Animal Health. Farmers may either have been unaware of the need to report the disease due to it being confused with endemic diseases of poultry such as Newcastle disease. At the time of the outbreak, HPAI was not a notifiable disease which would have further contributed to this delay. Thus, the failure to detect the outbreak of HPAI in December and to act to contain it meant that widespread movement of birds and hence disease had occurred before control measures could be implemented. Experience in countries such as Hong Kong (Ellis et al. 2004), Japan (Mase et al. 2005) and South Korea (Lee, Suarez, Tumpey, Sung, Kwon, Lee, Choi, Joh, Kim, Lee, Park, Lu, Katz, Spackman, Swayne & Kim 2005) has underscored the importance of early detection and slaughter of infected poultry in combination with other sanitary measures for controlling H5N1 epidemics. ProMed reported that infected and dead birds were sold by farmers to opportunistic middlemen as a means for recouping losses that occurred during the early weeks of the outbreaks (ProMED-mail 2004*c*). These events point to a need to improve both disease awareness and animal disease surveillance at the village and commune level in Vietnam.

The epidemic curve for this epidemic (Figure 4.2) showed a steep increase in cases with a peak occurring at the end of January 2004. The observed increase in cases may be a reflection of increased surveillance once HPAI was confirmed in the two initially infected provinces. The rapid rise in case numbers is indicative of a point source epidemic in which the exposure of communes to the H5N1 virus was simultaneous across the country. The peak of the epidemic coincided with the Tet festival on the 22 January 2004, a time of the year when poultry trade is typically vigorous, increasing the likelihood of movement of infected birds. The rapid decrease in case communes by the end of the second week of February is most likely due to the control strategies that were applied: stamping out and movement controls, which became more effective as more resources became available. Though control strategies were implemented as early as 9 January 2004 authorities admitted that they were unable to control the spread of disease which led to assistance being provided by the international community (specifically the FAO and OIE). These efforts no doubt played a role in interrupting the spread of virus throughout the country.

Ambient temperatures below 20° Celsius (Li et al. 2004) have been cited as a factor that contributed to the outbreak occurring during December and February, since low temperatures are critical for the survival of the viral agent in the environment (Shortridge et al. 1998). Influenza viruses of the H5N1 subtype have been shown to survive for 4 days at 25° Celsius in wet faeces (Shortridge et al. 1998) or 3 days at 30° Celsius in the environment. Poultry meat has been shown to contain H5N1 virus and serve as a possible means of transmission (Tumpey et al. 2003, Swayne & Beck 2005*b*). Since large amounts of virus are excreted in the faeces of infected birds, the favourable temperatures throughout December to February may have allowed the virus to survive in areas with high bird densities (e.g. poultry markets).

Our choropleth map of incidence risk (Figure 4.3a) shows a higher risk of HPAI in the north and south, compared with the central areas of the country. This broad spatial trend in risk of HPAI across Vietnam was not changed by the imputation of missing values but was enhanced by it, since this resulted in all of the provinces that had not reported HPAI as having anywhere from 2 to 24 positive communes. The high risk areas for HPAI identified in this study are consistent with the findings of Rushton et al. (2005) who reported that most losses due to HPAI occurred in the Mekong Delta and Red River Delta areas. The first order trend in province-level HPAI incidence risk may be associated with regional differences in the distribution of environmental risk factors such as the distribution of poultry farming systems, poultry population density and major waterways which support reservoir species for the virus such as wild birds (Morris & Jackson 2005).

Once HPAI was introduced into Vietnam, spread of disease was certainly exacerbated by the uncontrolled movement of infected birds, personnel and contaminated fomites and the system of marketing of live birds. The use of live bird markets is common in Asia and aggregation of various bird species kept in close proximity is likely to facilitate the spread of disease. Studies in Hong Kong and the US have identified a direct link between HPAI disease outbreaks in poultry and the presence of the virus circulating in birds found in live bird markets (Senne et al. 2003, Sims et al. 2003).

Inferences derived from piecing together the events of the 2003 – 2004 H5N1 outbreaks in Vietnam should be made with caution on account of the quality of the data available for analysis. Seven of the 64 provinces of Vietnam did not report the presence of HPAI for the period December 2003 to February 2004. Of the 57 HPAI-positive provinces, 3 had

no information on the number of affected communes. Use of complete data would have restricted the data suitable for analysis to only 54 provinces, excluding 15% of the total province population. Theoretically, imputation using a Bayesian framework should provide valid estimates of missing values, as long as the model describing the distribution is appropriate. The counts of affected communes within the 10 provinces (7 provinces that did not report disease and 3 that were HPAI-positive but had missing data) were considered to follow a Poisson distribution and were sampled from the conditional distribution of the missing values given the non-missing values in the remainder of the data set. A sensitivity analysis of the imputation procedure was conducted by comparing the counts of positive communes for the 10 provinces for six ranges of HPAI relative risk values. The imputed counts were consistent across the relative risk values. We interpret this to mean that the imputation model was rigorous and provided plausible estimates of HPAI positive commune counts.

The sources of bias in this study are numerous. First cases were defined as reported clinical cases, the majority of which were not confirmed by laboratory diagnosis, but due to a recognised epidemic underway in the country. Although imputation went some way to address the problem of missing data, it is likely that a tendency of survey respondents to report only known outbreaks (as opposed to estimating the place and time of outbreaks) meant that the overall estimate of HPAI incidence risk has been underestimated. Aggregation of case details presents the possibility of ecological bias and hence patterns found at the province level may not be reflective of the situation at higher levels of spatial resolution (for example, at the commune or village level).

The effect of the above mentioned biases on the inferences made from the results presented in this paper are difficult to quantify. If disease reporting was relatively uniform across provinces then our results should represent a filtered view of the actual situation and, while the actual number of outbreaks and incidence risk values would be larger than reported here, the spatial distribution of risk would be the same. If there was a differential tendency to report disease then one would expect that the recorded incidence risk estimates would fluctuate widely among provinces and that there would be no, or negative, spatial autocorrelation in the observed incidence risk. The moderate spatial autocorrelation in HPAI incidence risk identified in this study is not consistent with this interpretation, providing evidence (albeit weak) that the tendency for provincial veterinary authorities to

report disease was relatively uniform.

The analyses presented in this study are descriptive and provide a basis for further study into the epidemiological features of the HPAI epidemic in Vietnam. A novel feature of this study is that we used a Bayesian approach to impute missing data based on spatial dependency identified in descriptives analyses. Our results show that this epidemic of HPAI in Vietnam had features consistent with a point source epidemic in which exposure of communes to H5N1 virus was simultaneous and rapid throughout the country. Outbreaks of HPAI during the study period were concentrated in two areas of the country, the Mekong and Red River Deltas. This distribution may have been the result of the distribution of the population at risk and/or the presence of environmental risk factors for disease.

Risk factors for highly pathogenic avian influenza in Vietnam, December 2003 to February 2004

5.1 Introduction

Highly pathogenic avian influenza (HPAI) caused by the H5N1 virus (an influenza virus of the family Orthomyxoviridae) has become a disease of immense concern worldwide (Webster & Hulse 2004) and has been subjected to a wide range of control measures since its emergence in Guangdong province in southern China in 1996 (Chen et al. 2004) and reappearance in Southeast Asia in early 2004. Despite these measures, HPAI has spread to Europe, Africa and near East Asia during 2005 – 2007 where humans (ProMED-mail 2007c), wild birds (ProMED-mail 2007a) and domestic poultry (ProMED-mail 2007b) have been affected. As a consequence of the rapid transboundary spread of HPAI and field experience that indicates that epidemics in poultry can be extinguished by promptly culling the population at risk (Easterday et al. 1997) it is important that animal health authorities are able to quickly detect and respond to outbreaks if and when they occur. Effective surveillance is the cornerstone of early disease detection and is particularly necessary in the case of HPAI given the fact that ducks may act as silent carriers of the H5N1 virus (Chen et al. 2004, Gilbert et al. 2006, Songserm et al. 2006).

A small number of published studies have examined risk factors for avian influenza outbreaks in South East Asia, The Netherlands and the United States (see Gilbert et al. 2006 and Kung et al. 2007) but little has been published on the outbreaks in Vietnam from De-

cember 2003 to February 2004. During this phase of the Vietnamese epidemic, analysis of accumulated epidemic data showed a concentration of outbreaks centred around the Red River and Mekong River Deltas (Chapter 4). A number of factors have been implicated in the appearance and spread of HPAI in Vietnam and the other infected countries in Southeast Asia including the presence of wild birds, legal and illegal trade of poultry, and the presence of waterfowl in wetlands and rice paddies (Tiensin et al. 2005, Gilbert et al. 2007). While there is little doubt that each of these factors are component causes of the outbreaks that have been observed, the relative importance of each of these factors remains less clear. Determining the relative importance of these risks will provide a better understanding of the epidemiology of HPAI, which in turn will provide information that will allow surveillance activities for the disease to be better targeted.

In this paper we investigate the influence of environmental, human and animal demographic factors on the spatial distribution of HPAI H5N1 outbreaks in Vietnam from December 2003 to February 2004.

5.2   Materials and methods

The area of interest was the Socialist Republic of Vietnam. Data pertaining to the outbreaks of HPAI caused by the H5N1 virus which occurred between 1 December 2003 and 1 March 2004 (inclusive) were retrieved from the Department of Animal Health (DAH) database, compiled during a retrospective survey conducted in May 2004 (Morris & Jackson 2005).

To develop a model to quantify the effect of factors influencing the spatial distribution of outbreaks of HPAI we applied a regular grid across the territorial boundaries of Vietnam, creating a matrix of 1781 cells with each cell covering an area of 184 km^2 (13.60 km $\times$ 13.60 km). Each of the 10,073 communes that comprise the Socialist Republic of Vietnam were assigned to a cell of this grid on the basis of the easting and northing coordinates of their respective centroid. Details of the 1452 communes that reported HPAI outbreaks for the period 1 December 2003 to 1 March 2004 were retrieved from the DAH database and summarised as the total number of HPAI-positive communes per grid cell. For each of the $i = 1781$ cells that comprised the grid we calculated the expected number of HPAI-positive communes per grid cell, E_i, as:

$$E_i = n_i \left(\frac{\sum_{i=1}^{1781} O_i}{\sum_{i=1}^{1781} n_i} \right) \tag{5.1}$$

Where O_i was the total number of HPAI-positive communes in the ith grid cell and n_i the total number of communes in the ith grid cell. Standardised morbidity ratios (SMR) for HPAI (the ratio of the observed number of HPAI-positive communes in each grid cell to the number expected) and standard errors of the SMR estimates were plotted as choropleth maps.

Due to the relatively large number of grid cells that contained communes where HPAI was not reported (n = 1407), regression coefficients were estimated using a Bayesian zero-inflated Poisson (ZIP) model (Lambert 1992). This technique not allowed us to address the over dispersion that was present due the large number of grid cells where disease did not occur or was not reported but also allowed us to quantify the effect of factors influencing the number of HPAI-positive communes in each grid cell. Using this approach, the expected number of HPAI-positive communes per grid cell, Z_i, was modelled conditional on the observed number of HPAI-positive communes per grid cell, O_i:

$$Z_i \sim \begin{cases} \text{Bernoulli}(p) \text{ with probability } p \text{ if } O_i = 0, \\ \text{Poisson}(\mu) \text{ otherwise} \end{cases} \tag{5.2}$$

In Equation 5.2 O_i was an independent Bernoulli random variable with a mean of p if $O_i = 0$; otherwise O_i was assumed to follow a Poisson distribution with mean μ. The parameters p and μ were allowed to vary for each grid cell as a function of a series of explanatory variables as follows:

$$\text{logit}(p_i) = \alpha_0 + \alpha_1 x_{1i} + \ldots + \alpha_m x_{mi} \tag{5.3}$$

and

$$\log(\mu_i) = log E_i + \beta_0 + \beta_1 z_{1i} + \ldots + \beta_m z_{mi} \tag{5.4}$$

To account for the presence of spatial autocorrelation in the data the Poisson component of the model was extended as follows:

$$\log(\mu_i) = logE_i + \beta_0 + \beta_1 z_{1i} + \ldots + \beta_m z_{mi} + U_i + S_i \qquad (5.5)$$

In Equation 5.5 the terms U_i and S_i were included to represent the unstructured and spatially structured components of the data, respectively (Besag 1989, Besag & Mollié 1989, Besag et al. 1991, Mollié 1996).

We assumed uninformed normal prior distributions for the intercepts α_0 and β_0 and the regression coefficients $\alpha_1 \ldots, \alpha_m$ and $\beta_1 \ldots, \beta_m$ for the binomial and Poisson components of the model, respectively. The structured heterogeneity term was assumed to follow a conditional intrinsic Gaussian autoregressive (CAR) structure with mean 0 and precision λ dependent on a spatial proximity matrix based an adjacency where $w_{ij} = 1$ if grid cell i was defined as a neighbour of grid cell j and $w_{ij} = 0$ otherwise. The unstructured heterogeneity term was assumed to be normally distributed with mean 0 and precision τ.

The following variables were estimated for each grid cell and evaluated as explanatory variables in the zero-inflated mixed-effects Poisson model of HPAI risk: (1) the estimated number of humans, (2) the estimated number of domestic poultry, (3) median elevation (expressed as metres above sea level), (4) total road length (in kilometres), and (5) the proportion of land area under irrigation (Table 5.1). Human population size was included as a potential explanatory variable on account of the association between human population density and the presence of backyard (non-commercial) poultry rearing facilities and the frequency of movement of poultry to and from live bird markets (Bulaga et al. 2003, Nguyen et al. 2005, Kim et al. 2006, Pelzel et al. 2006, Wang et al. 2006, Terregino et al. 2007).

Given the observed spatial pattern of HPAI outbreaks could be explained by the spatial distribution of the susceptible host population, the contribution of the number of domestic poultry per grid cell to HPAI risk was evaluated. Road length was included as a proxy explanatory variable for access, the extent of which would determine the level of trade in poultry taking place across Vietnam. Areas that support water fowls (wild and domestic) such as irrigated farm lands have been implicated as a major contributor to the outbreaks of avian influenza in Thailand (Gilbert et al. 2006, 2007). The proportion of irrigated land in each grid cell provided a means for assessing the influence of this effect in Vietnam.

Estimates of human population, domestic poultry population and land use were derived

from remotely sensed (satellite) data. Each remotely sensed data set was projected onto a map of Vietnam and summary values derived for each of the 1781 grid cells that comprised the study area. Human population data was obtained from the LandScan 4 Population Dataset 2004 (Anonymous 2004*a*) presented as a raster surface of human population counts at a resolution of 30" × 30" (approximately 1 kilometre × 1 kilometre). Human population density for each grid cell was then estimated by summing the values from each cell of the human population raster surface that lay within the boundaries of each grid cell and dividing that value by grid cell area. Poultry population details were derived from the FAO Grided Livestock of the World Database for Asia (Anonymous 2007*e*) presented as a raster surface of poultry counts for 2000 at a resolution of 3' × 3' (approximately 5 kilometres × 5 kilometres). The number of domestic poultry in each grid cell of the study area was obtained by summing the values from each cell of the poultry population raster surface that lay within the boundaries of each grid cell. This provided an estimate of the number of domestic poultry in each grid cell, which was then expressed as poultry density (poultry numbers per square kilometre).

Elevation details at a resolution of 1 kilometre × 1 kilometre were obtained from the USGS GTOPO30 digital Dataset (Anonymous 1992). Median elevation in each grid cell was obtained from the median values of the corresponding cells from the elevation surface. The Global Landuse data set for Southeast Asia (Anonymous 2003), presented at a resolution of 1 kilometre × 1 kilometre, provided data on the distribution of irrigated farm lands and was expressed as the proportion of each grid cell occupied by irrigated land.

Vector maps of Vietnamese roads were obtained from the Digital Maps of the World database (Anonymous 1993). A raster surface of cell size 1 kilometre × 1 kilometre was generated from the vector feature and each cell of this raster surface assigned the total length of the line feature that fell within its boundaries. Total road length for each grid cell equaled the sum of road lengths calculated for each of the 1 kilometre × 1 kilometre cells that lay within the boundaries of the grid cell.

Frequency distributions of each of the five explanatory variables were inspected and variables dichotomised on the basis of the properties of their respective distributions. The cut-off values are shown in Table 5.2.

A three stage approach was used to develop a model to identify risk factors for HPAI

outbreaks in Vietnam. In the first stage, the relationship between the number of HPAI positive communes per grid cell and each of the four candidate explanatory variables was quantified using the Kruskal-Wallis test. In the second stage, explanatory variables associated with the number of HPAI-positive communes per grid cell at an alpha level of less than 0.20 were included in a fixed effects zero-inflated Poisson model implemented in the pscl package (Zeileis et al. 2007) in R (R Development Core Team 2008). The presence of spatial autocorrelation in the model residuals was assessed using Moran's I statistic (Moran 1950). Moran's I for model residuals for the 1st to the 10th spatial lag were calculated and plotted as a correlogram. A Moran's I statistic greater than the expected value over one or more spatial lags was indicative of unaccounted-for spatial autocorrelation in the data, justifying the mixed-effects model shown in Equation 5.5.

In the third stage, the model was extended to account for structured (S_i) and unstructured (U_i) heterogeneity using a Markov chain Monte Carlo algorithm implemented in Win-BUGS (Spiegelhalter et al. 2000). The Gibbs sampler was run for 200,000 iterations with a burn-in of 10,000 iterations. Convergence was visually assessed using cumulative path plots for each of the monitored parameters and quantified using the Raferty and Lewis convergence diagnostic (Raftery & Lewis 1992a,b) implemented in the Coda package (Plummer et al. 2006) in R.

5.3   Results

Three hundred and seventy four of the 1781 grid cells in Vietnam reported the presence of HPAI between December 2003 and March 2004. Thirteen of the 161 commune reports were accompanied by laboratory confirmation of the presence of disease; 149 reports were based on the presence of clinical signs. The incidence risk of disease for the period December 2003 to February 2004 was 21 HPAI-positive grid cells per 100 grid cells at risk (95% CI 19 – 23 cases per 100 grid cells).

Choropleth maps of the standardised morbidity (SMR) ratios and the standard errors of the standardised morbidity ratios for HPAI are shown in Figures 5.1a and 5.1b, respectively. Consistent with our descriptive analyses of the 2003 – 2004 epidemic (Chapter 4) Figure 5.1a shows high risk areas in the north east and south west of the country. The standard errors of the standardised morbidity ratios were large in the low SMR areas (Figure 5.1b),

reflecting the greater uncertainty in the SMR estimates in grid cells where there were relatively low numbers of communes.

Descriptive statistics of each of the explanatory variables eligible for inclusion in the fixed-effects model of HPAI risk are shown in Table 5.3. Human population density for each grid cell ranged from 0 to 268,000 humans per square kilometre with higher population densities in the northeast and southwest corresponding to the location of the cities of Hanoi and Ho Chi Minh, respectively. Poultry density ranged from 0 to 57,000 birds per square kilometre with the highest densities in the northeast of the country. Grid cells with the highest proportions of irrigated land were concentrated around the Red River and Mekong River Deltas (data not shown). Table 5.4 shows the Kruskal-Wallis test statistic, degrees of freedom and associated P-values for the association between grid-level HPAI risk and each of the four candidate explanatory variables.

A correlogram based on the residuals from the fixed effects model showed that significant spatial autocorrelation was present up to the seventh-order spatial lag (results not shown). On the basis of these analyses, the precision of the spatial heterogeneity term (S_i) was parameterised by a proximity matrix where grid cells were defined as neighbours on the basis of spatial lag to the seventh order.

Table 5.5 presents the posterior means and 95% credible intervals of the regression co-efficients estimated for the mixed-effects model of grid level HPAI risk. For the logistic part of the model, the odds of not reporting HPAI in grid cells where greater than or equal to two-thirds of the land area was irrigated was 0.12 (95% credible interval 0.07 – 0.19) times that of grids cells where less than two thirds of the land area was irrigated. Grid cells where median elevation was greater than or equal to 250 metres were 3.43 (95% credible interval 2.07 – 5.54) times as likely not to report HPAI, compared with cells where median elevation was less than 250 metres.

For the Poisson part of the model the risk of HPAI was 6.49 (95% credible interval 4.13 – 11.08) times greater in grid cells where the proportion of irrigated land was greater or equal to two thirds, compared with grids cells where less than two thirds of the land area was irrigated. The risk of HPAI in grid cells where median elevation was greater than or equal to 250 metres was 0.30 (95% credible interval 0.14 – 0.62) times that of cells where median elevation was less than 250 metres.

Plots of the structured (S_i) and unstructured (U_i) heterogeneity terms from the mixed-effects model, expressed as risk ratios are shown in Figures 5.2a and 5.2b, respectively. A single area of elevated, unaccounted-for HPAI risk was apparent in the north of the country. In contrast, the distribution of risk attributable to the unstructured random effect term was more variable and showed no obvious spatial pattern.

Table 5.1: Highly pathogenic avian influenza (HPAI) in Vietnam, 2003 – 2004. Covariates derived from satellite data considered for inclusion in a mixed-effects model of area-level HPAI risk.

Variable type	Description
Demographic	Human population density (number of humans per square kilometre)
Zoological	Poultry density (number of poultry per square kilometre)
Land use	Proportion of land area under irrigation
Topological	Height above sea level (metres)
Anthropogenic	Road density (estimated road length per square kilometre)

Table 5.2: Highly pathogenic avian influenza (HPAI) in Vietnam, 2003 – 2004. Criteria for dichotomising each of the covariates derived from satellite data considered for inclusion in a mixed-effects model of area-level HPAI risk.

Variable	Interpretation
Poultry population density [a]	
$< 10,000$	Areas of low poultry density
$\geq 10,000$	Areas of high poultry density
Proportion grid irrigated	
< 0.66	Areas where other land classification important
≥ 0.66	Areas where the irrigation was the predominant land classification
Median elevation [b]	
< 250	Areas of low elevation
≥ 250	Areas of high elevation
Road density [c]	
< 20	Areas with relatively low road density
≥ 20	Areas with relatively high road density

[a] Number of poultry ($\times$ 1000) per square kilometre.
[b] Height above sea level (metres).
[c] Estimated road length (kilometres) per square kilometre.

Table 5.3: Highly pathogenic avian influenza (HPAI) in Vietnam, 2003 – 2004. Descriptive statistics of each of the covariates derived from satellite data considered for inclusion in a mixed-effects model of area-level HPAI risk.

Variable	n	Mean (SD)	Median (min, max)
HPAI positive grids	374	0.69 (2.06)	0 (0, 21)
Human population density [a]	1781	4 (10)	1 (0, 268)
Poultry population density [b]	1781	3.6 (5.29)	2 (0, 57)
Proportion grid irrigated	1781	0.24 (0.33)	0.05 (0, 1)
Median elevation [c]	1781	380 (392)	253 (1, 2093)
Road density [d]	1781	17 (8)	17 (0, 68)

[a] Number of humans ($\times$ 1000) per square kilometre.
[b] Number of poultry ($\times$ 1000) per square kilometre.
[c] Height above sea level (metres).
[d] Estimated road length (kilometres) per square kilometre.

Table 5.4: Highly pathogenic avian influenza (HPAI) in Vietnam, 2003 – 2004. Kruskall Wallis test statistic, degrees of freedom and associated P-values for the association between grid cell-level HPAI risk and each of the covariates considered for inclusion in a mixed-effects model of area-level HPAI risk.

Variable	Test statistic	*df*	P
Poultry population density	241.7955	1	< 0.01
Proportion grid irrigated	459.0252	1	< 0.01
Median elevation	411.0685	1	< 0.01
Road density	157.5479	1	< 0.01

Table 5.5: Highly pathogenic avian influenza (HPAI) in Vietnam, 2003 – 2004. Posterior means and 95% credible intervals of the regression coefficients estimated for the mixed effects, zero-inflated Poisson model of HPAI risk.

Explanatory variable	Posterior mean	SD	MC error	RR	95% CI of RR
Poisson component:					
Intercept	-0.5573	0.2671	0.01		
Proportion grid irrigated					
< 0.66				1.00	
≥ 0.66	1.8780	0.2495	0.01	6.49	(4.13 – 11.08) [a]
Median elevation					
< 250 metres				1.00	
≥ 250 metres	-1.1870	0.2495	0.01	0.30	(0.14 – 0.62)
Structured heterogeneity [b,c]	0.3648	0.0881	< 0.01		
Unstructured heterogeneity [c]	1.3910	0.1192	< 0.01		
Logistic component:					
Intercept	0.8243	0.1678	< 0.01		
Proportion grid irrigated					
< 0.66				1.00	
≥ 0.66	-2.1170	0.2492	< 0.01	0.12	(0.07 – 0.19) [d]
Median elevation					
< 250 metres				1.00	
≥ 250 metres	1.2350	0.2507	< 0.01	3.43	(2.07 – 5.54)

[a] Interpretation: grid cells where greater than or equal to two-thirds of the land area was occupied by irrigated farm land, the risk of HPAI cases was increased by a factor of 6.49 (95% credible interval 4.13 – 11.08).
[b] Structured heterogeneity terms based on a spatial proximity matrix where grid cells defined as neighbours if up to the seventh spatial order.
[c] Variance of heterogeneity term.
[d] Interpretation: for grid cells where greater than or equal to two-thirds of the land area was occupied by irrigated farm land, the odds of reporting zero cases of HPAI was decreased by a factor of 0.12 (95% credible interval 0.07 – 0.19).
SD: Standard deviation.
MC error: Monte Carlo error.
RR: Risk ratio.
CI: Bayesian credible interval.
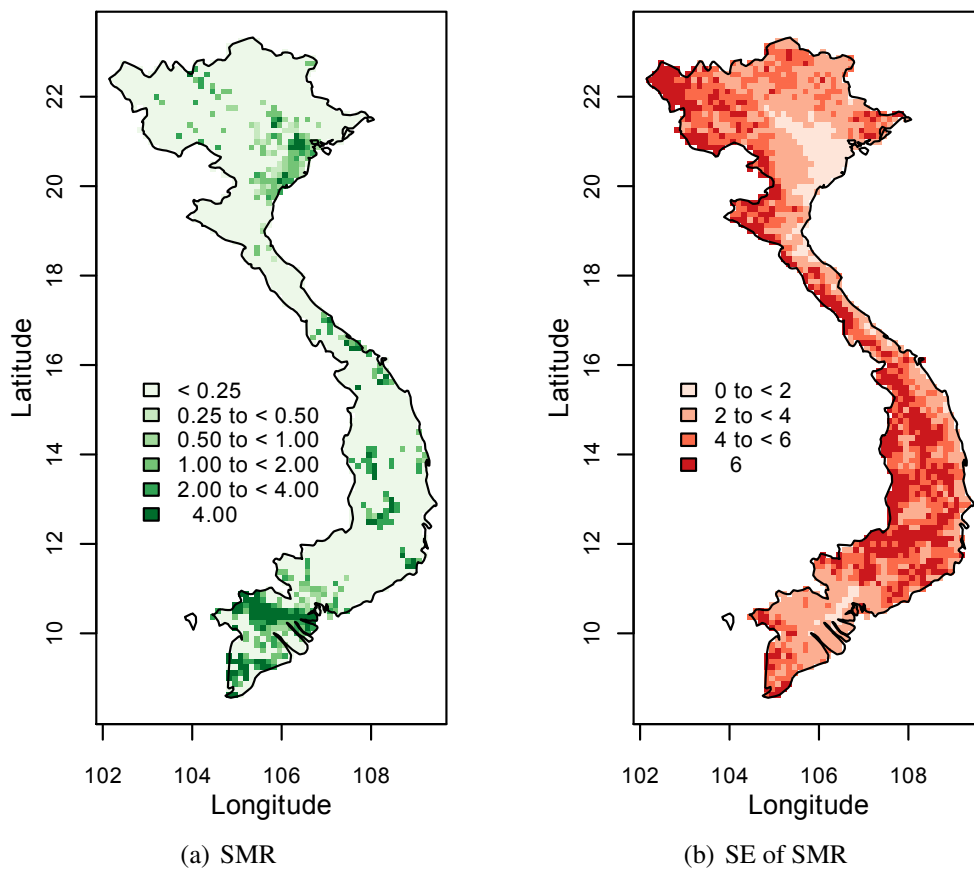
Figure 5.1: Choropleth maps of the: (a) standardised morbidity ratio and (b) standard errors of the standardised morbidity ratio for HPAI in Vietnam, December 2003 to March 2004.

(a) Structured heterogeneity   (b) Unstructured heterogeneity
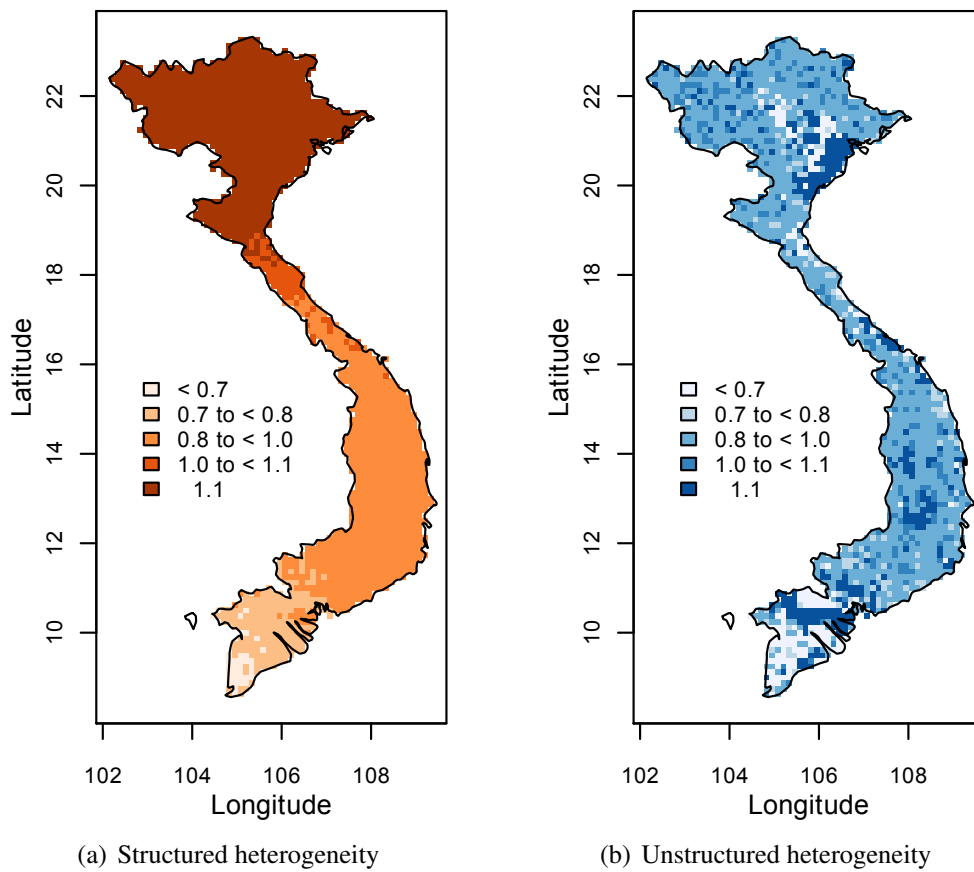
Figure 5.2: Highly pathogenic avian influenza (HPAI) in Vietnam, 2003 – 2004. Choropleth maps showing the grid cell risk ratio HPAI attributable to: (a) structured heterogeneity component, and (b) the unstructured heterogeneity component of the mixed effects zero-inflated Poisson model shown in Equation 5.5.

5.4   Discussion

The aim of this study was to identify factors associated with the spatial distribution of outbreaks of HPAI during the December 2003 to March 2004 epidemic in the Socialist Republic of Vietnam. We used a zero-inflated Poisson model including heterogeneity terms to account for spatial and non-spatial extra-Poisson variation in the data. The advantage of this approach was that it allowed us to quantify the effect of factors associated with the number of HPAI-positive communes per grid cell in a data set where the number of cells that reported disease was small, relative to the total number of cells. Inclusion of the heterogeneity terms allowed us to identify areas where there was a spatially correlated risk of disease unexplained by the explanatory variables included in the model.

The risk of HPAI in grid cells where greater than two-thirds of the land area was irrigated was six times that of cells where the proportion land irrigated was less than two-thirds (Table 5.5). These findings are consistent with those reported elsewhere (Gilbert et al. 2006) and may be attributed to the presence of larger numbers of silent carriers of the H5N1 virus such as ducks in these areas (Songserm et al. 2006). Throughout the outbreak period, Vietnam had a large domestic duck population which was maintained extensively throughout the irrigated areas of the Red River and Mekong River Deltas. The presence of large numbers of asymptomatic HPAI-susceptible species in these areas would have contributed to an increased likelihood of transmission of virus to other susceptible poultry species. A study in Thailand showed that areas where free-grazing ducks were abundant increased the risk of HPAI outbreaks by 1.5 times (Tiensin et al. 2005). A study conducted using details recorded from the 2004 to early 2006 outbreaks of HPAI in Vietnam reached the same conclusion (Pfeiffer et al. 2007).

Elevation was negatively associated with HPAI risk in grid cells where disease was reported. This finding is consistent with the association between HPAI risk and irrigation, since there is a negative association between elevation and use of irrigation (results not shown). These findings also reflect the fact that the bulk of poultry population in Vietnam is confined to low lying areas. Another explanation for the protective effect of elevation is that case ascertainment may have been poorer in elevated and more remote areas due to difficulties (or delays) in accessing veterinary services during the outbreak (Morris & Jackson 2005).

Our results show a single large region of elevated spatially structured risk in the Red River Delta area (Figure 5.2a). This represents areas of the country where spatially correlated factors other than irrigation and elevation were associated with either the presence or the reporting of HPAI outbreaks. An explanation for these areas would include similarities in the likelihood of reporting disease or the presence of factors increasing the likelihood of disease transmission and spread. One such factor is legal and illegal movement of birds. Although evidence is sparse, China has often been cited as the epicentre of influenza viruses (Webby & Webster 2001). It is therefore logical to assume that if trade in poultry occurred between Vietnam and China, infected animals could have been introduced into the north of Vietnam, leading to an increased probability of disease dissemination. The fact that this high risk area straddles the city of Hanoi reflects the presence of a high concentration of susceptible poultry species, located in wet markets and back yards. These factors have been cited as risk factors for the outbreaks of avian influenza in countries throughout Southeast Asia (Sims et al. 2005). This being the case, we would have expected to have identified an association between grid-level poultry density and risk of disease throughout the period of study. No such relationship was present, which might reflect errors or bias in the poultry population estimates used in these analyses. This is a reasonable explanation given that the poultry population data used for this study was based on the 2000 census estimates, collected three years before the 2003 – 2004 outbreak. This data may not have reflected the actual distribution of poultry numbers in Vietnam, due to the highly dynamic nature of the Vietnamese poultry industry. Additionally, the census data for Vietnam may have been incomplete, providing gaps in areas where poultry may have been present but were not recorded.

We identified no association between road density and HPAI outbreak risk. Our rationale for including road density as a covariate was that it provided an indirect measure of transport access and the amount of legal and illegal bird movement within each cell. Road density may not have been a suitable variable for this purpose for a number of reasons. Firstly, we were not able to differentiate between primary and secondary roads which would impact on the level of usage related to bird movements. Secondly, even if road density was an adequate predictor of the amount of bird transport, it provides no indication of the destination of movement activities (e.g. live bird markets, farms, households) and the time spent at these locations, which may be better predictors of outbreak risk in a

given area.

Our spatial analyses of the HPAI outbreaks that occurred in Vietnam between December 2003 and March 2004 identified areas of the country at higher risk of disease. The results presented here show that in areas where disease was reported, the presence of irrigated farm lands was associated with an increase in outbreak risk whereas higher elevations were associated with decreased outbreak risk. After accounting for these factors we identified a single large region of elevated risk in the Red River Delta, presumably due to similarities in the likelihood of reporting disease or the presence of factors increasing the likelihood of disease transmission and spread. Further investigations to elucidate transmission mechanisms, targeting this area of the country, would be a profitable area of future research.

A cross-sectional study of backyard poultry ownership in provincial New Zealand

6.1 Introduction

In New Zealand, as in other developed countries, there is a sizeable commercial poultry industry whose flocks are well characterised in terms of numbers, location, and management practices. However, the same cannot be said for non-commercial ('backyard') poultry flocks where relatively little is known about their spatial distributiion and how they are managed. Lack of knowledge about this sector of the domestic poultry population is of concern to both the commercial poultry industry and veterinary authorities because: (1) there is an increased likelihood of introduction of infectious disease into backyard flocks, due to inevitably varying levels of biosecurity, and (2) in the event of an infectious disease outbreak, backyard flocks may pose a risk to commercial poultry enterprises if links between the two enterprise types exist.

It is therefore important to have some knowledge of the characteristics of the backyard poultry sector in terms of numbers, management practices, and distribution in order to determine the risks (if any) they may pose to the commercial sector. The aim of this study was to describe the backyard poultry sector in a single area of provincial New Zealand in terms of quantifying the proportion of land parcels where domestic poultry and kept, details of bird numbers, and how flocks are managed. Recognising that the prevalence of poultry ownership might vary with land classification we selected two areas — one urban and the other an urban-rural fringe area. A secondary objective of this study was to identify factors that might assist animal health authorities to locate backyard poultry

flocks in the event of a disease emergency. To address this we determined if bird-positive parcels were clustered spatially and evaluated the relationship between mesh block-level deprivation index and the presence of backyard birds.

6.2   Materials and methods

6.2.1   Study design

A cross-sectional study was conducted to determine the proportion of land parcels in an urban and urban-rural fringe area where domestic poultry were kept. Two areas were selected. The first was an area 20.08 square kilometres in size located within the city limits of Palmerston North, in the North Island of New Zealand (longitude 175°, latitude 40°). The second was 16.39 square kilometres in size located in an urban-rural fringe area adjacent to the Palmerston North city limits (Figure 6.1). A questionnaire (Appendix A) was developed to provide a description of the type and number of birds kept, and details of management, and biosecurity practices. Emphasis was placed on recording direct and indirect contacts between wild birds and backyard poultry and the specific nature of management activities (e.g. poultry and product movements, feed type and sources, and aspects of hygiene).

We took a stratified random sample of land parcels within each of the selected study areas based on land area. The sampling frame for the urban area was comprised of 5,567 land parcels obtained from the Land Information New Zealand core record system (Land Information New Zealand 2007). The sampling frame for the rural area was comprised of 172 land parcels obtained from AgriBase, the national index of agricultural property ownership and location in New Zealand (Sanson & Pearson 1997). Land parcels were stratified into terciles and classified as small ($10 - 650$ m^2), medium ($650 - 780$ m^2), and large (>780 m^2). For sample size determination, we assumed that for a 95% confidence level, 50% of the parcels within each study area and each stratum would contain backyard poultry. A total of 435 land parcels (361 urban and 74 rural) were selected. Land parcels to be surveyed were selected from the sampling frame at random, for each size strata.

To ensure that property owners would be at home when visited, the survey was administered over a series of Saturday and Sunday afternoons from February to November 2006.

Each of the selected land parcels were visited and residents asked if domestic poultry were kept on the property. Where poultry were present, a questionnaire was administered. In the event that the resident of the selected parcel was not at home at the time of the visit a neighbouring land parcel was selected. Land parcels which were found to be commercial properties, schools, or non-residential were re-sampled and the re-selected land parcels visited at a later date. The survey of land parcels in the urban area was administered by the first and second authors, Caryl Lockhart and Mark Stevenson.

6.2.2 Statistical analyses

Survey responses were entered into a relational database and exported to a statistical package for analysis. To compare responses from the urban and rural areas we used Fisher's exact test for proportions and the Mann-Whitney U test for continuous variables. Results obtained for each study area were treated as independent samples and compared with each of the factors investigated. Significance was based on an alpha level of 0.05.

We tested the null hypothesis that the urban and rural study areas were significantly different from each other in terms of each of the factors listed in the questionnaire. In addition, we determined if there was any relationship between backyard poultry ownership and a quantitative measure of affluence. The point location of poultry-positive parcels were superimposed on a map of New Zealand deprivation index (Salmond et al. 2006) recorded at the mesh block block level and summary statistics generated for the number of bird-positive parcels for each of the 10 levels of deprivation (1 being least deprived and 10 the most deprived).

We assessed whether poultry-positive land parcels were spatially aggregated using the spatial scan statistic (Kulldorff & Nagarwalla 1995, Kulldorff 1997) and the inhomogeneous K-function (Ripley 1976, 1977). The spatial scan statistic can be applied as a non-focused test for spatial clustering and operates by imposing a series of circular windows around each of a series of possible cluster centroids (in this case poultry-positive land parcels) positioned throughout a study area. For each centroid the radius of the window varies continuously in size from zero to 50% of the total population at risk creating a number of distinct geographical circles with each being a possible candidate for a cluster. For each location and size of the scanning window, the alternative hypothesis is that there

is an elevated rate within the window, compared with outside. Once the window with the greatest likelihood ratio statistic is identified the sampling distribution of the likelihood ratio is evaluated using a Monte Carlo test. Used in this way, the spatial scan statistic is able to identify the location of the most likely cluster (in terms of its centroid and radius) and the probability that this cluster has arisen by chance.

In contrast to the spatial scan statistic, the inhomogeneous K-function is used to describe the second-order characteristics of a spatial point pattern, that is, the general tendency for poultry-positive land parcels to be located close to each other. Separate K-functions were generated for poultry-positive land parcels (K_{pos}) and poultry-negative parcels (K_{neg}). The difference in the two metrics as a function of distance was calculated as $D(s) = K_{pos}(s)$ - $K_{neg}(s)$. The observed difference can be interpreted as a measure of the aggregation of poultry-positive parcels over and above that observed for the poultry-negative parcels at relatively small distance scales (up to 2 kilometres). To test the hypothesis that there was no aggregation, we randomly permuted the location of the poultry-positive parcels and calculated the observed difference function for each of the permutations (Chetwynd & Diggle 1998). The upper and lower limits of the simulations were plotted to determine if the observed difference function fell outside the limits of the envelopes. If this was the case, this would indicate significant spatial aggregation of poultry-positive parcels, relative to land parcels without poultry.

To determine if there was any association between poultry-positive land parcels and enterprises that had poultry listed in AgriBase (some of which may have been commercial enterprises), we computed, for each AgriBase enterprise, the number of poultry-positive land parcels located within radial distances of 1 to 5 kilometres.

6.3 Results

Figure 6.1 shows the location of the two study areas. Figure 6.2 shows, for each study area, the point location of poultry-positive land parcels superimposed on a choropleth map of deprivation index.

Descriptive statistics for each quantitative variables collected by the survey, stratified by study area are provided in Table 6.1. Overall, 5% (20 of 435) of respondents kept domestic

poultry: 2% (6 of 361, 95% CI 1% – 4%) and 19% (14 of 74, 95% CI 12% – 30%) for the urban and rural areas, respectively. All poultry-positive parcel land occupiers were interviewed. The two study areas differed in two aspects — reason for bird ownership and carcass disposal methods (Table 6.1). Of the 20 poultry-positive land parcels, 10 cited production for food as the primary reason for keeping poultry while 3, 1, and 1 cited pleasure, manure, and other reasons as the primary reason. The median number of birds per parcel was 4 (minimum 1, maximum 15) and 7 (minimum 1, maximum 35) for the urban and rural areas, respectively.

Thirteen parcels housed birds in sheds while seven allowed their birds to free range within the property. All 13 parcels that housed birds also allowed them to range freely during the day. In the rural area 12 parcels provided housing while 2 allowed birds to continuously free range. In the urban area, two parcels kept birds in sheds whilst four allowed birds to continuously free range.

Methods for carcass disposal differed in the two study areas (Wilcoxon Rank Sum statistic 21; P = 0.03). For both areas, burial was the most frequently cited method for disposal of carcasses: 11 and 4 for the urban and rural areas, respectively. Respondents in both study areas cited purchased feeds as the primary feed source. Purchased feed was used in five of six poultry-positive parcels in the urban area and nine of 14 parcels in the rural area. The remainder used a mix of purchased feeds and kitchen scraps.

The two areas did not differ significantly in terms of movement of poultry onto (χ^2 0.01; df 1; P = 0.92) and off (χ^2 0.72; df 1; P = 0.39) land parcels. A total of nine of the 20 parcels reported either an off- or on-parcel movement of poultry in the past 12 months. These were related to the movement of eggs and adult birds gifted or sold to friends or members of poultry associations.

There were no significant clusters of poultry-positive parcels in either study area (log likelihood ratio statistic 6.74; P = 0.17 and log likelihood ratio statistic 3.45; P = 0.89 for the urban and rural study areas, respectively). There was no evidence to support spatial aggregation of poultry-positive parcels (Figure 6.3) or the existence of clusters of poultry-positive parcels within either study area or around commercial enterprises in the rural area (Figure 6.4). For the 10 enterprises in the rural area that had poultry listed in AgriBase, each had anywhere between 0 and 5 poultry-positive positive parcels within a 0 – 1 kilometre radius, 0 and 8 within a 1 – 2 kilometre radius, 1 and 7 within a 2 – 3

kilometre radius, and 0 and 4 for a 3 – 4 kilometre radius and 0 and 5 for a 4 – 5 kilometre radius.

Table 6.1: A cross-sectional study of backyard poultry ownership in an urban and rural area of New Zealand, February – November 2006. Details of selected management practices in the two study areas.

Variable	Area		Total	P
	Urban	Rural		
Study area (square kilometres):	20.08	16.39	36.47	
Number of land parcels:	361	74	435	
Parcels with backyard birds:	6 (2%)	14 (19%)	20 (5%)	< 0.01
Poultry-positive land parcels/100 km^2	30 (14, 52) [a]	85 (62, 95) [a]	55 (39, 70) [a]	
Reason poultry kept:				
Home use	2	8	10	
Hobby	0	3	3	
Commercial	0	1	1	
Pet	4	2	6	
Total	6	14	2 0	
Reason for bird ownership:				
Food	3	7	10	
Pleasure	3	0	3	
Manure	0	1	1	
Other	0	2	1	
Total	6	14	20	0.05
Number of birds per parcel:	4 (1, 15) [b]	17 (1, 35) [b]	7 (1, 35) [b]	0.26
Housing:				
Shed	2	11	13	
Free-range	4	3	7	
Total	6	14	20	0.13
Hours free range per day:	14 (4, 24) [b]	14 (0, 24) [b]	13 (0, 14) [b]	
Carcass disposal:				
Burial	4	11	15	
Rubbish dump	0	1	1	
Renderer	0	1	1	
Other	2	1	3	
Total	6	14	20	0.03
Feed source:				
Purchased	5	9	14	
Mixed	1	5	6	
Total	6	14	20	0.10
Movement (on):	2	6	8	0.13
Movement (of):	0	4	4	0.13
Movement (on and off):	3	6	9	0.13

[a] 95% confidence interval.
[b] Minimum, maximum.

(a)   (b)

(c)   (d)
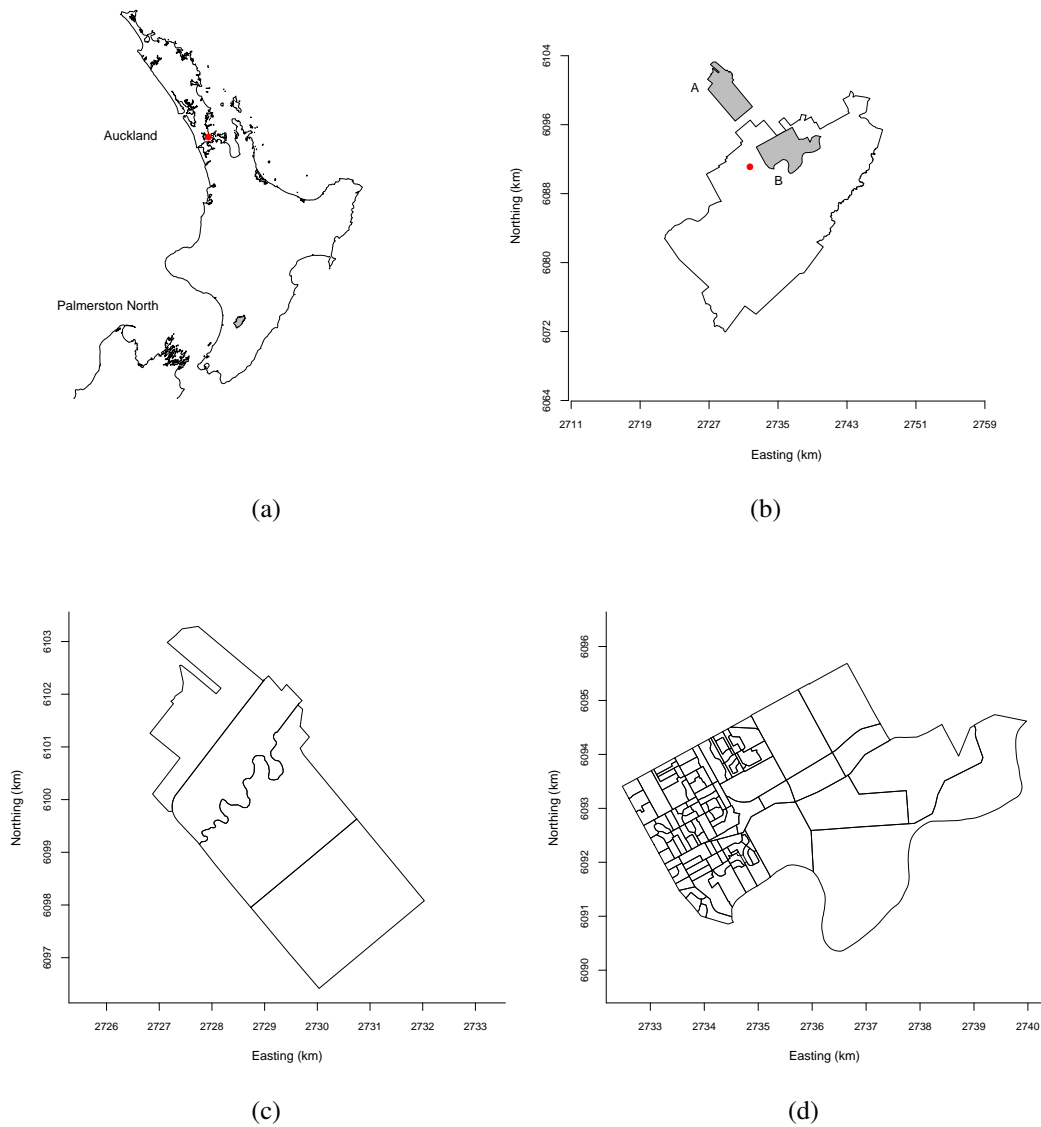
Figure 6.1: A cross-sectional study of backyard poultry ownership in an urban and rural area of New Zealand, February – November 2006. Maps showing: (a) location of Palmerston North (b) boundaries of Palmerston North city and the location of the two study areas, relative to the city boundaries, (c) the rural, and (d) urban study areas. The point (●) shown in (b) indicates the location of the Palmerston North central business district.
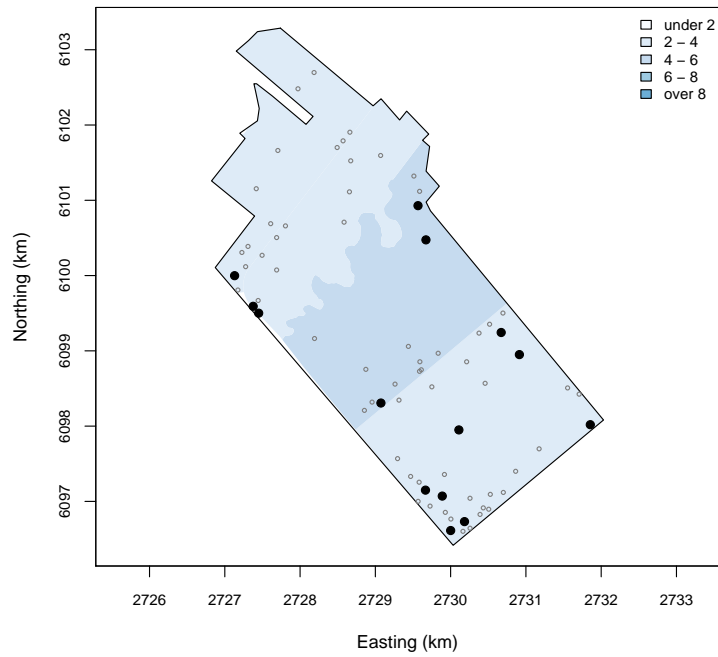
(a) Rural
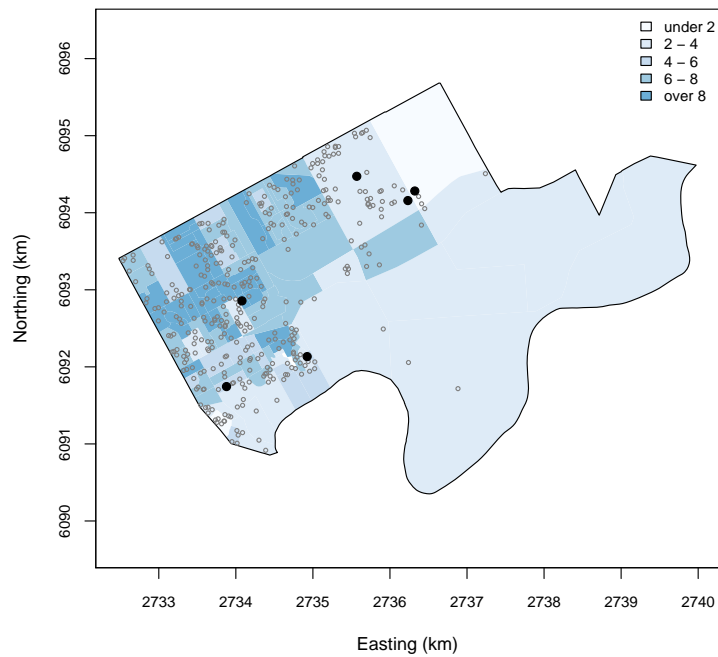
(b) Urban

Figure 6.2: A cross-sectional study of backyard poultry ownership in an urban and rural area of New Zealand, February – November 2006. Choropleth maps showing New Zealand deprivation index by census block for the: (a) rural and (b) urban study area. Superimposed on each map are the locations of the poultry positive (●) and negative (○) land parcels.
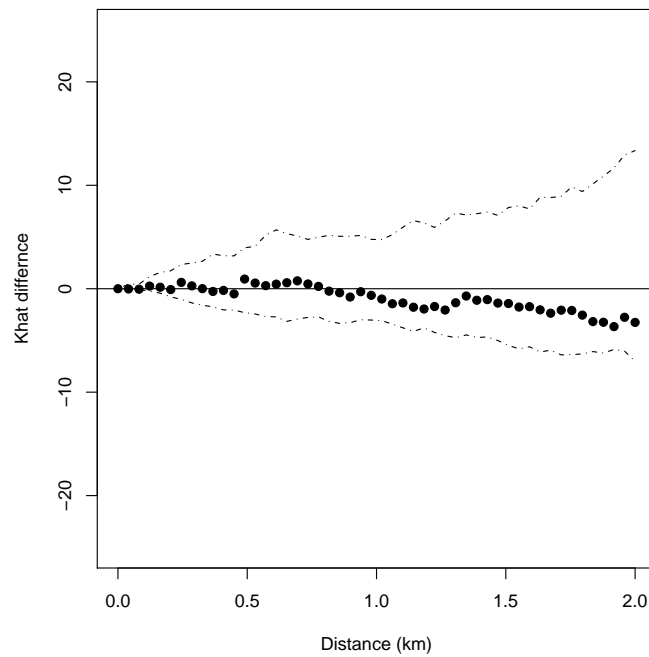
(a) Rural
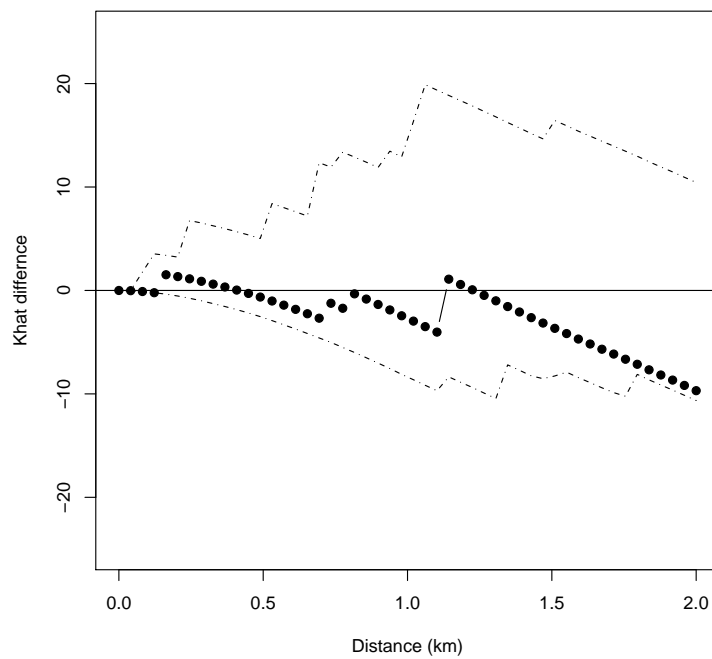
(b) Urban

Figure 6.3: A cross-sectional study of backyard poultry ownership in an urban and rural area of New Zealand, February – November 2006. K-function difference plot of the spatial distribution of poultry-positive parcels compared with the spatial distribution of poultry-negative parcels in the: (a) rural and (b) urban study area.
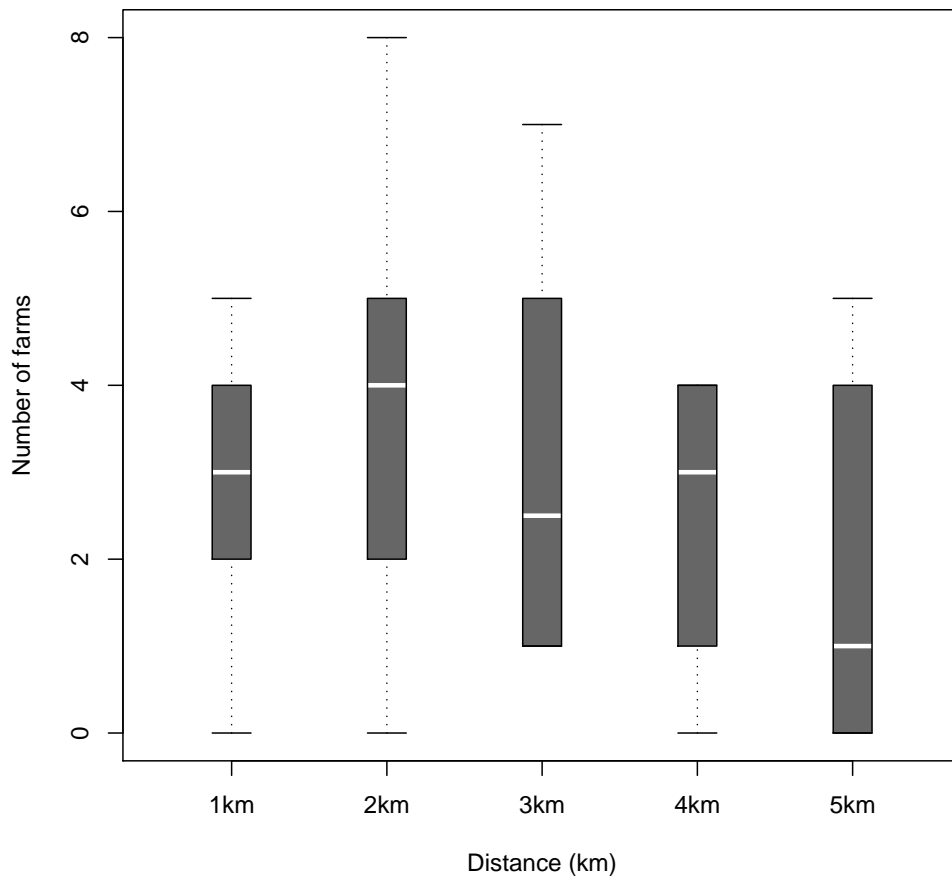
Figure 6.4: A cross-sectional study of backyard poultry ownership in an urban and rural area of New Zealand, February – November 2006. Box and whisker plot showing the distribution of the number of poultry-positive parcels in the rural study area located within a 1 – 5 kilometre distance of commercial poultry enterprises listed in AgriBase.

6.4 Discussion

This was a cross-sectional survey of residential properties in two areas in and around the city of Palmerston North, in the North Island of New Zealand. The first area was located within the city boundaries; the second area was located within a 10 – 15 minute drive of the central business district of the city in an area best classed as urban-rural fringe. Our aims were two fold: firstly, to determine the proportion of households in each area that keep backyard poultry, and secondly to document the way backyard poultry are managed. Previous experience has shown that backyard poultry flocks tend to be the first sector to be affected in the event of incursions of infectious diseases such as avian influenza and Newcastle disease into a country (Crespo et al. 1999, Capua et al. 2002). Furthermore, backyard poultry flocks can serve as a source of infection for commercial poultry if biosecurity on commercial poultry farms is poor. Characterisation of this sector of the poultry industry is of strategic importance in terms of setting priorities for surveillance and for epidemic contingency planning.

Our results show that few residential parcels (5%, 95% CI 3% – 7%) kept backyard poultry and, if birds were kept, the size of flocks were small (mean 7 95% CI 1 – 35). The prevalence of backyard poultry ownership was significantly greater in the rural area compared with the urban area (Table 6.1). The number of birds kept on rural premises was greater than in the urban area, though differences in bird numbers for the two study areas were not significant (Mann Whitney U test statistic 3; P = 0.50). The difference in the prevalence of keeping backyard poultry among the two areas may be due to the presence of council by-laws that limit the numbers of birds that may be kept in built-up areas of the city or due to a higher prevalence of bird ownership on 'lifestyle' blocks in the rural area. The relatively low numbers of poultry-positive land parcels and the low numbers of birds present on each indicates that both urban and urban-rural fringe areas, in the event of an exotic disease incursion, are unlikely to pose a large risk for spread of infectious agents. Infectious diseases of poultry such as avian influenza and Newcastle's disease with short incubation periods (Mishra et al. 2001) and a tendency towards a rapid clinical course require high bird densities to spread (Mannelli et al. 2007, Thrusfield 2007). Our findings indicate that if backyard poultry in these areas were to become infected with either of these pathogens, disease would be unlikely to spread unless infection was transported to

areas of high bird density (i.e. commercial poultry farms) via contaminated shoes, clothing and/or live birds (Halvorson et al. 1980, Webster et al. 1992). Consideration of these risks play an important role when providing advise to owners of backyard flocks regarding biosecurity. With regards to registration, mandatory registration determinations are generally based on enterprise size cut-offs that pose a significant risk to disease transmission (Houston et al. 2006).

We enumerated the prevalence of a range of practices that may increase the risk of exposure of backyard poultry to infectious disease. Free ranging of birds was permitted for periods of up to 24 hours in all poultry-positive parcels, a practice likely to increase the probability of contact with wild birds. A number of studies have implicated wild birds as an exposure source for avian influenza incursions into both commercial and non-commercial poultry sectors (Kaoud 2007, Saad et al. 2007). As part of epidemic contingency planning effort should be applied to educate backyard poultry owners regarding the risks that wild birds might pose in terms of disease transmission (Muller et al. 1999). Carcass disposal method was predominantly by burial in both study areas. This would imply that the risk of spread of disease via infected carcasses would be unlikely in the event of an infectious disease outbreak. Similar findings were reported by McBride et al. (1991) in a study of backyard poultry flocks in California.

We found no evidence of formal or informal links between residents on land parcels where backyard poultry were kept and the commercial poultry sector. This probably reflects the condition of employment practiced by most of the major commercial poultry companies requiring workers not to keep domestic poultry on their home premises. This is an encouraging finding as movements between informal and commercial poultry sectors have, in other countries, been associated with widespread dissemination of disease (Panigrahy et al. 2002, Garber et al. 2007). There were no reported movements of product from poultry-positive parcels to commercial premises (and *vice versa*) and poultry-positive parcels were randomly distributed within radial distances of 1 to 5 kilometres from those parcels that had poultry listed in AgriBase (Figure 6.4). These findings imply that there is little or no relationship between commercial poultry enterprises (as recorded in AgriBase) and the presence of land parcels where backyard birds are kept. The implication of this for animal health authorities is that, in this area of New Zealand at least, in the event of an outbreak in a commercial poultry unit, identification of poultry-positive land parcels

through tracing within defined zones around affected premises would yield less results than an appropriately designed survey of residents within the same area.

Purchased feed was by far the feed of choice for birds in both study areas although the use of kitchen scraps as a source of feed was common. Determining the content of kitchen scrap was not an objective of this study, but it's use may result in a potential pathway for disease introduction into backyard flocks if contaminated meat is fed. Diseases such as avian influenza and Newcastle disease could potentially be spread in this way. A recent study conducted to determine the ability of chicken meat to transmit avian influenza found that feeding breast or thigh meat from H5N1 infected chickens to other chickens resulted in infection and death (Swayne & Beck 2005*a*). Additionally, these findings indicate that a sampling frame of backyard poultry owners might be rapidly obtained in the event of an emergency by contacting commercial feed suppliers (Freier et al. 2004). This is especially important as most owners did not belong to an association.

We found no association between the presence of backyard poultry and socio-economic deprivation, as measured by the 2001 New Zealand Deprivation Index (Salmond et al. 2006). Further studies — perhaps to investigate the relationships between (say) ethnicity and the likelihood of bird ownership in other areas of the country, particularly in and around the larger cities (characterised by higher densities of ethnically diverse populations) would provide a means for investigating these relationships in greater detail. Our experience from this study was that it was relatively easy to survey large numbers of properties over a short period of time, given the opening question to respondents was simply 'Do you keep poultry?' and, in the majority of cases, when the answer to this question was no, the questionnaire was terminated allowing us to move onto the next premises. We believe that AgriBase and human census data could be combined to carry out the same type of survey was that described in this paper at multiple sites throughout the country (i.e. encompassing a wider range of cities, towns and rural areas) to build up a more comprehensive picture of backyard poultry ownership. Studies of this type would allow factors associated with backyard poultry ownership to be defined such as population density, distance from urban centres, land parcel area, and ethnicity. The distribution of this somewhat difficult to quantify sector of the poultry industry might then be better defined, based on predictions made from these identified factors.

CHAPTER 7

Patterns of contact in the commercial sector of the New Zealand poultry industry

7.1 Introduction

The entry and establishment of infectious diseases such as highly pathogenic avian influenza, Newcastle disease and infectious bursal disease would have severe consequences for the New Zealand poultry industry. Knowledge of industry 'weak points' or areas of vulnerability where these pathogens might enter the country and establish is important, since it provides better focus for border control and disease surveillance activities. Furthermore, knowledge of the means by which an infectious agent might disperse from an entry point into the country is useful for disease control authorities: eliminating transmission pathways will help to reduce the number of enterprises affected if (and when) an incursion occurs (Rawdon, McFadden, Stanislawek & Bingham 2007).

To better understand how disease might be transmitted between farms by direct and indirect contact, information is needed on the type and magnitude of contacts between farm enterprises and those that provide services to the agriculture sector. Social network analysis (Wasserman & Faust 1994) provides a means for formalising this process, allowing patterns of contact to be described and quantified. Although this methodology has been widely used in the social sciences and human epidemiology (see Fitzpatrick et al. 2001, Bearman et al. 2004, and Hufnagel et al. 2004 for examples) it has only recently been applied to understand the potential for disease spread among animal populations. Examples of the use of social network analysis in animal populations include studies of trainer networks in the British horse racing industry (Christley & French 2003), patterns

of movement among British and Danish cattle farms (Christley et al. 2005, Bigras-Poulin et al. 2006, Ortiz-Pelaez et al. 2006, Robinson & Christley 2007), and the spread of tuberculosis among captive possums (Corner et al. 2003). An accessible review of this technique is provided by Newman (2003).

We describe the results of a cross-sectional survey where enterprise managers within the commercial sector of the New Zealand poultry industry were asked to describe the type and frequency of contacts with other poultry enterprises and industry service providers. We describe the topology of these contacts using social network analyses and provide a commentary on how this information might be used refine strategies to contain and eradicate outbreaks of infectious disease and to develop effective surveillance activities for exotic disease incursions.

7.2 Materials and methods

7.2.1 Study population

The Poultry Industry Association of New Zealand (PIANZ) is an organisation that provides and support and advocacy for commercial poultry farmers throughout New Zealand. Although exact details are unknown, it has been estimated that over 95% of the total number of enterprises selling poultry product for human consumption in New Zealand are PIANZ members (Michael Brooks, personal communication). We accessed details of the 440 members listed on the PIANZ database in June 2007. Duplicate records, enterprises that were no longer in production and enterprises that were listed but had no production facilities were removed from the member database.

The eligible population for this study comprised the 420 valid enterprises on the PIANZ database (including feed plants, hatcheries, breeding units, processing plants and layer and broiler production units) who were sent a questionnaire by post on 1 August 2007. Questionnaires were addressed to the contact person listed in the PIANZ database for each enterprise. In the remainder of this paper we use the term 'respondent' to refer to the person who completed the questionnaire on behalf of each enterprise. The study population comprised those members of the eligible population who returned a completed, valid set of questionnaire responses to the authors by 31 October 2007.

7.2.2 Questionnaire

The questionnaire was comprised of 28 questions, asking respondents to describe the type and frequency of on- and off-enterprise movements of: (1) feed, (2) live birds and hatching eggs, (3) table eggs and poultry product, and (4) manure and waste litter. We use the term 'movement' to describe the physical transfer of material (e.g. feed, live birds, eggs, or manure) from one location to another. The period of interest was the last complete month of production for farms, hatcheries and processing plants and the last six months of sales for feed plants. For each of the four movement categories, respondents were asked to provide information relating to: (1) the identity of enterprises or town location of the enterprises they had contact with, (2) the type of contact, (3) how often these contacts occur, (4) the quantity of material that was moved and, (5) how the frequency of these contacts varied over the previous 12 months. General information about the enterprise such as company affiliation, production type, current and total holding capacity, the number of sites and their locations was also obtained.

The questionnaire was piloted on six PIANZ members during July 2007 in an effort to ensure clarity of the questions that were being asked. Of the 6 members that took part in the pilot survey, 4 returned the survey forms with comments and suggestions as to how the questionnaire could be improved. One week before the questionnaire mail-out, a one-page pre-survey sensitisation letter was sent. At regular intervals between 1 September 2007 and 31 October 2007 members who had not returned a completed questionnaire were contacted by PIANZ staff to encourage a response.

7.2.3 Data management and analysis

Data from the completed and returned questionnaires were entered into a relational database. The database contained four tables comprised of: (1) the eligible population (PIANZ members who received a questionnaire), (2) survey respondents (contact and enterprise details of those who returned a complete and valid set of responses to the questionnaire), (3) survey respondents and all their named contacts, and (4) details of movements between enterprises and their named contacts. Contacts were defined in terms of enterprise name and location. For example, if feed was purchased from a single company from two sites (e.g. Feed Company A Auckland, Feed Company A Christchurch) these were

recorded as two separate entries in the list of enterprise contacts. Survey responses from the database were exported to a statistical package for analysis (UCINET v6.137 Analytic Technologies Inc., Harvard, Massachusetts, USA).

In February 2008 the completed network descriptions were presented to a panel of poultry industry consultants for comment. This provided the opportunity to seek clarification around unusual contact patterns that were apparent. Following the meeting a list of issues was drafted and the relevant enterprises were contacted by PIANZ staff to seek clarification. Individual enterprise records were corrected, where appropriate.

Descriptive analysis of the data consisted of summary statistics of surveyed enterprises stratified by location and production type. We plotted the location of the surveyed enterprises geo-referenced by their town location over a density map of poultry enterprises listed in the PIANZ database (produced using the town of the listed mailing address to define geographic location).

The presence of a recorded movement event between poultry enterprises and their named associates allowed us to construct a network of named contacts. Using this approach, industry participants (commercial poultry enterprises and those that provided goods and services to the poultry industry) formed the nodes of the network and the stated movement of material from one node to another formed the ties. Under the assumption that ties between enterprises were not reciprocal all contact networks were treated as directed.

Contact networks were constructed for movements relating to: (1) feed, (2) live birds and hatching eggs, (3) table eggs and poultry product and (4) manure and waste litter. Each network was described in terms of: (1) the number of nodes and the number of directed links; (2) network size, diameter and density; and (3) the number of reachable pairs of nodes and the proportion of pairs that were reachable. The following parameters were calculated for each node of the network and summarised for the entire network (in terms of frequency histograms and descriptive statistics): (1) in- and out-degree, (2) in- and out-degree centralisation, (3) betweenness, and (4) geodesic distance, and (5) network clustering coefficient. Network diagrams were constructed for each of the four networks to allow visual assessment of network structure.

Small world networks are those where there are clusters of connected individuals (social groups), which have contacts with 'nearby' groups as well as 'far-off' groups via sparse

long range links. To identify networks as small world we compared the observed network with a network with a similar number of nodes and ties generated at random based on Erdös and Rényi random graph theory (Erdös & Rényi 1960). Small world networks are characterised by short geodesic distances and large clustering coefficients, compared with random networks of equivalent size. Identifying a network as small world is important, since the spread of disease from one group to another can be prevented by targeting the links that connect each group.

In scale-free networks (Albert & Barabási 2002, Newman 2003, Li et al. 2005) the degree distribution of the observed network is skewed, which means that while large numbers of nodes have few contacts, smaller numbers have many contacts (so-called 'super-spreaders' Anderson & May 1991). Effective disease control strategies can be applied in scale-free networks if they focus on these highly connected nodes.

7.3   Results

Counts of respondents who responded to the questionnaire, stratified by Biosecurity New Zealand zone and production type are provided in Table 7.1. Counts of PIANZ member enterprises, stratified by production type and Biosecurity New Zealand zone are provided in Table 7.2. Figure 7.1 shows the town location of survey respondents in relation to the geographical distribution of PIANZ members.

The response rate for this survey was 58% (244 out of 420). This included responses from 67% (38 of 57) of all breeder units and hatcheries, 58% (103 of 179) of all broiler units, 41% (11 of 27) of all feed plants, 57% (69 of 120) of all layer units, 55% (11 of 20) of all processing plants, and 35% (6 of 17) of enterprises classified as 'other'. A horizontal bar plot, showing counts of PIANZ member enterprises stratified by response status and production type is shown in Figure 7.2.

Summary statistics of the installation capacity of the study population, stratified by production type are provided in Table 7.3. Summary statistics for the feed, live bird and hatching eggs, table egg and poultry product and manure and waste litter networks are provided in Table 7.4. The footnotes that accompany Table 7.4 provide a brief explanation of each of the network descriptors used in this paper.

A total of 284 of the 1162 feed and manure/waste litter movement events provided data suitable for analysis. A trellis plot, showing the number of tonnes ($\times$ 1000) of feed and manure/waste litter moved on or off enterprises as a function of calendar month is shown in Figure 7.3. No seasonal trend in the quantity of material moved was evident.

Figures 7.4, 7.5, and 7.6 provide graphical representations of key aspects of the feed network: Figure 7.4 is a graph showing key aspects of the network structure; Figure 7.5 shows the same graph, respecting enterprise location. In each network plot the size of each node is proportional to its betweenness, providing an indication of the amount of flow within the network 'controlled' by individual nodes. Figure 7.6 shows the distributional features of network in- and out-degree, and the distance feed moved when being moved onto and off enterprises. Figures 7.7 to 7.15 show the same data for the live bird and hatching egg, table egg and poultry product, and manure and waste litter networks, respectively.

7.3.1 Feed

The network created from feed-related movements was comprised of 519 nodes (enterprise locations) with a total of 638 direct ties between them. The feed network was the largest of the four networks, reflecting the requirement for feed by all enterprises where live birds are kept and the infrastructure required to service this requirement.

Of the total possible number of ties in this network (n = 268,842) 10,316 were actually present. The proportion of possible ties that were present was 0.04 (10,316 $\div$ 268,842), indicative of a network of relatively low density. This is confirmed in Figure 7.4, where the network is characterised by a series of 'hub and spoke' type structures, with poultry enterprises making small numbers of connections to individual feed companies (the hubs). Centralisation indices provide a means for quantifying this network characteristic: a large centralisation index implies that a single node in the network has ties with many other nodes, but that the remaining nodes are not tied to each other. The out-degree centralisation index for the feed network was greater than that recorded for the live bird, table egg and manure and waste litter network (0.28 *vs* 0.18, 0.13, and 0.02, respectively) meaning that, compared with the other three networks, the off-enterprise movement of feed was organised around focal nodes. This finding is consistent with feed supplier chains where

many poultry enterprises source feed from a small number of suppliers (Figures 7.4 and 7.5). The highly skewed distribution of node in- and out-degree (Figures 7.6a and 7.6b) indicates that this network has scale-free properties.

Small world networks are characterised by short geodesic distances and relatively high clustering coefficients. The mean geodesic distance for the feed network was 4.08. The mean geodesic distance for a random network of similar size was 6.75. The clustering coefficient for the observed feed network was 0.021. The clustering coefficient for a random network of similar size 0.001. We conclude that the feed network described in this paper has small world properties.

Frequency histograms showing the distance travelled by feed moving on- and off-enterprises are shown in Figure 7.6c and 7.6d, respectively. For both directions feed-related movements were in two broad distance categories: less than 100 kilometres and between 600 and 1000 kilometres. The median distance feed travelled was 26 kilometres (range 0 – 1170 kilometres).

7.3.2   Live birds and hatching eggs

The network of live bird and hatching egg related movements (Figures 7.7 and 7.8) was comprised of 445 nodes with a total of 788 direct contacts. Of the total possible number of ties in this network ($n = 197,580$) 11,135 were actually present. Although this network exhibited a hub and spoke type structure (Figure 7.7) the degree of clustering around focal nodes was not as great as in the feed network (out-degree centralisation index 0.18 *vs* 0.28 for the feed network). Similar to the feed network the distribution of in- and out-degree was highly skewed (Figures 7.9a and 7.9b) consistent with a network with scale-free properties. Most nodes had contact with at least one other node from which they received live birds and/or hatching eggs.

The mean geodesic distance for the observed live bird and hatching egg network and a random network of similar size was 3.45 and 4.92, respectively. The clustering coefficient for the observed live bird and hatching egg network and a random network of similar size was 0.064 and 0.010 (respectively), consistent with a network with small world properties.

The distributions of live bird and hatching egg movement distances are shown in Figure 7.9c and 7.9d. The median distance live birds and hatching eggs travelled was 18

kilometres (range 0 – 1129 kilometres). Most movements occurred over relatively small distances (less than 100 kilometres), with smaller numbers occurring over distances of greater than 500 kilometres consistent with live birds and hatching eggs moving from the North to the South Island and *vice versa*.

7.3.3 Table eggs

The contact structure created from the movement of table eggs was comprised of 274 nodes with 288 direct ties. In common with the feed and live bird and hatching egg networks, the table egg and poultry product network was characterised by an out-degree centralisation index (0.13) greater than the in-degree centralisation index (0.03) indicative of the presence of hub nodes that distribute table eggs and poultry product to other network members. The distribution of node in- and out-degree was skewed (Figures 7.12a and 7.12b), indicating that this network had scale-free properties. The betweenness centralisation index was 0.022 (the highest of all the networks examined) reflecting the role of bridge nodes controlling the flow of material through this network.

The mean geodesic distance for the table egg and poultry product network was 3.72. The mean geodesic distance for a random network of similar size was 6.36. Clustering coefficients for the table egg and poultry product network and random networks were 0.045 and 0.018 (respectively), consistent with a network with small world properties. The median distance table eggs and poultry product travelled was 63 kilometres (range 0 – 1013 kilometres).

7.3.4 Manure and waste litter

The contact structure created from the movement of manure and waste litter (Figures 7.13 and 7.14) was comprised of 465 nodes with 565 direct ties. The proportion of reachable pairs was 0.01, the smallest of the four networks. In contrast to the other networks, this network was characterised by an in-degree centralisation index greater than the out-degree centralisiation index (0.07 *vs* 0.02). This is consistent with the presence of focal nodes (e.g. contract cleaners) acting as receivers of movement events. The skewed distribution of node in- and out-degree (Figures 7.15a and 7.15b) indicates that this network, in common with the others, had scale-free properties.

This network had the smallest betweenness centralisation index (0.003 *vs* 0.019, 0.021, and 0.022 for the feed, live bird and hatching egg, and table egg and poultry product networks, respectively). This finding reflects a small, if not negligible role of hubs in this network.

Mean geodesic distance for this network and a random network of similar size was 2.20 and 6.69, respectively. Clustering coefficients for this network and a random network of similar size were 0.003 and 0.005, respectively. In contrast to the other three networks, the manure and waste litter network did not have small world properties. The median distance over which manure and waste litter travelled was 15 kilometres (range 0 – 744 kilometres), considerably less than that in the feed, live bird and hatching egg, and table egg and poultry product networks (Figures 7.15c and 7.15d).

Table 7.1: Social network analysis of contacts in the commercial sector of the New Zealand poultry industry. Counts of poultry industry participants who responded to the survey, stratified by enterprise type and Biosecurity New Zealand zone. Zone 1: Northland, Auckland; Zone 2: Taranaki; Zone 3: Waikato, Bay of Plenty; Zone 4: Hawke's Bay, Manawatu, Wellington; Zone 5: Tasman, Nelson, Marlborough, West Coast, Canterbury; Zone 6: Southland, Otago.

Type	North Island				South Island		Total
	Zone 1	Zone 2	Zone 3	Zone 4	Zone 5	Zone 6	
Breeder	5	20	6	1	6	0	38
Broiler	27	19	26	7	24	0	103
Feed plants	0	0	3	2	3	3	11
Hatchery	3	1	0	0	2	0	6
Layer	7	1	13	29	13	6	69
Other	1	0	0	0	5	0	6
Processor	3	1	2	2	3	0	11
Total	46	42	50	51	56	9	244

Table 7.2: Social network analysis of contacts in the commercial sector of the New Zealand poultry industry. Counts of poultry industry participants registered with PIANZ, stratified by enterprise type and Biosecurity New Zealand zone. Zone 1: Northland, Auckland; Zone 2: Taranaki; Zone 3: Waikato, Bay of Plenty; Zone 4: Hawke's Bay, Manawatu, Wellington; Zone 5: Tasman, Nelson, Marlborough, West Coast, Canterbury; Zone 6: Southland, Otago.

Type	North Island				South Island		Total
	Zone 1	Zone 2	Zone 3	Zone 4	Zone 5	Zone 6	
Breeder [a]	6	17	12	7	14	1	57
Broiler	57	38	40	7	34	3	179
Feed plants	6	0	6	2	7	6	27
Layer	27	1	15	38	24	15	120
Other [b]	1	0	3	0	13	0	17
Processor	7	1	3	3	5	1	20
Total	104	57	79	57	97	26	420

[a] Includes hatcheries.

[b] Includes duck, quail and turkey enterprises.

Table 7.3: Social network analysis of contacts in the commercial sector of the New Zealand poultry industry. Descriptive statistics of enterprise installation capacity of surveyed enterprises, stratified by type.

Type	n	Mean (SD)	Median (Q1, Q3)	Range	Missing
Breeder [a]	38	3 (2)	3 (2,3)	0.8 – 14	13
Broiler [a]	103	10 (6)	9 (6,12)	0.3 – 36	14
Hatchery [b]	6	47 (75)	12 (7,53)	6 – 160	2
Layer [a]	69	5 (9)	2 (1,6)	0 – 45	13
Other [a]	6	1 (1)	1 (1,2)	0.4 – 3	1

SD: standard deviation.
Q1, Q3: first and third distribution quartiles, respectively.
[a] Number of birds ($\times$ 10,000).
[b] Number of fertile eggs ($\times$ 10,000).

Table 7.4: Social network analysis of contacts in the commercial sector of the New Zealand poultry industry. Descriptive statistics of network and node-level parameters for the feed, live birds and hatching eggs, table eggs and poultry product, and manure and waste litter networks.

Parameter	Feed	Live birds	Table eggs	Waste litter
Number of nodes [a]	519	445	274	465
Number of directed links [b]	638	788	288	565
Size [c]	268,842	197,580	74,802	215,760
Diameter [d]	8	10	9	6
Density (directed) [e]	0.002	0.004	0.004	0.003
Number of reachable pairs [f]	10,316	11,135	2,799	1,999
Proportion reachable pairs [g]	0.04	0.06	0.04	0.01
Mean in-degree (range) [h]	1 (0 – 14)	2 (0 – 27)	1 (0 – 10)	1 (0 – 33)
Mean out-degree (range) [i]	1 (0 – 107)	2 (0 – 70)	1 (0 – 23)	1 (0 – 16)
Normalised mean in-degree (range) [j]	0.2 (0 – 3)	0.4 (0 – 6)	0.4 (0 – 4)	0.3 (0 – 7)
Normalised mean out-degree (range) [k]	0.2 (0 – 21)	0.4 (0 – 16)	0.4 (0 – 8)	0.3 (0 – 3)
In-degree centralisation [l]	0.02	0.06	0.03	0.07
Out-degree centralisation [m]	0.28	0.18	0.13	0.02
Normalised mean betweenness (range) [n]	0.02 (0 – 2)	0.03 (0 – 2)	0.04 (0 – 2)	0 (0 – 0.2)
Betweenness centralisation [o]	0.019	0.021	0.022	0.003
Mean geodesic distance (mode) [p]	4.08 (4)	3.45 (3)	3.72 (4)	2.20 (2)
Clustering coefficient [q]	0.021	0.064	0.045	0.003

[a] Number of nodes: the total number of network members.

[b] Number of directed links: the total number of connections between nodes.

[c] Size: the total possible number of unique pairs of nodes.

[d] Diameter: the number of links in the largest path between two nodes.

[e] Density: the proportion of all contacts that could be present that actually are.

[f] Number of reachable pairs: a node is 'reachable' by another if there exists any set of connections by which one can trace from the source to the target node, regardless of how many others fall between them.

[g] Proportion of reachable pairs: the number of reachable pairs divided by the network size.

[h] In-degree: the number of contacts to a node (i.e. on-enterprise movements).

[i] Out-degree: the number of contacts from a node (i.e. off-enterprise movements).

[j] Normalised in-degree: the number of contacts to a node divided by the maximum number of possible contacts.

[k] Normalised out-degree: the number of contacts from a node divided by the maximum number of possible contacts.

[l] In-degree centralisation: a large in-degree centralisation score means that a small number of nodes in the network receive material from many other nodes, but the remaining nodes are not tied to each other.

[m] Out-degree centralisation: a large out-degree centralisation score means that a small number of nodes in the network send material to many other nodes, but the remaining nodes are not tied to each other.

[n] Betweenness: the frequency with which a node falls between pairs of other nodes on the path connecting them. Betweenness provides an indication of the amount of flow within the network that is 'controlled' by a node.

[o] Betweenness centralisation: provides an overall measure of the disparity in the centralised roles of nodes in the network. Higher values indicate the presence of large numbers of nodes that act as mediators.

[p] Geodesic distance: the shortest path between two nodes.

[q] Clustering coefficient: a metric that represents the density of triangles in the network. In a complete network where all vertices are connected to each other the clustering coefficient will be 1.
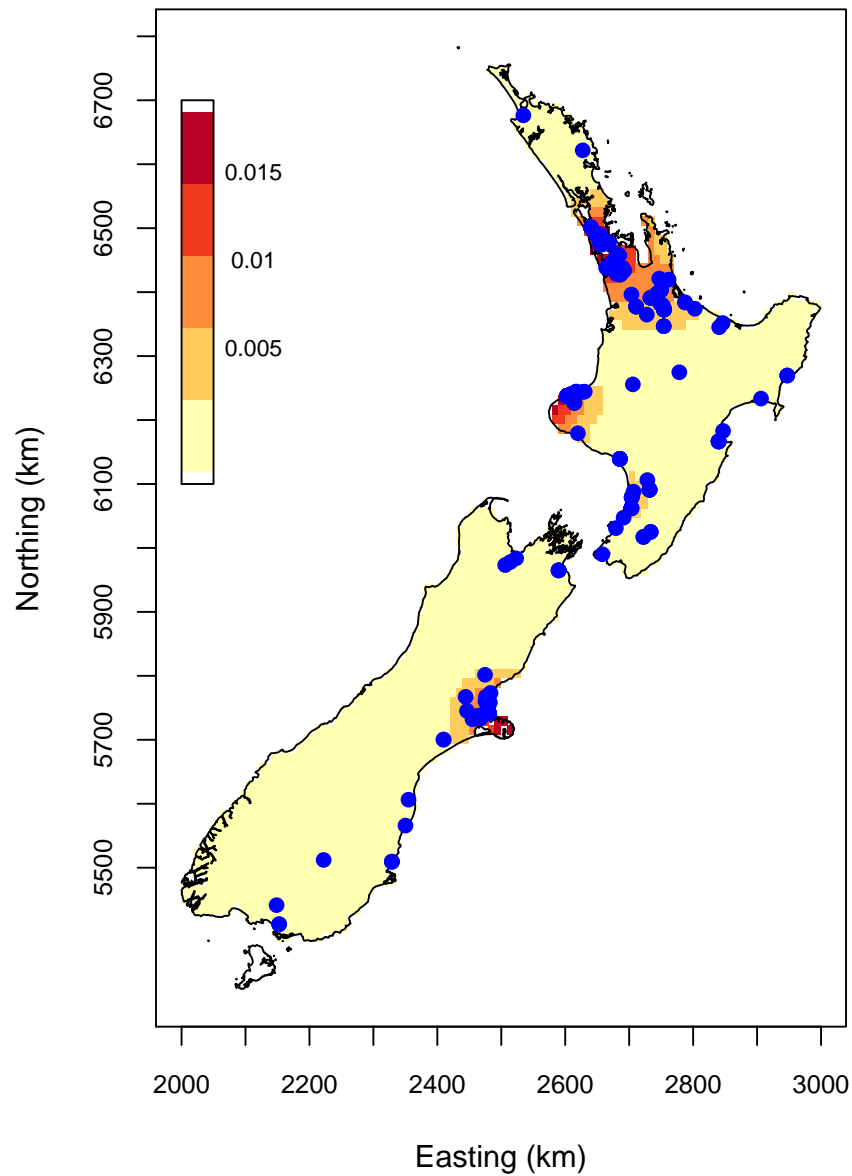
Figure 7.1: Social network analysis of contacts in the commercial sector of the New Zealand poultry industry. Map of New Zealand showing the location of survey respondents ($blue\bullet$)) superimposed on a density plot of enterprises listed in the PIANZ database. Densities are expressed as the number of enterprises per square kilometre.
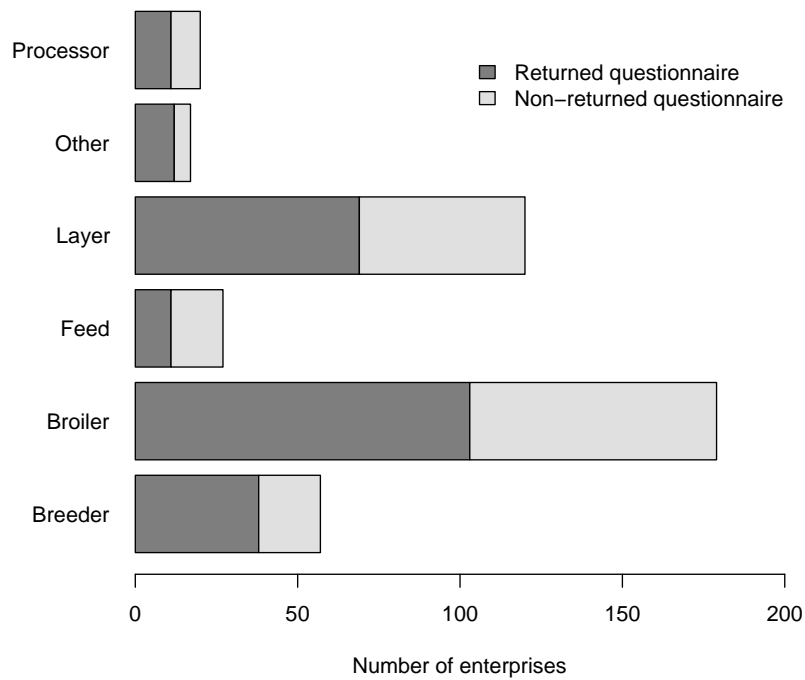
Figure 7.2: Social network analysis of contacts in the commercial sector of the New Zealand poultry industry. Horizontal bar plot showing counts of the eligible population stratified by production type and whether or not they returned a completed questionnaire.
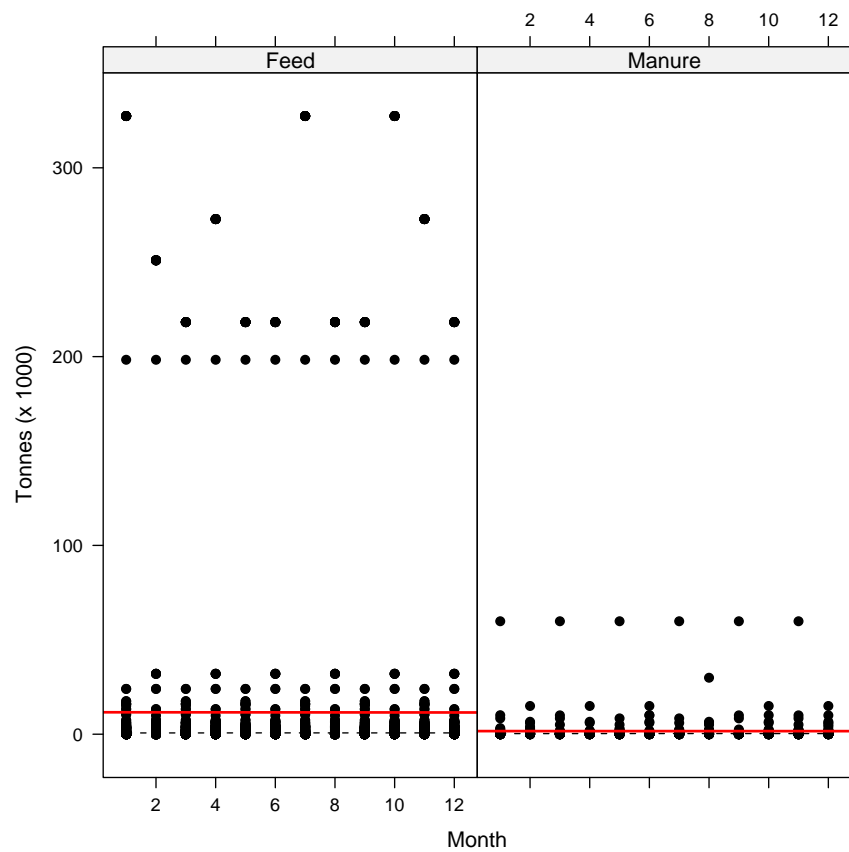
Figure 7.3: Social network analysis of contacts in the commercial sector of the New Zealand poultry industry. Trellis plot showing the number of tonnes ($\times$ 1000) of feed and manure/waste litter moved on or off poultry enterprises as a function of calendar month (1 = January; 12 = December). A lowess smoothed curve has been fitted to each plot to indicate trend over the 12-month period.
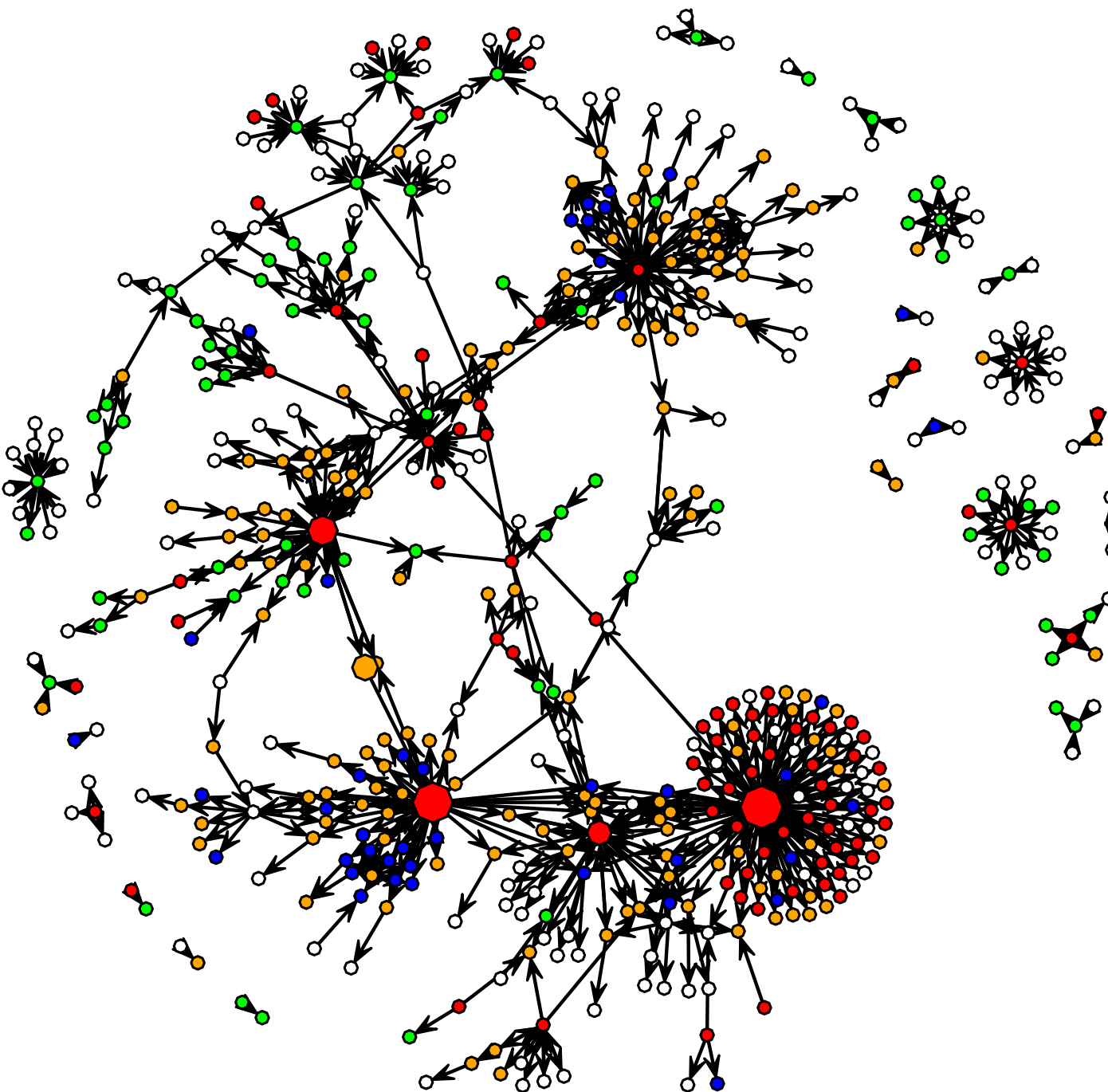
Figure 7.4: Social network analyses of feed related contacts in the commercial sector of the New Zealand poultry industry. Network graph constructed using a force-based algorithm proposed by (Fruchterman & Reingold 1991) with the size of the nodes proportional to node betweenness (an indicator of the amount of flow within the network 'controlled' by a node). Key: feed producers (red), breeders and hatcheries (blue), layer farms (green), broiler and other poultry farms (orange), other enterprise types (open circles).
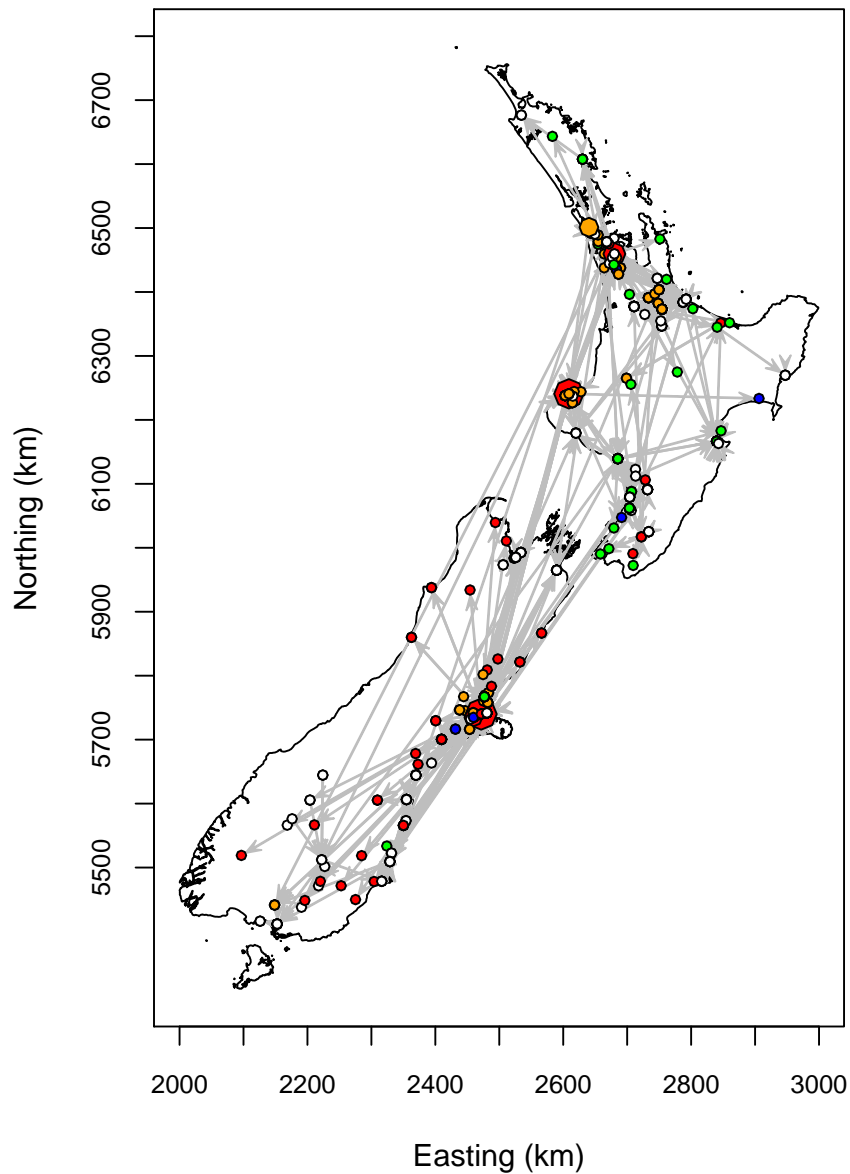
Figure 7.5: Social network analyses of feed related contacts in the commercial sector of the New Zealand poultry industry. Map of New Zealand showing the point location of enterprises that reported a feed related movement with the size of the nodes proportional to node betweenness. Lines define the movement of material from one enterprise to another, with arrows indicating the direction of movement. Key: feed producers (red), breeders and hatcheries (blue), layer farms (green), broiler and other poultry farms (orange), other enterprise types (open circles).
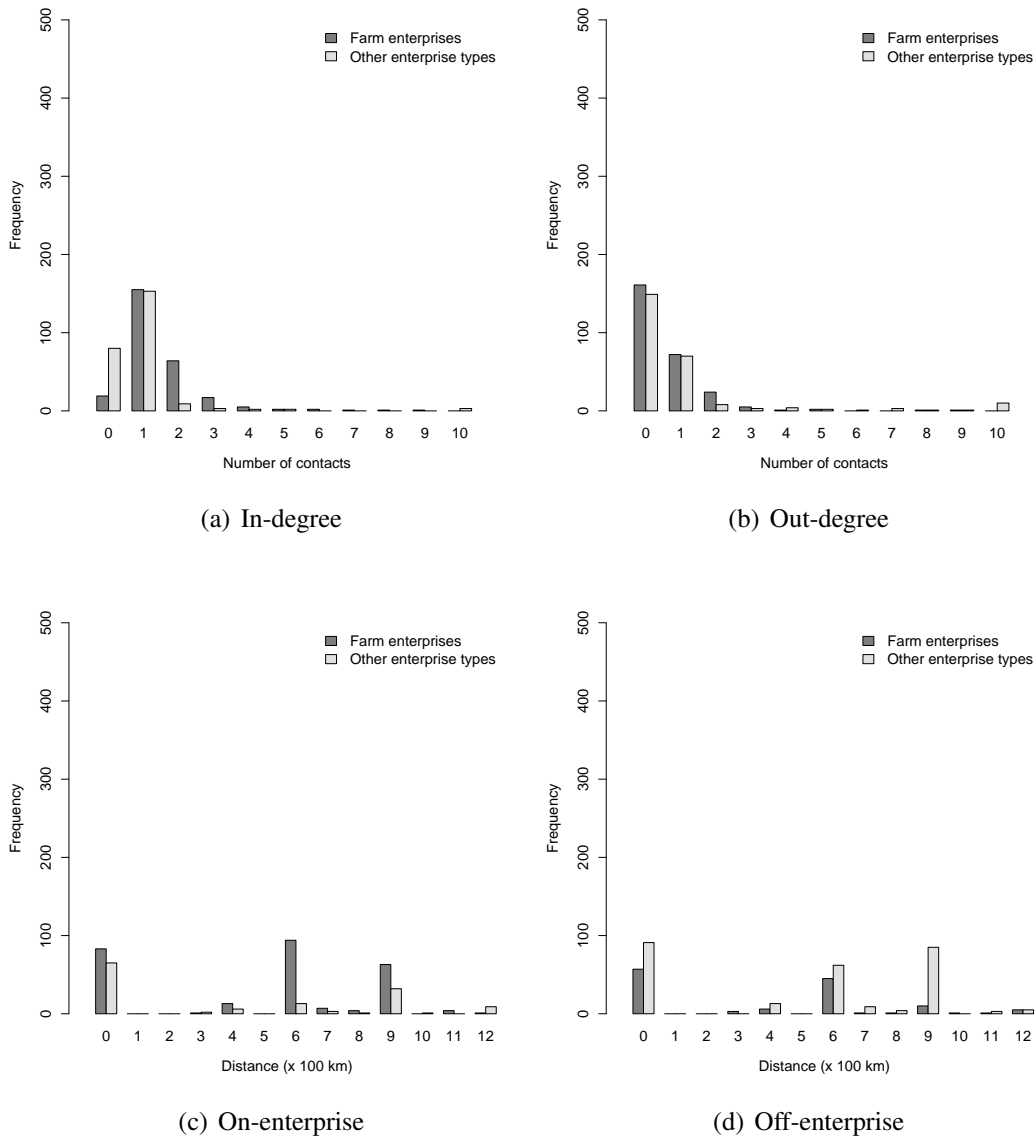
Figure 7.6: Social network analyses of feed related contacts in the commercial sector of the New Zealand poultry industry. (a) Bar plot showing the distribution of the number of contacts arising from movement events onto farm and non-farm enterprises, (b) bar plot showing the distribution of the number of contacts arising from movement events off farm and non-farm enterprises, (c) frequency histogram showing the distance material has moved when coming onto farm and non-farm enterprises, and (d) frequency histogram showing the distance material moves when going off farm and non-farm enterprises.
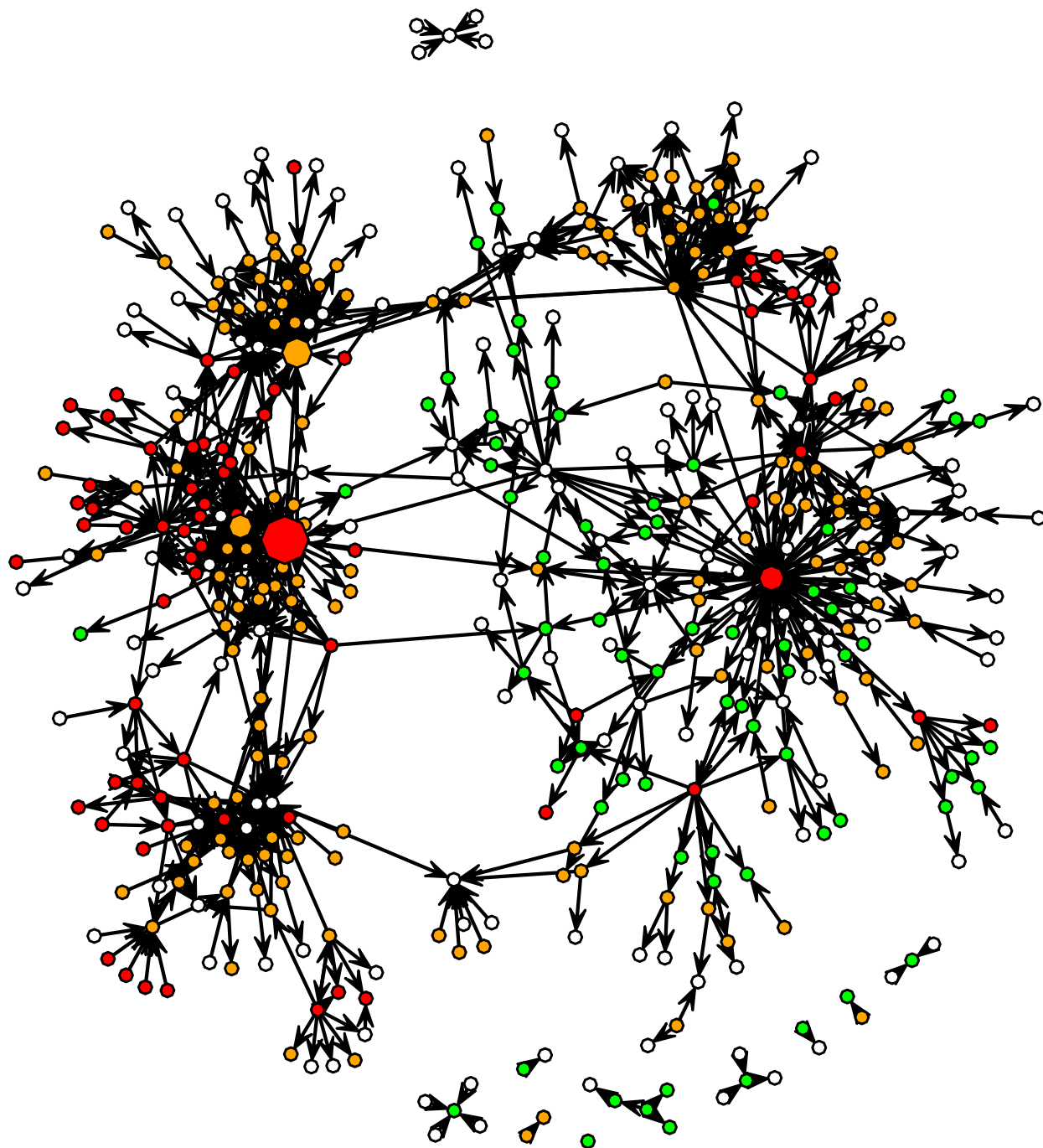
Figure 7.7: Social network analyses of live bird and hatching egg related contacts in the commercial sector of the New Zealand poultry industry. Network graph constructed using a force-based algorithm with the size of the nodes proportional to node betweenness. Key: breeders and hatcheries (red), layer farms (green), broiler and other poultry farms (orange), other enterprise types (open circles).
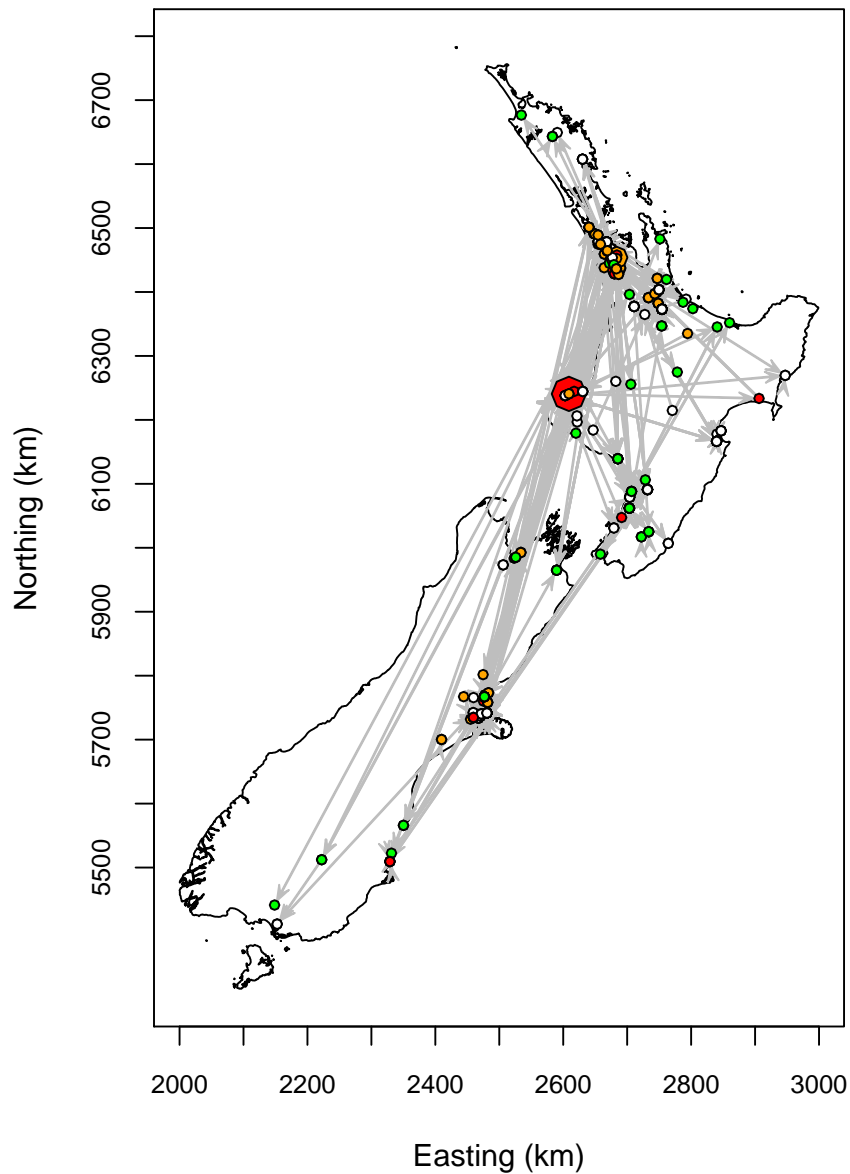
Figure 7.8: Social network analyses of live bird and hatching egg related contacts in the commercial sector of the New Zealand poultry industry. Map of New Zealand showing the point location of enterprises that reported a live bird or hatching egg related movement with the size of the nodes proportional to node betweenness. Lines define the movement of material from one enterprise to another, with arrows indicating the direction of movement. Key: breeders and hatcheries (red), layer farms (green), broiler and other poultry farms (orange), other enterprise types (open circles).

(a) In-degree

(b) Out-degree

(c) On-enterprise

(d) Off-enterprise
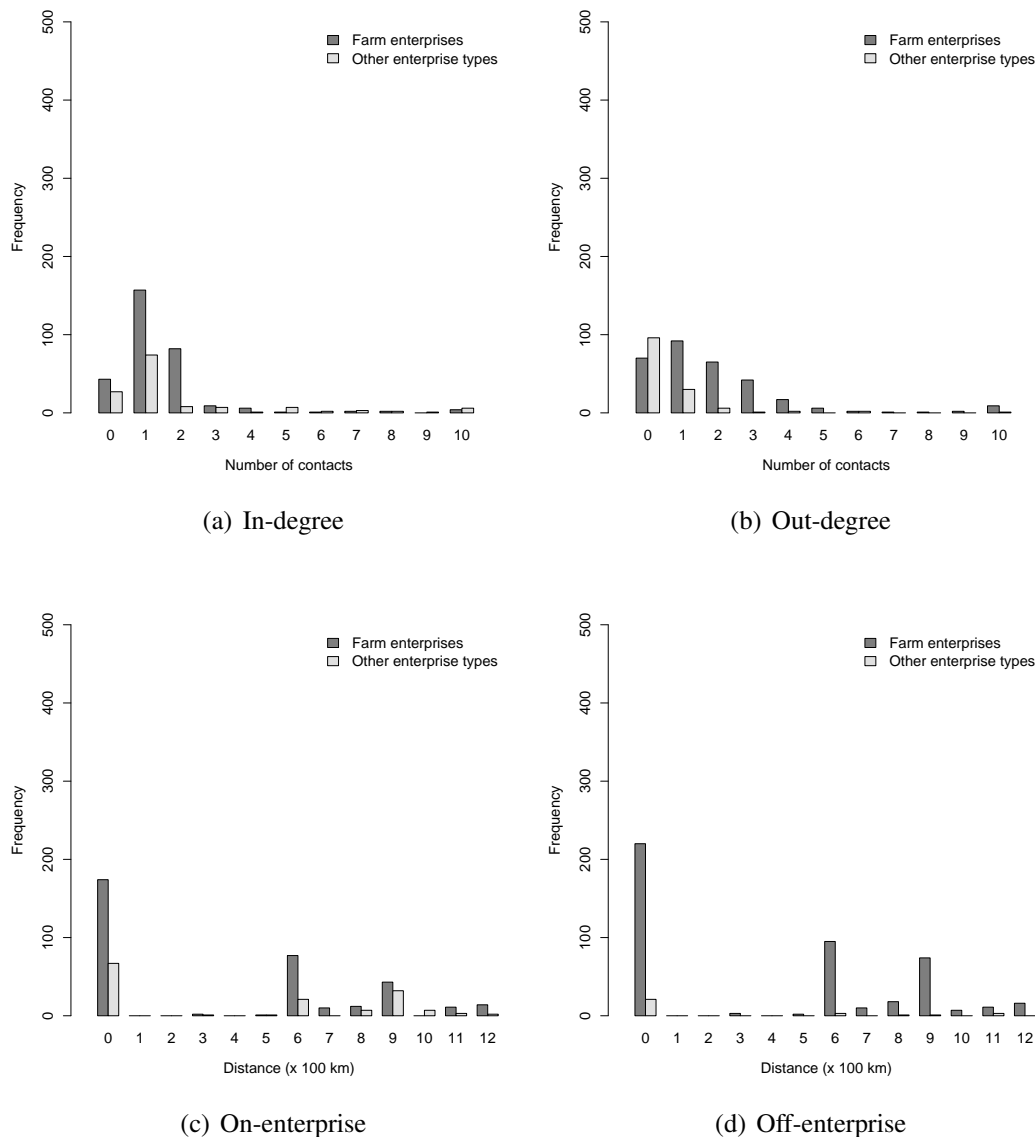
Figure 7.9: Social network analyses of live bird and hatching egg related contacts in the commercial sector of the New Zealand poultry industry. (a) Bar plot showing the distribution of the number of contacts arising from movement events onto farm and non-farm enterprises, (b) bar plot showing the distribution of the number of contacts arising from movement events off farm and non-farm enterprises, (c) frequency histogram showing the distance material has moved when coming onto farm and non-farm enterprises, and (d) frequency histogram showing the distance material moves when going off farm and non-farm enterprises.
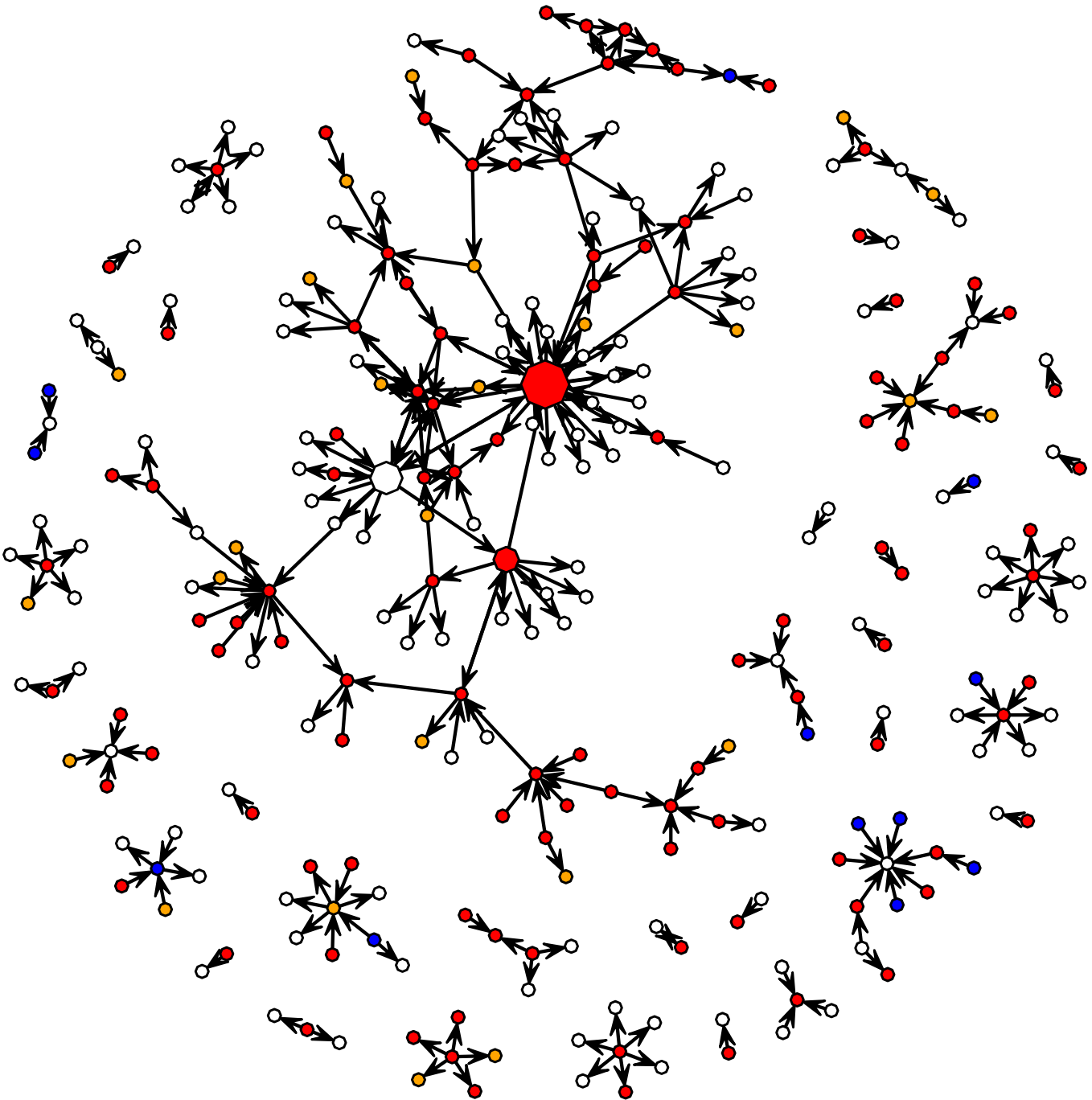
Figure 7.10: Social network analyses of table egg and poultry product related contacts in the commercial sector of the New Zealand poultry industry. Network graph constructed using a force-based algorithm with the size of the nodes proportional to node betweenness. Key: breeders and hatcheries (blue), layer and broiler farms (red), other poultry farms (orange), other enterprise types (open circles).
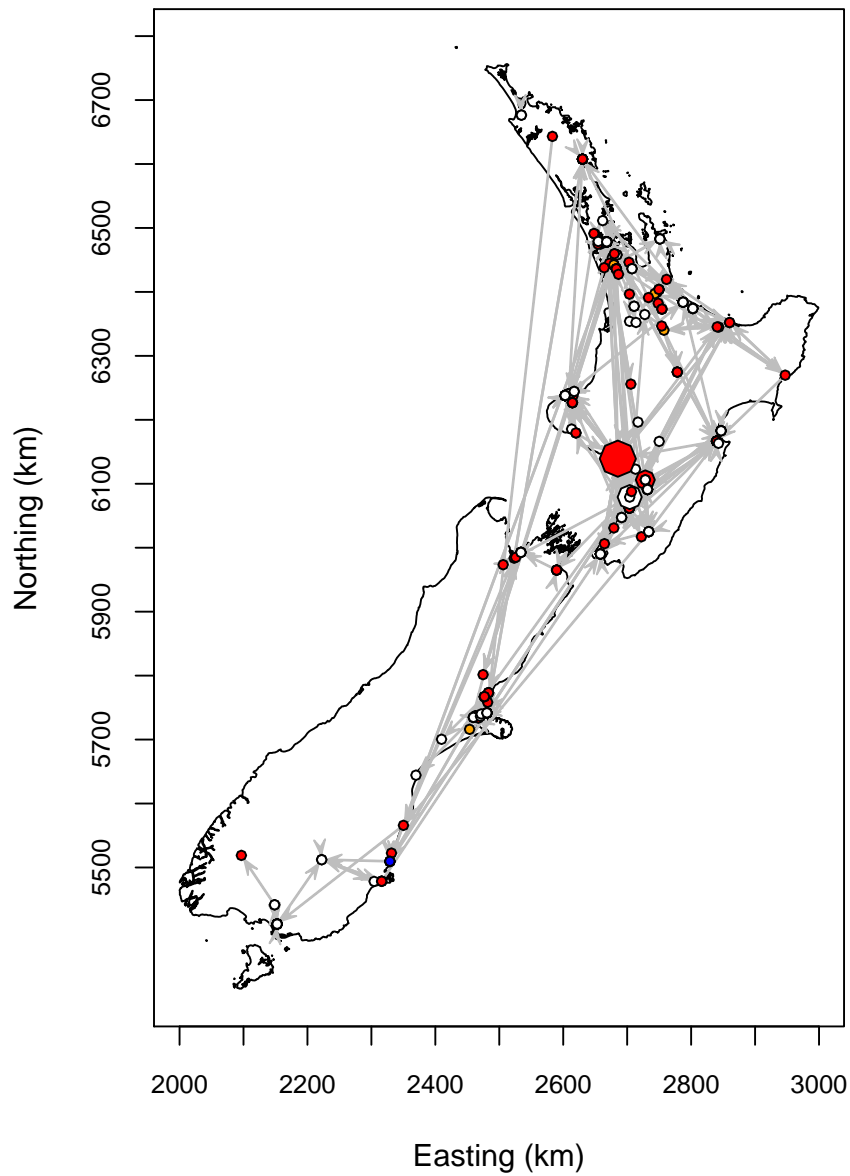
Figure 7.11: Social network analyses of table egg and poultry product contacts in the commercial sector of the New Zealand poultry industry. Map of New Zealand showing the point location of enterprises that reported a table egg and/or poultry product related movement with the size of the nodes proportional to node betweenness. Lines define the movement of material from one enterprise to another, with arrows indicating the direction of movement. Key: breeders and hatcheries (blue), layer and broiler farms (red), other poultry farms (orange), other enterprise types (open circles).

(a) In-degree

(b) Out-degree

(c) On-enterprise

(d) Off-enterprise
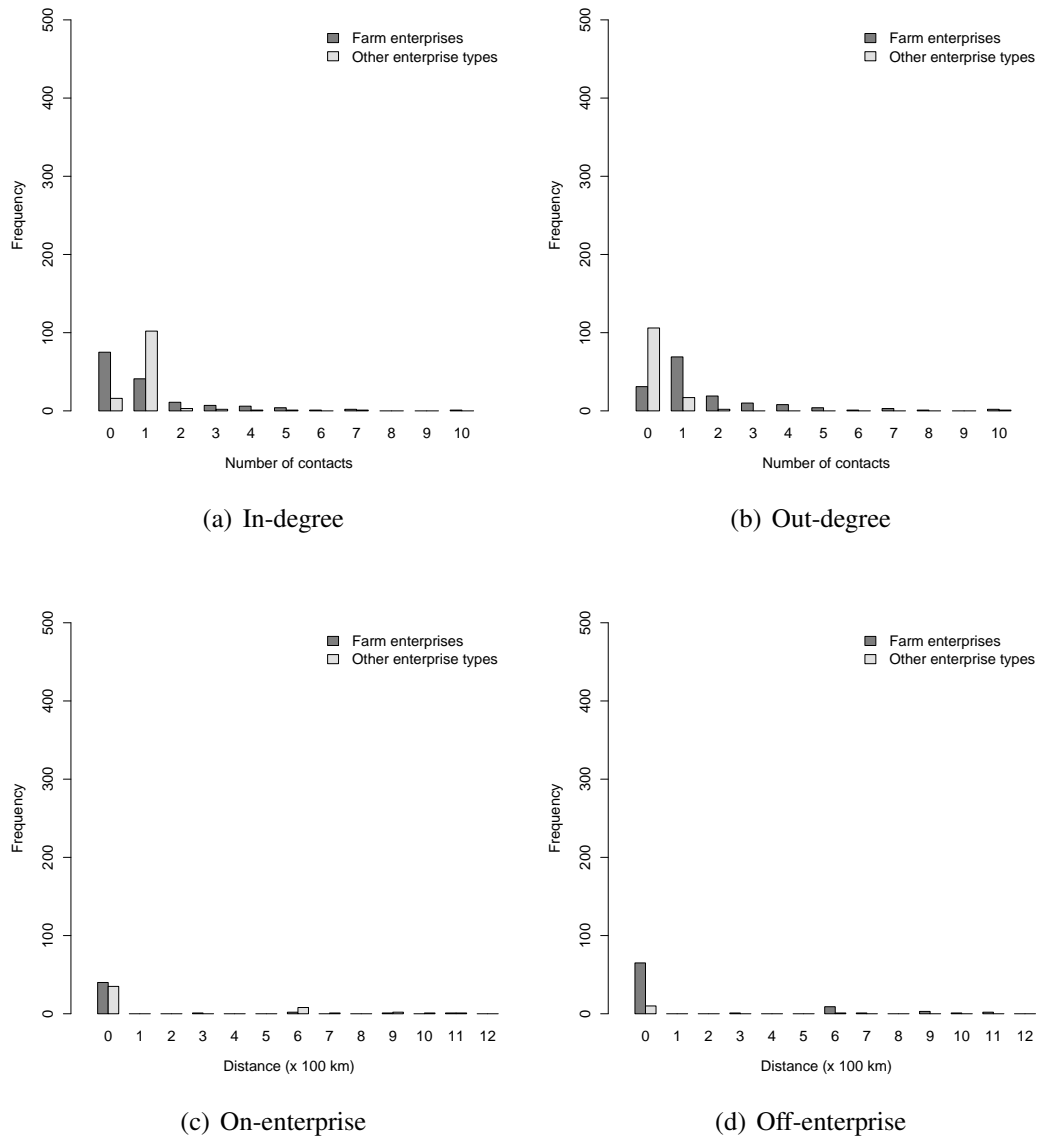
Figure 7.12: Social network analyses of table egg and poultry product contacts in the commercial sector of the New Zealand poultry industry. (a) Bar plot showing the distribution of the number of contacts arising from movement events onto farm and non-farm enterprises, (b) bar plot showing the distribution of the number of contacts arising from movement events off farm and non-farm enterprises, (c) frequency histogram showing the distance material has moved when coming onto farm and non-farm enterprises, and (d) frequency histogram showing the distance material moves when going off farm and non-farm enterprises.
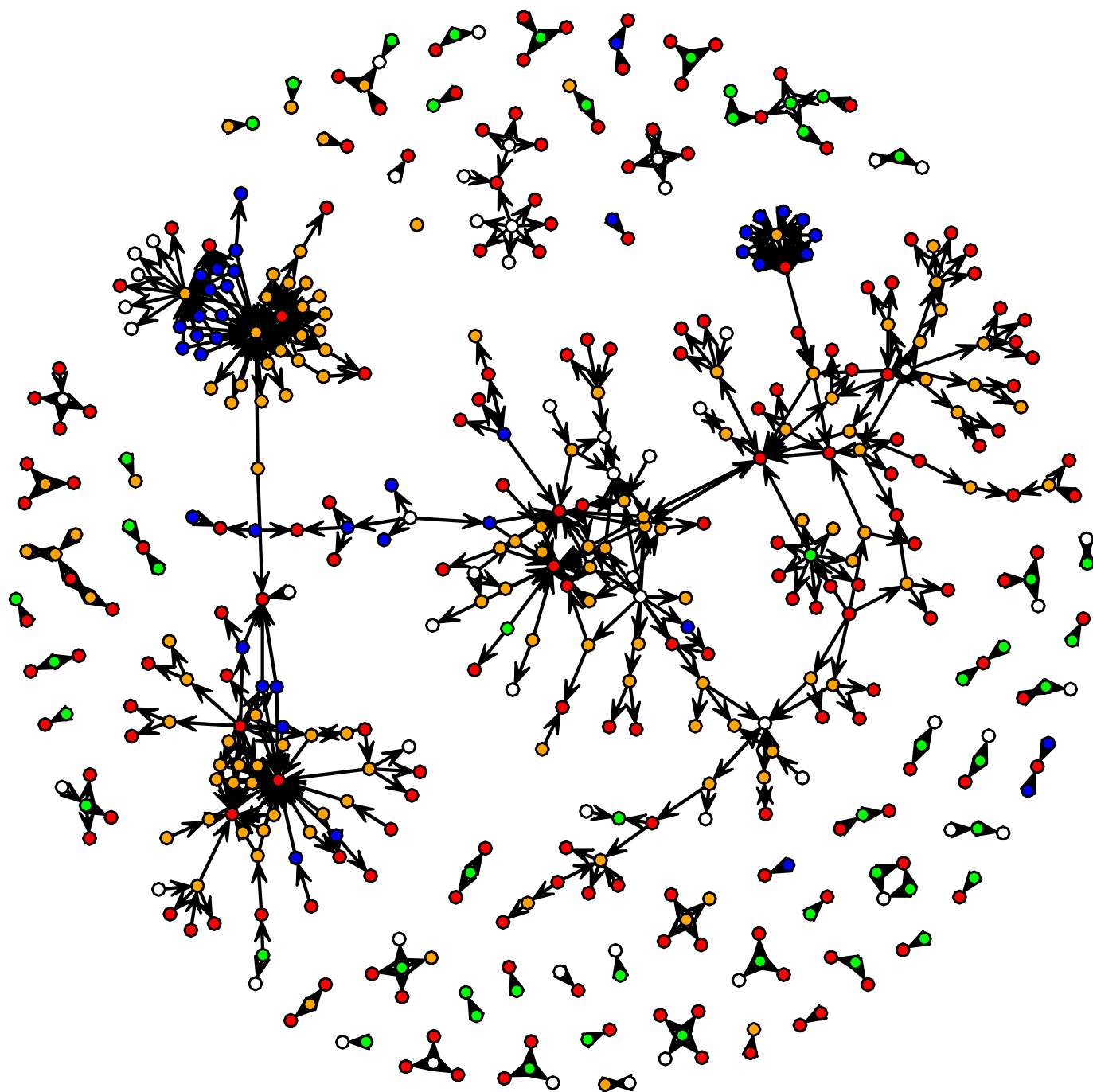
Figure 7.13: Social network analyses of manure and waste litter related contacts in the commercial sector of the New Zealand poultry industry. Network graph constructed using a force-based algorithm with the size of the nodes proportional to node betweenness. Key: breeders and hatcheries (blue), layer farms (green), broiler and other poultry farms (orange), service providers (red), other enterprise types (open circles).
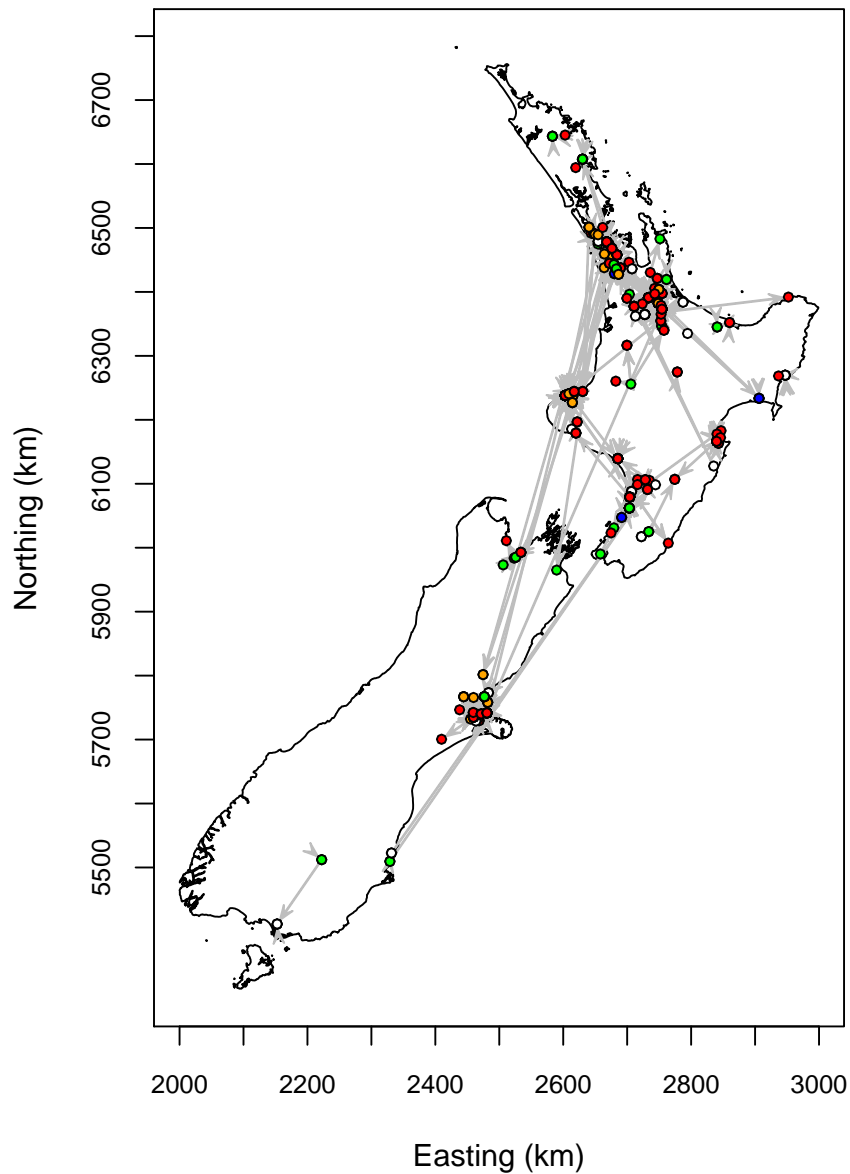
Figure 7.14: Social network analyses of manure and waste litter contacts in the commercial sector of the New Zealand poultry industry. Map of New Zealand showing the point location of enterprises that reported a manure and/or waste litter related movement with the size of the nodes proportional to node betweenness. Lines define the movement of material from one enterprise to another, with arrows indicating the direction of movement. Key: breeders and hatcheries (blue), layer farms (green), broiler and other poultry farms (orange), service providers (red), other enterprise types (open circles).

(a) In-degree

(b) Out-degree

(c) On-enterprise

(d) Off-enterprise
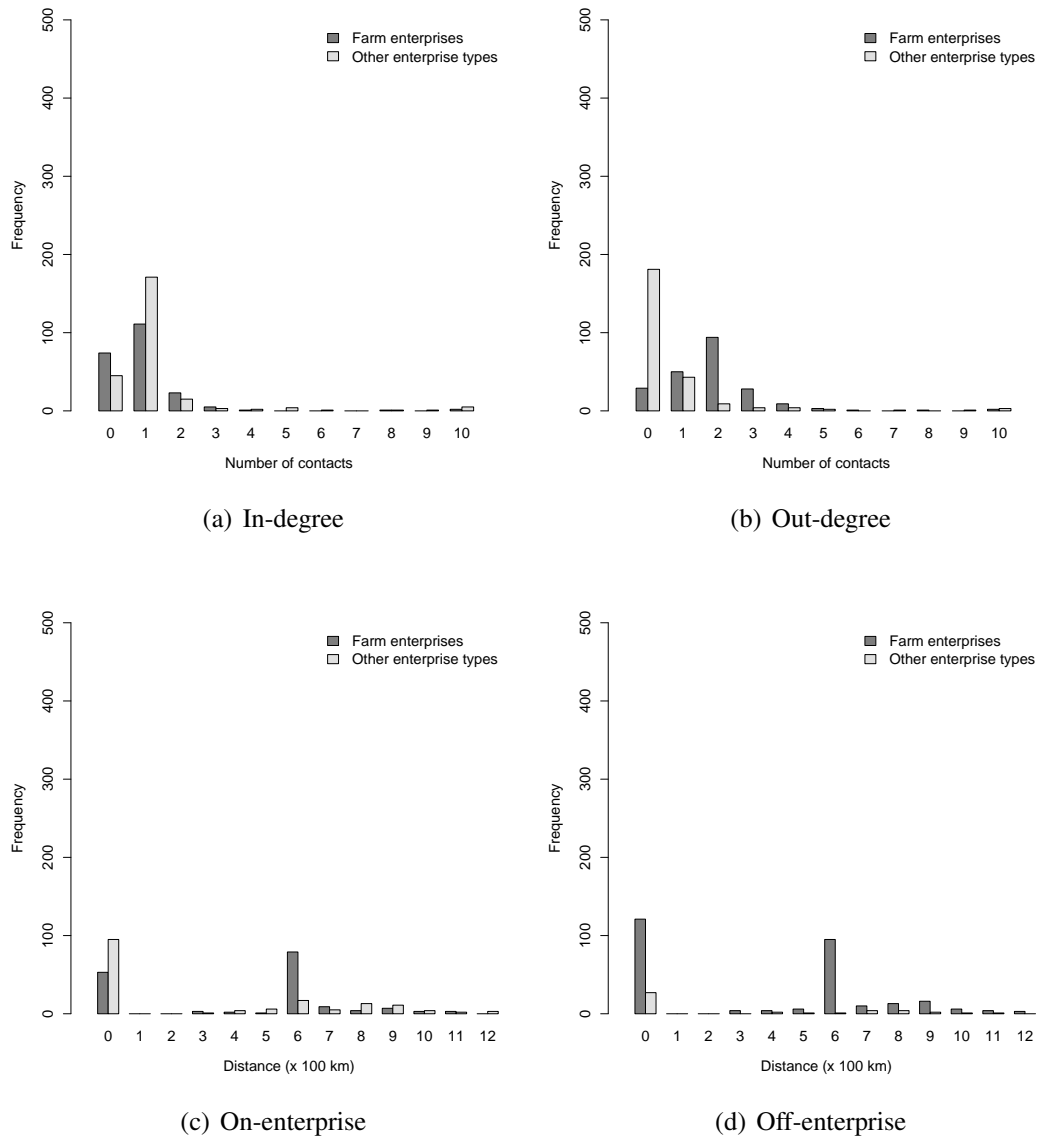
Figure 7.15: Social network analyses of manure and waste litter contacts in the commercial sector of the New Zealand poultry industry. (a) Bar plot showing the distribution of the number of contacts arising from movement events onto farm and non-farm enterprises, (b) bar plot showing the distribution of the number of contacts arising from movement events off farm and non-farm enterprises, (c) frequency histogram showing the distance material has moved when coming onto farm and non-farm enterprises, and (d) frequency histogram showing the distance material moves when going off farm and non-farm enterprises.

7.4 Discussion

This was a cross-sectional survey of the commercial sector of the New Zealand poultry industry. We elicited details of contacts arising from the movement of four commodity types that could potentially play a role in the transfer of infectious disease or contaminants from one location to another. Knowledge of network characteristics provides the opportunity to tailor surveillance and control strategies for particular hazards of concern. For example, the widespread distribution of a dioxin-contaminated batch of feed (similar to that which occurred in Belgium in 2001, van Larebeke et al. 2002) could have been averted by firstly taking the obvious step of restricting the movement of feed by feed distributors (many of the network 'hubs' shown in Figures 7.4 and 7.5) and secondly by targeting non-feed distributor enterprises identified as having relatively high out-degree and/or betweenness scores. A benefit of this approach is that at a time of crisis, it allows resources and investigational effort to be targeted on enterprises most likely to be contributing to the problem. Information derived from studies of this type can also be used to inform simulation models of disease spread. Knowledge of destination enterprise types, location and the frequency of movement events allows simulation models to more accurately reflect long distance spread of disease.

The response rate to our questionnaire was reasonable (244 of 420, 58%), given the number and type of questions asked. The distribution of respondents matched the distribution of PIANZ members in terms of geographical location (Figure 7.1) and enterprise type (Figure 7.2). Incomplete enumeration of contacts made by the population represents an inherent form of selection bias in this study and its effect on the validity of the network statistical measures (representativeness of the actual situation) is difficult to quantify (Borgatti et al. 2006). It would be reasonable to assume that direction and magnitude of bias would be similar across each of the evaluated networks. For this reason we believe that appropriate inferences can be drawn from this study by focussing on how the parameters for each of the four networks vary in relative, rather than absolute terms.

During the process of transferring responses from the completed questionnaires to the relational database for analysis, it was apparent that the quality of record keeping related to on- and off-enterprise movements varied widely among industry participants. The quality of record keeping was not associated with enterprise type. Identifying those enterprise

managers with effective systems to record movement event data, and encouraging them to share their knowledge and experience with other industry participants should mean that, in future, completion of a questionnaire similar to the one described in this paper would present little difficulty. This should enhance survey response rates and allow more complete network descriptions to be compiled. Complete network details would allow surveillance strategies based on network characteristics (e.g. betweenness scores, as in the feed contamination example cited above) to be designed with greater precision.

The networks described in this paper fell into two broad categories. The first, comprised of the feed, live bird and hatching egg, and table egg and poultry product networks was characterised by relatively high out-degree centralisation scores consistent with a 'hub and spoke' network structure (Figures 7.4, 7.7, and 7.10). This pattern is indicative of small numbers of enterprises (e.g. feed suppliers and hatcheries) providing goods and services to larger numbers of client farms. The out-degree centralisation index was greatest for the feed network implying that this network is comprised of a relatively small number of feed suppliers and that, in general, feed moves directly from a single supplier to a single farm without an intermediary. The same general pattern was evident for the live bird and hatching egg network (Figure 7.7) however, in contrast to the feed network, significant numbers of farms received live birds and/or hatching eggs from multiple sources and there were greater numbers of farms that moved live birds and/or hatching eggs onto other farms.

The manure and waste litter network comprised the second network category. In this network in-degree centralisation was greater than out-degree centralisation, meaning that enterprises receiving manure and waste litter (i.e. contract cleaners) were the hubs in this network. Centralisation scores for the manure and waste litter network were lower compared with the other three networks reflecting the greater numbers of contract cleaners (relative to feed suppliers and hatcheries) servicing the industry.

Each of the four networks had scale-free properties, meaning that for each movement type there were small numbers of enterprises that had contacts with large numbers of enterprises ('super-spreaders'). The presence of an undetected infectious disease in those enterprises with super-spreader characteristics increases the likelihood that an epidemic will propagate rapidly through the population, assuming there is a directly proportional relationship between the number of contacts an enterprise makes and the probability that

disease will be transferred from one location to another (Albert et al. 2000, Liljeros et al. 2001). While the finding that feed suppliers had large numbers of poultry farm contacts in the feed network came as no surprise, what was of greater interest was that there were small numbers of poultry farms that reported off-farm movements of feed. This should serve as an important reminder for disease control authorities: movement (and other) restrictions applied during the course of an animal health emergency should be applied across a range of industry sectors, recognising that some industry participants may practice activities that are not entirely typical for their enterprise type (e.g. poultry farms on-selling feed to other farms). Surveys of movement patterns (indeed, real-time capture of movement events, Stevenson et al. 2007) and social network analyses of recorded movement patterns provide a convenient means for identifying enterprises with these 'atypical' behaviours, which in turn allows strategies to enforce disease control activities to be carried out with greater precision. In the absence of perfect and up-to-date network data, knowledge of the characteristics of individual enterprises that render them more likely to be atypical (e.g. size, type, and geographic location) would be of value, since this information could be used to inform a risk based approach to disease surveillance and control.

Georeferencing the town location of each industry participant referred to in this questionnaire provided useful information relating to the range of distances over which each of the four commodity types are moved (Figures 7.6, 7.9, 7.12, and 7.15). Median movement distances for feed, live birds and hatching eggs, table eggs and poultry product, and manure and waste litter were 26, 18, 63, and 15 kilometres, respectively. In general, movement distances were greater for commodities of greater value. The movement distances reported here not only provide guidelines for the range of distance over which infectious materials might spread from an infected source, but also provide some indication as to how large surveillance zones need to be in the event of an animal disease emergency.

Network structures for enterprise-to-enterprise movement of feed, live birds and hatching eggs, and table egg and poultry product were characterised by a 'hub and spoke' type structure with small numbers of network hubs (e.g. feed suppliers and hatcheries) providing goods and services to large numbers of client farms. In addition to hubs acting as the predominant source of material moving onto farms, we identified smaller numbers of intermediary (high betweenness score) enterprises that were influential in movement

of material through each network. Surveillance and disease control strategies should not only focus on the obvious network hubs, but also these identified intermediaries.

Demonstration of New Zealand's freedom from highly pathogenic avian influenza

8.1 Introduction

Despite the worldwide spread of HPAI H5N1 virus during 2003 – 2008, New Zealand has remained free of disease, primarily a result of geographic isolation and the application of stringent biosecurity measures. The continued global spread of influenza viruses and the possibility that low pathogenic H5 and H7 influenza viruses may mutate to highly pathogenic forms has made animal health authorities in New Zealand increasingly aware of the need to enhance surveillance activities for avian influenza, allowing low and highly pathogenic forms to be promptly detected on the basis of scientifically identified risks.

Within- and between-country spread of avian influenza viruses has occurred via a number of routes including the importation of live bird products, trade in wild birds (Kilpatrick et al. 2006), and transfer of infection via wild, migratory birds. An assessment of incursion routes by Pharo (2003) cited the importation of live birds or avian product as the most likely means by which avian influenza might enter New Zealand. An additional route, thought to be of lesser importance, is via wild, migratory birds. In this respect Pharo identified two potentially important events: (1) the mutation of endemic H5 influenza subtypes (in wild birds) into virulent forms, and (2) the introduction of new viruses, either existing highly pathogenic avian influenza viruses or low pathogenic avian influenza that might mutate to virulence. An epidemic of HPAI in a naïve poultry population would result in significant mortalities and would be readily detected (Elbers et al. 2004). However the same may not be the case for low pathogenic influenza viruses in which mild or

subclinical signs may predominate (Swayne & Halvorson 2003).

To limit the consequences of an incursion of notifiable avian influenza (NAI) into the commercial poultry population New Zealand, like other NAI free countries, has established an early warning strategy to monitor the appearance of avian influenza in its wild bird (Stanislawek et al. 2007, Tana et al. 2007) and commercial poultry populations (Rawdon, Thornton, McKenzie & Gerber 2007). The system devised for wild birds is an active surveillance approach using targeted sampling of resident waterfowls and migratory shorebirds (Stanislawek et al. 2007). In the absence of superior methods, passive surveillance based on clinical reports by farmers, veterinarians and laboratories form the backbone of the commercial poultry surveillance system (Rawdon, Thornton, McKenzie & Gerber 2007). Once a new disease incursion is suspected via passive surveillance, an investigation is intitiated and active surveillance measures applied to identify new cases (Dufour et al. 2006). A major disadvantage of passive surveillance is the possibility of reporting delays (Bates et al. 2003, Doherr et al. 2001), which in turn affects the timeliness of outbreak detection (Farrington & Andrews 2004). The longer the period between first incursion of disease and reports to authorities, the more difficult an outbreak is to deal with (Yoon et al. 2006, McLaws & Ribble 2007). This underlies the need to critically evaluate surveillance systems which allows differences between proposed methods to be compared (Campbell et al. 2007).

Recently Martin, Cameron & Greiner (2007) and Martin, Cameron, Barfod, Sergeant & Greiner (2007) proposed a method to combine details of the elements that make up a surveillance to provide an overall quantitative assessment of the system's performance. The method uses a systematic approach called scenario tree modeling allowing the probability that the system will detect an infected animal (i.e. surveillance sensitivity) to be estimated as well as an overall estimate of the probability that a country (or region) is free of disease, given a sustained period of negative findings. In this paper we provide an assessment of the passive surveillance system currently in place to detect an incursion of a NAI HPAI (subsequently referred to as HPAI) into New Zealand using a scenario tree approach informed by geographic and seasonal changes in risk.

8.2 Materials and methods

The approach presented in this paper shows how geographic risk factors can be incorporated into a scenario tree to provide a country-specific assessment of proposed surveillance strategies. The approach is undertaken in two stages: (1) development of a spatial risk model and, (2) development of a scenario tree model of the passive surveillance system. In the first stage, factors thought to influence the geographic distribution of HPAI risk of introduction and spread are combined to assign each area of the country a semi-quantitative score of HPAI entry and spread risk. In the second stage, a scenario tree model of the passive surveillance system for HPAI is developed on the basis of spatial risk zones identified in step 1.

8.2.1 Spatial risk modeling

We used multi-criteria evaluation (MCE) (Eastman et al. 1995, Bonham-Carter 1997) to identify areas of New Zealand where avian influenza virus (the hazard) might first enter and subsequently spread to domestic poultry populations. For each risk pathway (i.e. entry and spread) we followed the sequence of steps involved in the MCE process: (1) definition of objectives, (2) identification and definition of factors influencing risk of introduction and spread, (3) definition of the relationship between risk factors and the likelihood of HPAI incursion, (4) standardisation of the identified risk factors to a common scale, (5) development of weights to be applied to each factor, and (6) combination of the factors to obtain a final estimate of risk.

The land area of New Zealand was divided into a regular grid comprised of 3,137 cells with each cell having dimensions of 10 kilometres × 10 kilometres. For each of the four seasons of the year (spring, September to November; summer, December to February; autumn, March to May, and winter, June to August) we developed raster surfaces expressing the likelihood of HPAI incursion or spread. The identified risk factors for entry and spread were: (1) sites throughout the country visited by five species of wild, migratory birds, (2) areas where wild, migratory birds and resident wild bird species are likely to make physical contact, (3) locations where material from other countries first enter New Zealand (ports of entry), (4) areas with large numbers of domestic poultry (commercial poultry enterprises, game bird enterprises, and backyard birds) and, (5) major road

networks, thought to facilitate infection spread by movement of poultry and/or poultry product. A raster surface was constructed for each of these five risk factors and each cell of the regular grid classified as either a 1 or 0 subject to the presence or absence of the factor within it's boundaries. These five raster surfaces were then combined to provide a raster surface of semi-quantitative scores, allowing us to distinguish high and low risk areas of the country for HPAI incursion and spread.

Areas of introduction by wild birds

To identify areas of New Zealand where the likelihood of introduction of virus via wild, migratory birds was high, we identified migratory bird species according to the method developed by Crick et al. (2006) (Table 8.1). With these species defined we identified the important aggregation sites based on the monthly frequency of recorded sightings, compiled in the Atlas of Bird Distribution in New Zealand (Robertson et al. 2007).

Areas of contact between wild birds

To define areas of the country where transfer of virus could potentially occur from wild, migratory birds to resident (both wild and domestic) species, migratory bird species were selected based on their reported occurrence on farmlands, freshwater and coastal areas. The resident species included in these analyses included local shorebirds and waders, native waterfowls and wild domestic species such as turkeys, pheasants and quails (Table 8.1). Data relating to the seasonal records of bird sightings were obtained from the Atlas of Bird Distribution in New Zealand (Robertson et al. 2007). This allowed us to develop a map showing areas where virus, if it were to enter the country via migratory birds, would likely be introduced to resident species which would then facilitate the spread of infection to domestic and commercial poultry. Five wild, migratory bird species and 32 resident species were included in these analyses (Table 8.1).

We created four raster surfaces to represent the presence or absence for each of the selected wild bird species (migratory and resident) for summer, autumn, winter, and spring. The number of observations made for each species and season were summed to obtain an aggregated count of the total number of observations in each cell, irrespective of species. Each cell was then classified as one if the number of observations in each cell was greater than one and zero otherwise.

Backyard and commercial poultry

The national farm animal database, AgriBase (Sanson & Pearson 1997), was used to define the spatial distribution of commercial and backyard poultry enterprises throughout New Zealand. For the purpose of this study commercial poultry enterprises included broiler, layer and game (emu and ostrich) farms. Recognising that Agribase provided incomplete coverage of backyard flocks, defined as poultry enterprises with less than 100 birds, a simulation approach (described subsequently) was used to estimate the distribution of this population. The point location of commercial poultry enterprises were buffered by 20 kilometres and converted to a raster surface where each cell received a value of one if poultry were present and zero otherwise.

The distribution of backyard poultry flocks throughout New Zealand was derived from two sources of data. In areas of the country classified as rural we used poultry counts recorded for each enterprise in AgriBase. The distribution of backyard poultry in urban areas was based on human census data. Our premise here was that the probability of an urban household keeping backyard poultry was inversely proportional to human population density (that is, the probability of keeping backyard poultry was greater in areas of low population density and *vice versa*). Human population counts from the 2001 Census of Population and Dwellings (Anonymous 2001) comprised counts of individuals per mesh block. These data were converted to the regular grid of 3,137 cells and human population density calculated for each cell. Cut points defining the bottom third, middle third, and top third of the distribution were calculated. We then used population counts for each cell to estimate the number of households present. This was done by selecting each cell in turn and by taking a random draw from a Poisson distribution (with a mean of 4 individuals) to simulate the number of individuals within a single household. This process was repeated until the sum of individuals within each simulated household equalled the total population size for the respective cell. With an appropriate estimate of the number of households per cell our next task was to estimate the number of households that kept backyard poultry. The population density for each cell was noted and the probability of a household keeping poultry was chosen from the values shown in Table 8.2. For example, if population density was between 30 and 60 individuals per square kilometre the probability of a household within the cell keeping backyard poultry was set to 20%. Each household was then selected in turn and a random draw from a binomial distribution used to determine whether or not backyard poultry were present. Each cell of the raster surface

was then given a value of one if backyard poultry were estimated to be present in any household within the cell and zero otherwise.

Roads and ports of entry

To account for risk arising from importation of live birds and/or poultry products at points where material enters the country we used the location of international air and sea ports and location details of the major road networks throughout the country. The point location of air and sea ports were buffered by a distance of 3 kilometres and roads buffered by 5 kilometres. This map was then converted to a 3,137 cell raster surface where each cell was given a value of one if a major road and/or air or sea port was present and zero otherwise.

Risk estimation

The raster layers for each of the risk factors described above were combined to obtain an overall summary of HPAI incursion and spread risk using the technique of Boolean overlay. Boolean overlay involves summing each of the five binary evidence themes to obtain a final score for each cell. For example, using this method, a cell where all of the risk factors were present (wild birds, backyard, commercial birds, ports of entry and roads) received a score of 5, whilst another cell with only one risk factor, received a score of 1. The resulting risk surface was then smoothed using kernel smoothing techniques to provide a final, semiquantitative estimate of HPAI incursion and spread risk. Smoothing the data allowed us to identify areas of the country where there were relatively large numbers of cells with high risk scores in close proximity. The risk score density estimates were plotted as a frequency histogram and dividing the distribution into terciles allowed us to define low, medium and high HPAI incursion and spread risk zones. Four risk surfaces were created to represent seasonal changes in geographical risk of HPAI incursion and spread across New Zealand.

8.2.2 Scenario tree modeling

A scenario tree model was developed to evaluate New Zealand's passive surveillance system for HPAI. The main output of this model was an estimate of the probability that domestic poultry were free of disease at the end of a specified surveillance period. The evaluation process involved: (1) definition of the structure of the scenario tree, (2) definition of the input parameters for the tree, (3) estimation of the probability that a randomly

selected unit processed by the surveillance system will be detected given that infection is present (unit sensitivity) at specified design prevalences, (4) estimation of the overall probability of detecting at least one infected unit given infection is present (surveillance system sensitivity) and finally, (5) estimation of the probability of freedom on the basis of the estimated surveillance sensitivity (confidence in disease freedom).

Model description

Using a scenario tree model, the probability that New Zealand could be considered free of HPAI at a pre-defined design prevalence depends on the sensitivity of the surveillance system (detection probability) and the prior probability of infection (probability of introduction and probability of residual infection). The overall sensitivity of the system is defined as the probability that the surveillance system will detect at least one infected unit given that it is present. This depends on the unit sensitivity and the number of units processed.

A period of one calendar month was selected as the time interval for surveillance, reflecting the highly contagious nature of the disease. The reference population comprised 453 commercial and 5,473 backyard enterprises, representing over 2 million birds. The surveillance unit was the individual house within each enterprise. For each season, enterprises processed by the passive surveillance system were assigned a risk category according to the risk zone of their physical location (described in Section 8.2). The steps necessary for each unit processed to give a positive outcome from the surveillance system, represented by nodes in the scenario tree, are shown in Figure 8.2. Table 8.3 provides further details for each node.

Data sources

Passive surveillance for HPAI in New Zealand is dependent on farmers, veterinarians and laboratories reporting the presence of birds with signs consistent with HPAI to the Ministry of Agriculture and Forestry (MAF). In the usual case MAF is alerted to the presence of an unusual animal health event by a toll-free number which is accessible to the general public of New Zealand 24 hours each day. Reports deemed to be worthy of further investigation on the basis of risk profiling are investigated by the Investigation and Diagnostic Centre (IDC) (Rawdon, McFadden, Stanislawek & Bingham 2007). In these cases, the IDC supervises the collection of appropriate samples for screening for

avian influenza using a generic real-time RT-PCR Taqman followed by conventional RT-PCR assays to exclude H5 and H7 subtypes. Virus isolation is performed on all positive samples to the RT-PCR assay (Rawdon, McFadden, Stanislawek & Bingham 2007).

To evaluate New Zealand's passive surveillance for HPAI H5N1, data on the distribution of the population at risk (commercial and backyard poultry) and members of the population actually processed by the system were required. Data on the distribution of enterprises where poultry were present were obtained from three sources: AgriBase, the poultry industry database and the results of a survey of the New Zealand commercial poultry industry conducted in 2007 (Chapter 7). These sources provided enterprise-level data on commercial poultry through-out New Zealand, and backyard poultry located in rural areas across New Zealand. The information required to describe each poultry enterprise included the number of houses (units), the enterprise production type (indoor or outdoor), and the easting and northing coordinates of the main farm building. All backyard poultry enterprises in Agribase were classified as outdoor and assumed to have one house in which birds were kept. Each enterprise was assigned the risk zone of the cell within which it was located for each season of the year based on the spatial risk model (described earlier). These data were used to estimate the proportion of poultry units (houses) in each risk zone for each season.

Data on the actual reporting patterns of HPAI for commercial and backyard poultry enterprises were not available. We therefore simulated the number of units within each enterprise that might report the presence of clinical signs consistent with NAI per month by taking random draws from a binomial distribution. This was assumed to vary with enterprise type (i.e. commercial *versus* backyard), where commercial enterprises were considered more likely to report an adverse event relative to backyard enterprises. For backyard enterprises, the probability that each enterprise was likely to report the presence of disease on a monthly basis was fixed at 0.025, chosen to reflect the low likelihood of reporting. For commercial poultry enterprises, the number of houses present was assumed to range between 1 and 3 and the probability of a report being made each month set to 0.05. We simulated reporting patterns for each month of a 12-month study period. Each enterprise was selected in turn and the binomial distribution, using the probability estimates described above, used to determine whether or not the enterprise made a notification of signs consistent with HPAI to either their veterinarian or a MAF representative.

Input values for the baseline scenario

Our first task was to define appropriate parameters for input into the model to represent as closely as possible the passive HPAI surveillance system currently in place in New Zealand. This baseline surveillance scenario was then modified to reflect nine alternative scenarios. Development of the baseline scenario required specification of input parameters relating to: (1) branch probabilities, (2) the values to be used for each risk group, (3) the unit- and herd/enterprise design prevalence, (4) an estimate of the prior probability of disease freedom and, (5) estimates for the probability of introduction for each surveillance period. Parameters estimated for each branch in the baseline scenario were informed by a combination of expert opinion and a review of the literature. The source of information used to inform each input parameter for the baseline scenario are provided in Table 8.4. Details of the input parameters are provided in Table 8.5. Values for input parameters were either defined as fixed or as probability distributions to account for uncertainty (lack of knowledge) in the estimated values.

The monthly probability of introduction of virus was set to a fixed value of 0.01. We defined two levels of design prevalence: enterprise/herd prevalence (P_H) and unit prevalence (P_U). Values of 0.01 and 0.50 were selected for enterprise/herd prevalence and unit prevalence, respectively. These values were considered appropriate, given the highly contagious nature of HPAI and the high likelihood that disease, if present, would cluster within an enterprise.

Within the model, risk nodes were defined for the geographical zone in which the enterprise was located and for enterprise type (indoor or outdoor). For the risk zone node three categories were defined: high, medium and low. The low risk category was the reference category (risk 1) and the medium and high risk zones were assigned values of 3 and 5, relative to the low risk zone. These values were selected to represent the relative likelihood that a farm or unit within a farm in each of the geographical risk zones would be infected given that infection was present at the specified design prevalence. Similarly, risk values were defined for farm type. Risk values for an outdoor farm within each risk zone were assigned a value of 2 relative to indoor farms. These values were assumed to be constant across risk zones and across seasons.

For each risk node, the relative risk values were adjusted in order to ensure that the average relative risk over the whole population summed to one. The adjusted relative risks were

subsequently multiplied by the design prevalence at the herd/enterprise and unit level
to provide an estimate of the effective probability used to replace the design prevalence
values in the model. The formula for adjusting the relative risk values was (Martin 2008):

$$AR_i = \frac{RR_i}{\sum_{i=1}^{I} \times PrP_i} \qquad (8.1)$$

In Equation 8.1 AR_i refers to the adjusted risk for the ith branch of the node; RR_i is the
risk for the ith branch relative to the reference branches; PrP_i is the proportion of farms
or units falling into the ith branch of the node; and I the total number of branches in the
node.

The parameter for the probability of observing clinical signs (PrClinic, node 3) when
HPAI enters a naïve population was based on a review of the literature and modeled using
a Pert(0.95, 0.99, 1.0) distribution, reflecting the likelihood that high levels of mortality
within a poultry unit would be observed if HPAI was present (Swayne & Halvorson 2003).
The Pert distribution was chosen to account for uncertainty in the estimates. Following
from the probability of observing clinical signs, the probability that a farmer decides to
seek assistance, given the appearance of clinical signs, (PrFarmer) was considered to be
highly likely and modeled using a Pert(0.60, 0.70, 0.80) distribution. The estimate of the
probability that a farmer makes a notification to an industry veterinarian (PrFarmerVet)
as opposed to calling MAF (PrFarmerMAF) was modeled as a Pert(0.60, 0.80, 0.90) dis-
tribution. This was intended to reflect the situation where producers are more likely to
report directly to industry veterinarians as opposed to MAF.

The estimated branch probabilities for laboratory diagnoses from submitted samples com-
prised two components: the probability that the laboratory would decide to test for HPAI
H5N1 virus (PrTestCL or PrTestPM) and the diagnostic sensitivity of the RT-PCR test
available (RT-PCRSe). Four nodes in the scenario tree relating to laboratory diagnosis
were described dependent on the source of the surveillance samples. These included
the probability of a positive laboratory result from samples submitted by: (1) a veteri-
narian as a result of direct contact with a farmer (PrVetSubDiag), (2) MAF as a result
of a veterinarian's call for assistance (PrMAFVetDiag), (3) MAF, as a result of investi-
gating a farmer call (PrMafFarmerDiag) and, (4) the result of *post mortem* examinations
(PrPMDiag) where specimens are submitted to a laboratory by a veterinarian as a result of

an autopsy conducted for other reasons. For these laboratory nodes, the estimated values were based on the product of the estimate of the probability that samples would be tested for HPAI (PrTestCL) and the diagnostic sensitivity of the available test (RT-PCRSe). We assumed that the decision to test samples from *post mortem* submissions for HPAI H5N1 was less likely than testing clinical samples and defined PrTestCL and PrTestPM accordingly.

The probability of testing for HPAI H5N1 virus from samples submitted on the basis of clinical signs (PrTestCL) was modeled to reflect a high likelihood (i.e. most likely probability of 90%, but greater than 70%). This estimate was obtained using BetaBusta software.[1] This resulted in the probability of PrTestCL being modeled as a Beta(71, 13) distribution. The probability of testing for HPAI from samples submitted as the result of *post mortem* examination was modeled to reflect a lower likelihood (i.e. most likely probability of 20%, but greater than 10%) and modeled using a Beta(31, 71) distribution. The sensitivity of the RT-PCR test for avian influenza was defined using a Pert(0.90, 0.95, 0.99) distribution based on expert opinion.[2]

Calculating sensitivity of the surveillance system

The estimated sensitivities of the surveillance system for each month of the study period were calculated allowing for grouping of houses (units) within each poultry enterprise. This meant that it was necessary to estimate the enterprise-level sensitivity of detection for each enterprise that was processed. Enterprise-level sensitivity was defined as the probability that one or more positive outcomes will be obtained when a certain number of houses are processed and the enterprise is infected at the specified design prevalence. Formally, the estimate of enterprise level sensitivity (SeH_i) for the ith enterprise was calculated as follows (Martin, Cameron & Greiner 2007):

$$\text{SeH}_i = 1 - \prod_{j=1}^{J} \left(1 - \text{AR}_U \text{RG}_j \times \text{P}_U \times \text{Se}_U\right)^{n_j} \tag{8.2}$$

Where AR_URG_j refers to the adjusted risk values for each of the jth branches of the risk group within which the enterprise is classified, n_j the number of units processed in the jth unit risk group, P_U the unit prevalence, and Se_U the unit-level sensitivity within enterprise.

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[1] http://www.epi.ucdavis.edu/diagnostictests/betabuster.html
[2] W. Stanislawek, Investigation and Diagnostic Centre – Wallaceville, Biosecurity New Zealand, personal communication.

Unit-level sensitivity was obtained as the product of all detection nodes in the scenario tree involving the nodes from observation of clinical signs to laboratory diagnosis (nodes 5 – 19 in Table 8.3 and Figure 8.2). In this application there were two levels of grouping of risk nodes (risk zone and enterprise type), therefore the farm-level sensitivity for a farm processed by the surveillance system that was classed as outdoor farm in a high risk zone was given as:

$$\text{SeH}_i = 1 - (\text{ARHR} \times \text{ARHROD} \times \text{P}_U \times \text{Se}_U)^{n_i} \tag{8.3}$$

Where ARHR and ARHROD refer to the adjusted risk in high risk zones and outdoor farms in high risk zones, respectively and n_i is the number of houses (units) processed from each enterprise. The estimate of the enterprise/herd-level sensitivity (SSe_{tp}) for each surveillance time period was combined to provide an estimate of the probability that at least one infected enterprise will be detected by the system at the specified design prevalence:

$$\text{SSe}_{tp} = 1 - \prod \text{SeH}_i \tag{8.4}$$

Estimation of the probability of disease freedom

On the basis of overall system sensitivity for each time period we estimated the posterior probability that New Zealand was free of HPAI considering a prior estimate of disease freedom (conversely, 1 - the prior estimate that NAI was present) and the probability of introduction. Specifically, the posterior probability of freedom at time period tp, PostPFree_{tp} is given as:

$$\text{PostPFree}_{tp} = \frac{1 - \text{PriorPInf}_{tp}}{1 - \text{PriorPInf}_{tp} \times \text{SSe}_{tp}} \tag{8.5}$$

Where the prior estimate of the level of disease in the population (PriorPInF_{tp}) in the first month of surveillance (PriorPInf1) is the reciprocal of the prior probability of freedom (1 - PriorFree$_{tp}$) and estimated on the basis of expert opinion. In subsequent surveillance periods the prior probability of infection depends on the previous period's estimate of the posterior probability of freedom (PostFree1$_{tp}$). In this case, the posterior probability of infection (PostPInf2) in the current period is defined as a function of the residual

probability of infection (PriorPInf1) in the last time period and the probability of disease introduction (PriorPIntr2) in the current period:

$$PostPInf2 = PostPInf1 + PrIntr2 - (PostPInf1 \times PrIntr2) \qquad (8.6)$$

We used an initial prior probability of infection of 0.5 as recommended by Martin, Cameron & Greiner (2007). We subsequently introduced probabilities of introduction for the 11 succeeding months as described in the model specifications. For the baseline scenario, the monthly probability of introduction was kept constant at 0.01 whereas in scenarios 1 – 3 we introduced higher values during the spring (September to November) to reflect a relative increase in the risk of infection during this period by wild migratory birds. Thus, by allowing the probability of introduction to change on a seasonal basis, the increased risk posed by new disease incursions was incorporated into our final probability estimate of disease freedom.

The model was implemented in @RISK version 4.5 (Palisade Corporation, Newfield, NY, USA) within Microsoft Excel (Microsoft Corporation, Redmond, WA, USA). For each month of the surveillance period, values were sampled from 1000 iterations using Monte Carlo simulations.

8.2.3 Sensitivity analysis

Nine alternative scenarios were defined in order to identify which inputs had the most impact on the surveillance sensitivity estimates. To evaluate the effect of seasonal introduction of infection into poultry units on the estimated confidence of disease freedom, three alternative scenarios were run where the monthly probability of introduction was changed from 0.01 in the spring (months 7 – 9) to 0.02, 0.05, and 0.10 (scenarios 1 – 3, Table 8.6). To evaluate the effect of relative risk values on the estimated probability of disease freedom, we varied the baseline scenario relative risk values from 5, 3, and 1 (high, medium, and low) to 1, 1, and 1 and 20, 10, and 1 (scenarios 4 – 5).

To evaluate the effect of the probability of observing clinical signs, the baseline scenario values were changed from Pert(0.95, 0.99, 1.00) to Pert(0.2, 0.3, 0.5) and Pert(0.3, 0.5, and 0.7) (scenarios 6 – 7). To evaluate the effect of changing the between farm prevalence,

the baseline scenario values were changed from 0.01 to 0.001 and 0.050 (scenarios 8 – 9). Sensitivity of the probability of disease freedom for the last month of surveillance to the input parameters in the baseline scenario were assessed using Pearson's rank correlation coefficient.

8.3 Results

A list of the wild bird species considered for input into the spatial risk model is provided in Table 8.1. These represent the wild bird species most likely to introduce or cause secondary spread of HPAI in New Zealand. Maps of the final risk density scores for incursion and spread arising from wild, migratory birds and spread of HPAI for the four seasons considered are shown in Figure 8.1. The wild migratory bird incursion and spread risk areas are similar throughout the year and are primarily concentrated in the far north of the North Island with small pockets located in the lower North Island and east coast of the South Island. The risk estimation for HPAI incursion and spread roughly followed the distribution of commercial poultry enterprises and wild bird locations with relatively large areas of high risk in the Northland region.

The results from the baseline scenario for the 12 months study period are presented in Table 8.7 and Figure 8.3. These represent the medians and 95% confidence intervals of the output distributions for the estimated surveillance system sensitivity, prior and posterior probability of freedom obtained from 1000 iterations of the model. Figure 8.3 shows the changes in the estimated parameters and the simulated proportion of units processed for each month of surveillance. The estimated sensitivity of the surveillance system fluctuated slightly over the 12 month period with the lowest value of 0.14 (95% CI 0.09 – 0.22) and the highest value of 0.18 (95% CI 0.12 – 0.27) for the second and sixth month, respectively. These estimated sensitivity values were dependent on the between-farm prevalence values used. Between farm prevalence values of 0.001 and 0.050 resulted in month 12 sensitivity estimates of 0.02 (95% CI 0.01 – 0.02) and 0.60 (95% CI 0.41 – 0.79), respectively.

The posterior probability of disease freedom for the study period returned an estimate of 0.54 (95% CI 0.53 – 0.57) in the first month of surveillance and increased to 0.85 (95% CI 0.73 – 0.93) by month 12, indicative of a moderate increase in confidence that HPAI was

not present in New Zealand domestic poultry at the designated design prevalence. The estimate of the surveillance system sensitivity and therefore the estimate of the posterior probability of freedom for the first month was most strongly correlated with the probability that a farmer seeks a diagnosis ($r^2 = 0.72$), moderately correlated with the probability of a farmer observing clinical signs ($r^2 = 0.313$), and weakly correlated with the remaining input parameters. This relationship was consistent across the entire 12 month study period. These findings indicate the importance of each step in the surveillance process in contributing to the sensitivity of the system.

Figure 8.4 shows the posterior probability of disease freedom for the baseline scenario and three alternative scenarios where the probability of introduction of infection during the spring (months $7 - 9$) was increased to reflect the increased risk of introduction at this time of the year by wild migratory birds. Probabilities of introduction set to 0.02 (scenario 1) and 0.05 (scenario 2) resulted in non-significant reductions in the baseline posterior probabilities of freedom estimates, whereas of probability of introduction of 0.10 (scenario 3) produced a significant reduction in posterior probability of disease freedom.

Changes in the relative risk values assigned to the geographic risk zones had an insignificant effect on the posterior estimate of freedom (Figure 8.5). Allowing equal risk values across zones (scenario 4) caused an increase in the posterior probability of freedom whilst increasing the risk values for high and medium risk zones in comparison to low risk zones (scenario 5) resulted in a decrease in the estimated posterior probability of freedom.

The effect of changing the input parameter values for the probability of observing clinical signs for HPAI on the posterior estimate of disease freedom is shown in Figure 8.6. Specification of low and medium probabilities of observing clinical signs represented by scenarios 6 and 7 (respectively) decreased the posterior estimate of disease freedom compared with the baseline model. This indicates the importance of observing clinical signs and therefore disease awareness on the sensitivity of the surveillance system.

Figure 8.7 shows the effect of changing between-farm prevalence values on the estimate of disease freedom probability. Higher prevalence values of 0.05 (scenario 9) resulted in an increase in the estimate of probability of freedom, whilst values of 0.001 (scenario 10) resulted in an overall decrease. At the end of the surveillance period, the estimated posterior probability of freedom for the baseline and scenarios 9 and 10 were 0.85 (95% CI $0.73 - 0.93$), 0.50 (95% CI $0.48 - 0.52$) and 0.99 ($0.98 - 1.00$), respectively. These

results confirm the dependence of the surveillance system sensitivity on design prevalence that the system is directed at detecting.

Table 8.1: Demonstration of freedom from disease using multiple complex data sources for highly pathogenic avian influenza in New Zealand. List of wild migratory bird species and local wild bird species selected for inclusion in the spatial risk model.

Category	Type	Species
Migrant	wader	Godwit, Eastern Bar-Tailed
	wader	Knot, Lesser
	wader	Plover, Pacific Golden wader
	wader	Stint, Red-Necked
	wader	Turstone
Resident	domestic wild	Peafowl
	domestic wild	Pheasant, Ring-Necked
	domestic wild	Quail, Brown
	domestic wild	Quail, Californian
	domestic wild	Turkey, Feral
	wader	Dotterel, Black-Fronted
	wader	Gull, Southern Black-Backed
	wader	Plover, Spur-Winged
	wader	Stilt, Australasian Pied
	wader	Dotterel, New Zealand
	wader	Gull, Black-Billed
	wader	Gull, Red-Billed
	wader	Oystercatcher, South Island Pied
	wader	Oystercatcher, Variable wader
	wader	Scaup, New Zealand
	wader	Shoveler, New Zealand
	wader	Stilt, Black
	wader	Stilt, Black $\times$ Pied
	wader	Tern, Caspian
	wader	Tern, White-Fronted
	water fowl	Duck, grey
	water fowl	Duck, Muscovy
	water fowl	Goose, Canada
	water fowl	Goose, Cape Barren
	water fowl	Goose, Feral
	water fowl	Mallard
	water fowl	Teal, Grey
	water fowl	Swan, Black
	water fowl	Swan, Mute
	water fowl	Shelduck, Paradise
	water fowl	Tern, Black-Fronted
	water fowl	Teal, Brown

Table 8.2: Demonstration of freedom from disease using multiple complex data sources for highly pathogenic avian influenza in New Zealand. Distribution of population density and the estimated probability of households keeping poultry in mesh blocks across New Zealand.

Population density (persons/km^2)	Probability of household keeping poultry
< 10.00	0.90
10.00 – 30.00	0.50
30.00 – 60.00	0.20
60.00 – 90.00	0.10
> 90.00	0.00

Table 8.3: Demonstration of freedom from disease using multiple complex data sources for highly pathogenic avian influenza in New Zealand. Nodes in the scenario tree model of the New Zealand passive surveillance system.

Node	Name	Type	Branches	Variable	Next node
1	Risk zone	Risk	High	$PrSSCHR/RR_{HR}$	2
			Medium	$PrSSCHR/RR_{MR}$	2
			Low	$PrSSCHR/RR_{LR}$	2
2	Farm status	Infection	Infected	PH	3
			Uninfected	1 - PU	3
3	Farm type	Risk	Indoor	$PrSSCID^a$	4
			Outdoor	PrSSCOD	4
4	Unit status	Infection	Infected	PU	5
			Uninfected	1 - PU	End
5	Clinical signs	Detection	Yes	PrCLSigns	6
			No	1 - PrCLSigns	17
6	Farmer seeks assistance	Detection	Yes	PrFarmer	7
			No	1 - PrFarmer	End
7	Farmer notifies	Detection	Vet	PrFarmerVet	8
			MAF 0800	1 - PrFarmerVet	14
8	Vet seeks diagnosis	Detection	Yes	PrVetDiag	9
			No	1 - PrVetDiag	End
9	Vet samples or calls MAF	Detection	Sample	PrVetSamples	10
			MAF 0800	PrVetMAF	11
10	Lab diagnosis (vet)	Detection	Positive	$PrVetSubDiag^b$	End
			Negative	1 - PrVetSubDiag	End
11	MAF investigates (vet)	Detection	Yes	PrMAFVetcalls	12
			No	1 - PrMAFVetcalls	End
12	MAF takes samples (vet)	Detection	Yes	PrMAFSampVet	13
			No	1 - PrMAFSampVet	End
13	Lab diagnosis (MAF – vet)	Detection	Positive	PrMAFVetDiag	End
			Negative	1 - PrMAFVetDiag	End
14	MAF investigates (farmer)	Detection	Yes	PrMAFFarmercalls	15
			No	1 - PrMAFFarmercalls	End
15	MAF samples (farmer)	Detection	Yes	PrMAFSampFarmer	16
			No	1 - PrMAFSampFarmer	End
16	Lab diagnosis (farmer)	Detection	Positive	PrMAFFarmDiag	End
			Negative	1 - PrMAFFarmDiag	End
17	*Post mortem* other reasons	Detection	Yes	PrPM	18
			No	1 - PrPM	End
18	Samples for other reasons	Detection	Yes	PrPMSamp	19
			No	1 - PrPMSamp	End
19	Lab diagnosis (other)	Detection	Positive	$PrPMDiag^c$	End
			Negative	1 - PrPMDiag	End

[a] PrSSCID: proportions for each risk zone are high risk (PrSSHRCID), medium risk (PrSSMRCID) and low risk (PrSSLRCID).

[b] PrVetSubDiag: the product of the probability that the laboratory will test samples for HPAI and the sensitivity of the RT-PCR test.

[c] PrPMDiag: the product of the probability that the laboratory will test samples for HPAI from *post mortem* submission and the sensitivity of the RT-PCR test.

Table 8.4: Demonstration of freedom from disease using multiple complex data sources for highly pathogenic avian influenza in New Zealand. Data sources for the scenario tree model of the New Zealand passive surveillance system.

Node	Name	Type	Data	Source
1	Risk zone	Risk	Number of farms in each risk zone	AgriBase
1			Number of farms processed	Estimated
1			Risk estimates	Expert opinion
2	Farm status	Infection	Design prevalence	Specified
3	Farm type	Risk	Indoor-outdoor	AgriBase
3			Risk estimates	Expert opinion
4	Unit status	Infection	Design prevalence	Expert opinion
5	Clinical signs	Detection	Probability clinical signs present	Expert opinion
6	Farmer seeks assistance	Detection	Probability farmer seeks assistance	Expert opinion
7	Farmer notifies MAF	Detection	Probability farmer notifies MAF	Expert opinion
8	Vet seeks diagnosis	Detection	Probability vet responds to farmer	Expert opinion
9	Vet samples or calls MAF	Detection	Probability vet notifies MAF	Expert opinion
10	Lab diagnosis (vet)	Detection	Probability lab tests for NAI	Expert opinion, literature
11	MAF investigates (vet)	Detection	Probability MAF investigates vet	Expert opinion
12	MAF takes samples (vet)	Detection	Probability MAF takes samples vet	Expert opinion
13	Lab diagnosis (MAF – vet)	Detection	Probability lab tests for NAI	Expert opinion
14	MAF investigates (farmer)	Detection	Probability MAF investigates farmer	Expert opinion
15	MAF samples (farmer)	Detection	Probability MAF takes samples vet	Expert opinion
16	Lab diagnosis (farmer)	Detection	Probability NAI diagnosed if present	Expert opinion
17	PM for other reasons	Detection	Probability PM done for other reasons	Expert opinion
18	Samples for other reasons	Detection	Probability samples submitted to lab	Expert opinion
19	Lab diagnosis (other)	Detection	Probability lab will test for NAI	Expert opinion

Table 8.5: Demonstration freedom from disease using multiple complex data sources for highly pathogenic avian influenza in New Zealand. Details of input variables used for the base scenario tree, described in the text.

Node	Variable	Distribution
-	Prior probability of freedom	Constant(0.5)
-	Probability of introduction	Constant(0.01)
2	Between-farm prevalence	Constant(0.01)
3	Within-farm prevalence	Constant(0.50)
2	Relative risk in zone	Constant(5), Constant(3), Constant(1)[a]
3	Relative risk for farm type	Constant(2), Constant(1)[b]
10,13,16,19	RTPCRSe [c]	Pert(0.90, 0.95, 0.97)
5	Clinical signs	Pert(0.95, 0.99, 1.00)
10,13,16	Probability samples tested clinicals	Beta(71, 13)
19	Probability samples tested PM	Beta(31,71)
6	Farmer seeks assistance	Pert(0.60, 0.70, 0.80)
7	Farmer notifies	Pert(0.6, 0.8, 0.9)
8	Vet seeks diagnoses	Pert(0.6, 0.9, 1.0)
9	Vet samples or calls MAF	Pert(0.4, 0.5, 0.6)
10	Lab diagnoses NAI (vet)	Pert(0.75, 0.9, 0.99) $\times$ Beta(15.03, 2.55)
11	MAF investigates (vet)	Pert(0.00, 0.70, 0.90)
12	MAF takes samples(vet)	Pert(0.00, 0.70, 0.90)
13	Lab diagnoses NAI (MAF)	Pert(0.75, 0.90, 0.99) $\times$ Beta(71, 13)
14	MAF investigates (farmer)	Pert(0.10, 0.50, 0.60)
15	MAF takes samples (farmer)	Pert(0.00, 0.70, 0.90)
16	Lab diagnoses NAI (farmer)	Pert(0.75, 0.90, 0.99) $\times$ Beta(15.03, 2.55)
17	PM for reasons other than clinical signs	Pert(0.05, 0.10, 0.20)
18	Samples to lab for other reasons	Pert(0.00, 0.10, 0.20)
19	Lab diagnoses NAI (other)	Pert(0.75, 0.90, 0.99) $\times$ Beta(3.13, 7.39)

[a] Relative risk in each risk zone: high = 5, medium = 3, low = 1.
[b] Relative risk for farm type: outdoor = 2, indoor = 1.
[c] RTPCRSe: RTPCR diagnostic sensitivity.

Table 8.6: Demonstration of freedom from disease using multiple complex data sources for highly pathogenic avian influenza in New Zealand. Details of input variables used for the alternative scenario tree, described in the text.

Scenario	Details	Value
Baseline	See Table 8.5.	See Table 8.5.
1	Probability of introduction PIntr	0.02
2	Probability of introduction PIntr	0.05
3	Probability of introduction PIntr	0.10
4	Relative risk in risk zones	1, 1, 1[a]
5	Relative risk in risk zones	20, 10, 1 [b]
6	Probability of observing clinical signs	Pert(0.20, 0.30, 0.50)
7	Probability of observing clinical signs	Pert(0.30, 0.50, 0.70)
8	Enterprise/herd prevalence	0.001
9	Enterprise/herd prevalence	0.050

[a] Relative risk in each risk zone: high = 1, medium = 1, low = 1.
[b] Relative risk in each risk zone: high = 20, medium = 10, low = 1.

Table 8.7: Demonstration of freedom from disease using multiple complex data sources for highly pathogenic avian influenza in New Zealand. Posterior medians and 95% credible intervals of the monthly surveillance system sensitivity, prior probability of freedom and posterior probability of freedom estimated for the baseline scenario tree model.

Month	System sensitivity (95% CI)	PriorPFree (95% CI)	PostPFree (95% CI)
1	0.16 (0.10 – 0.24)	0.50 (0.50 – 0.50)	0.54 (0.53 – 0.57)
2	0.14 (0.09 – 0.22)	0.54 (0.52 – 0.56)	0.57 (0.54 – 0.62)
3	0.15 (0.10 – 0.23)	0.57 (0.54 – 0.61)	0.61 (0.56 – 0.67)
4	0.16 (0.10 – 0.25)	0.60 (0.56 – 0.67)	0.64 (0.59 – 0.73)
5	0.15 (0.10 – 0.23)	0.64 (0.58 – 0.72)	0.68 (0.60 – 0.77)
6	0.18 (0.12 – 0.27)	0.67 (0.60 – 0.76)	0.71 (0.63 – 0.81)
7	0.17 (0.11 – 0.25)	0.70 (0.62 – 0.81)	0.74 (0.65 – 0.85)
8	0.16 (0.10 – 0.24)	0.73 (0.64 – 0.84)	0.77 (0.67 – 0.87)
9	0.16 (0.10 – 0.24)	0.76 (0.66 – 0.86)	0.79 (0.68 – 0.89)
10	0.17 (0.11 – 0.26)	0.78 (0.68 – 0.88)	0.81 (0.70 – 0.91)
11	0.17 (0.11 – 0.25)	0.80 (0.69 – 0.90)	0.83 (0.72 – 0.92)
12	0.16 (0.10 – 0.24)	0.82 (0.71 – 0.91)	0.85 (0.73 – 0.93)

CI: Bayesian credible interval.

PriorPFree: Prior probability of freedom.

PostPFree: Posterior probability of freedom.

Figure 8.1: Demonstration freedom from disease using multiple complex data sources for highly pathogenic avian influenza in New Zealand. Raster maps showing the distribution of HPAI incursion risk density estimates obtained from combining the listed risk factors using Boolean addition for: (a) summer, (b) autumn, (c) winter and (c) spring. In each figure shading is used to represent the estimated risk score density per square kilometre.
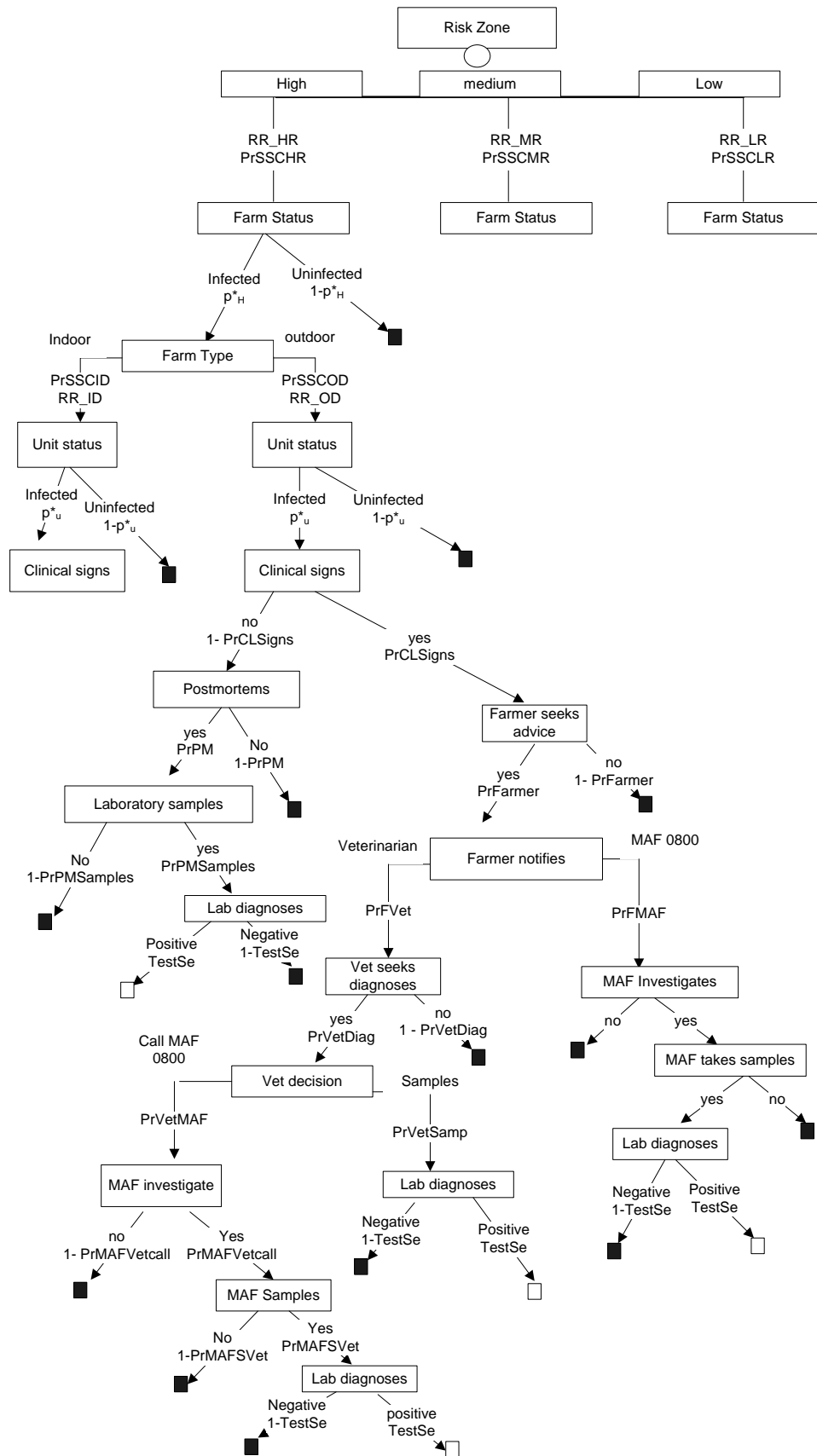
Figure 8.2: Scenario tree representing passive surveillance for HPAI in New Zealand.
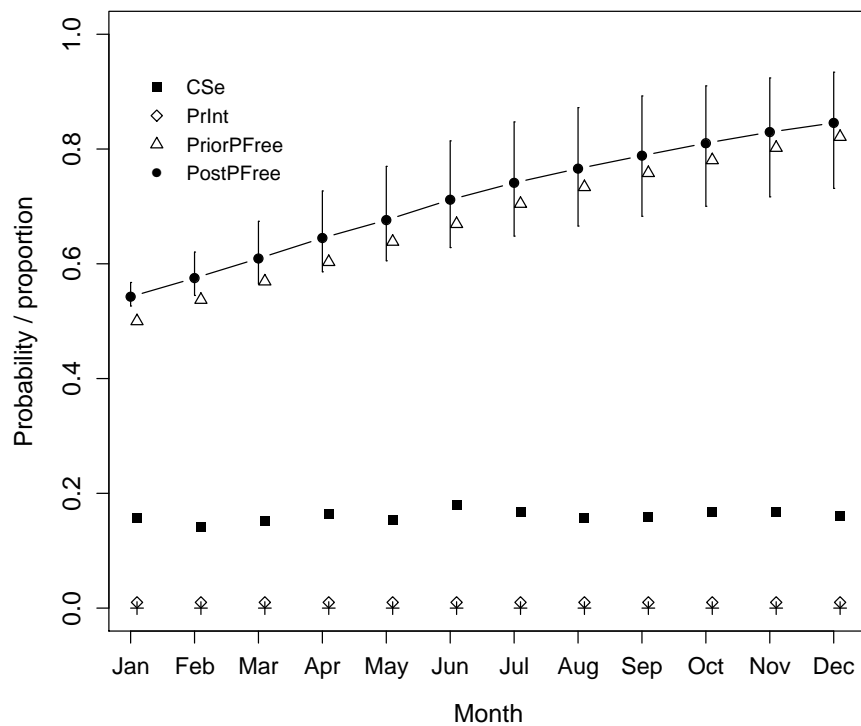
Figure 8.3: Demonstration freedom from disease using multiple complex data sources for highly pathogenic avian influenza in New Zealand. Error bar plot showing the median posterior probability of HPAI freedom (and associated 95% credible intervals), surveillance system sensitivity, probability of introduction of HPAI, and proportion of units processed as a function of calendar month for the baseline surveillance scenario.
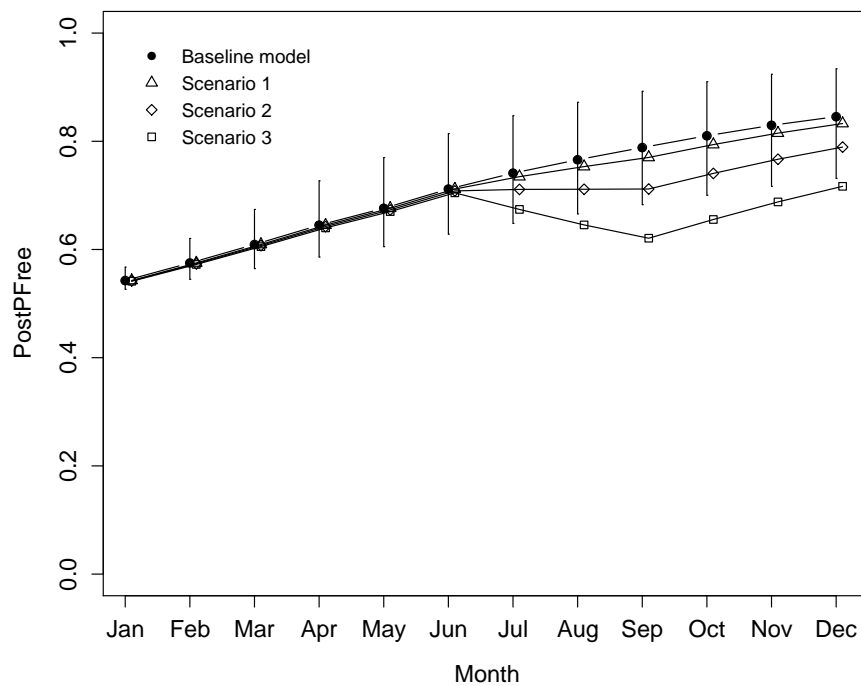
Figure 8.4: Demonstration freedom from disease using multiple complex data sources for highly pathogenic avian influenza in New Zealand. Error bar plot showing the median posterior probability of HPAI freedom (and associated 95% credible intervals) for the baseline surveillance scenario and alternative scenarios related to changes in the probability of introduction during spring months (scenarios 1, 2 and 3).
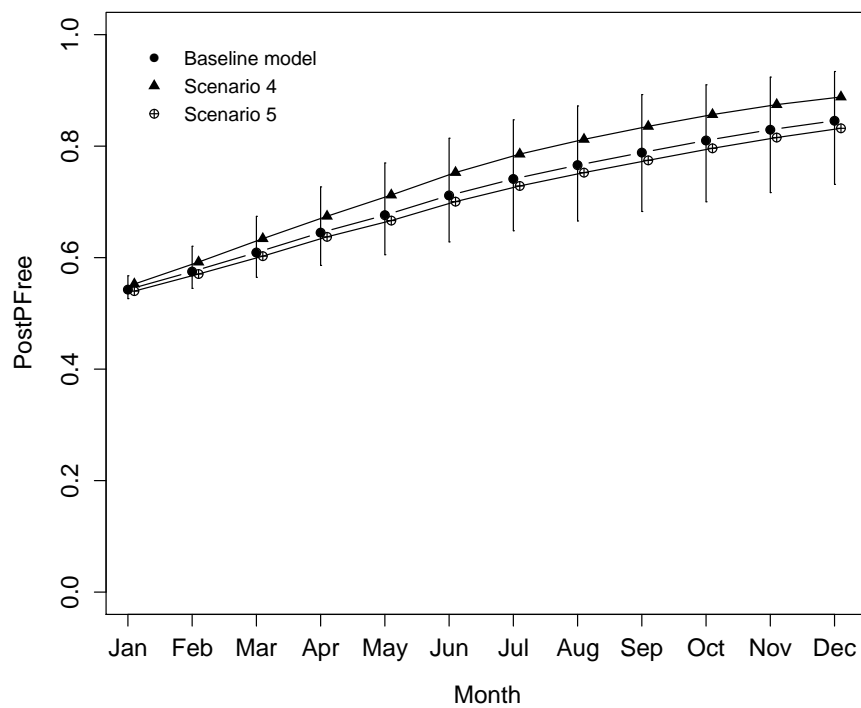
Figure 8.5: Demonstration freedom from disease using multiple complex data sources for highly pathogenic avian influenza in New Zealand. Error bar plot showing the median posterior probability of HPAI freedom (and associated 95% credible intervals) for the baseline surveillance scenario and alternative scenarios related to changes in the relative risk values for each risk zone (scenarios 4 and 5).
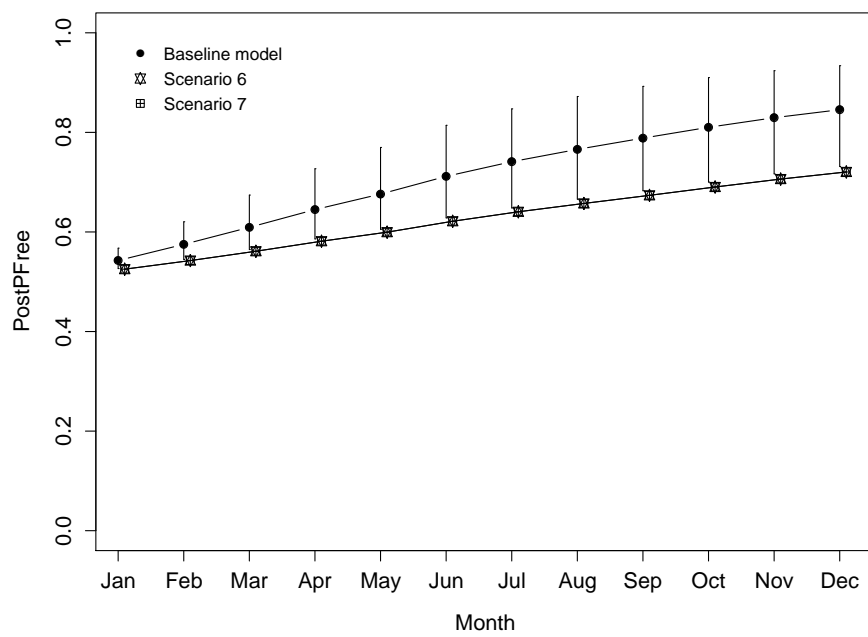
Figure 8.6: Demonstration freedom from disease using multiple complex data sources for highly pathogenic avian influenza in New Zealand. Error bar plot showing the median posterior probability of HPAI freedom (and associated 95% credible intervals) for the baseline surveillance scenario and alternative scenarios related to changes in the probability of observing clinical signs (scenarios 6 and 7).
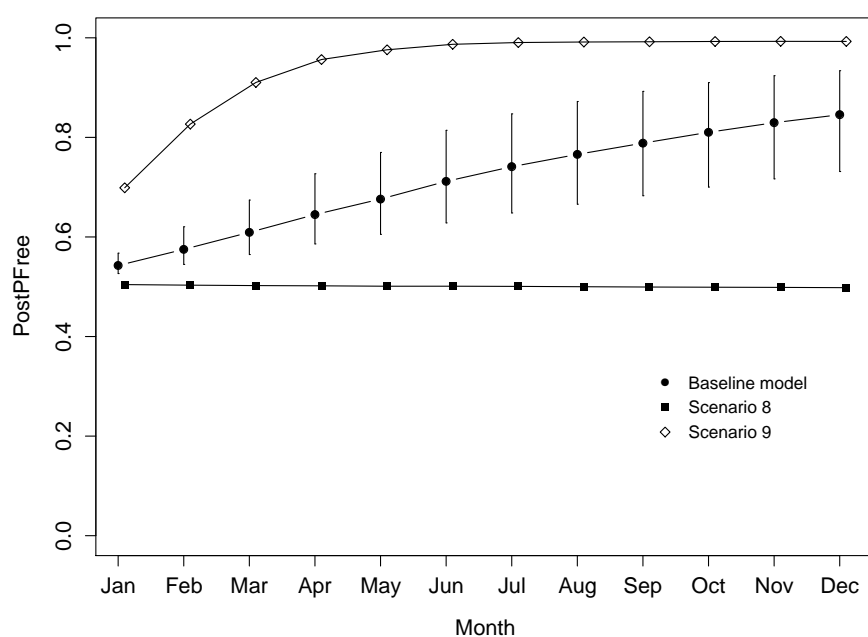
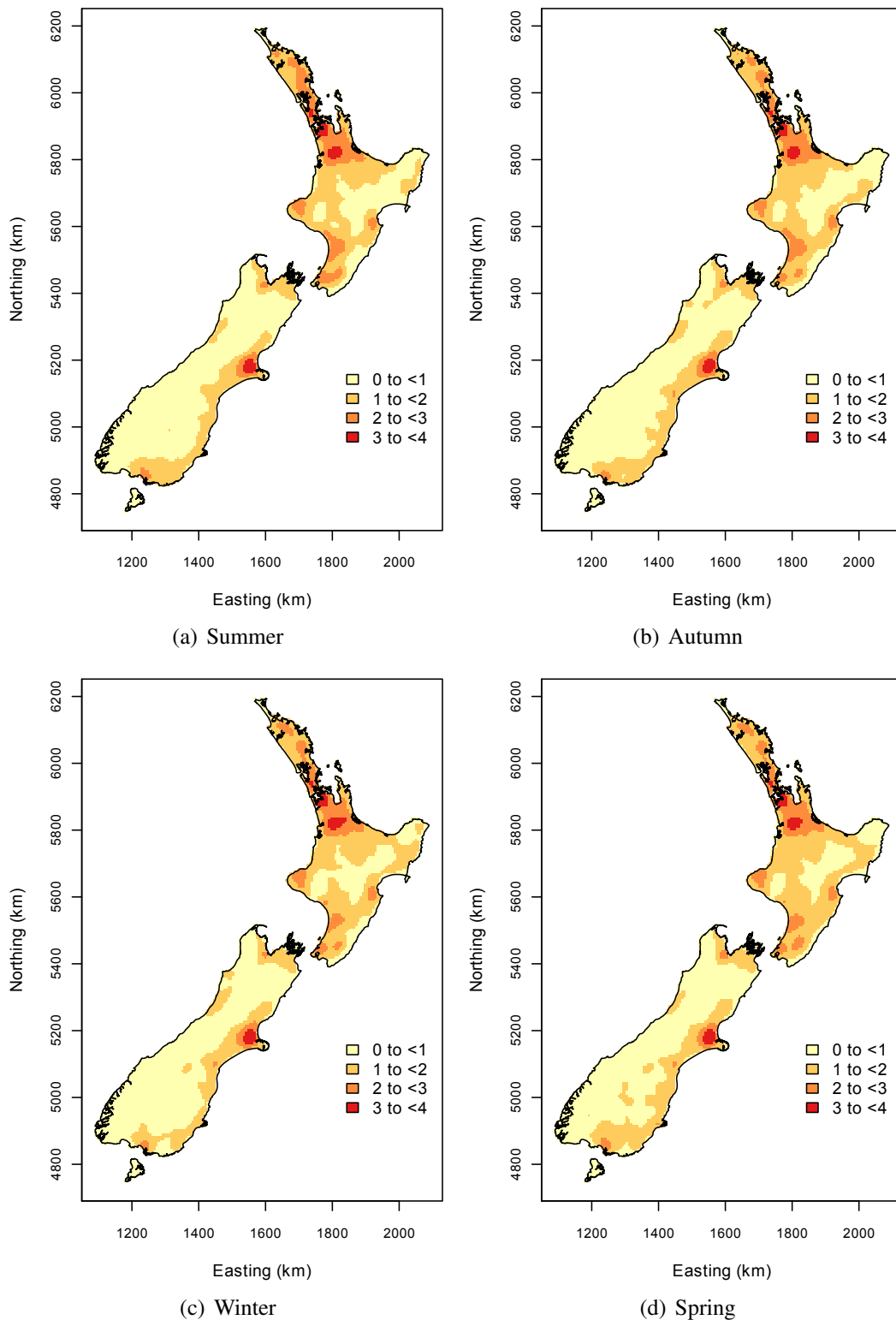**Figure 8.7:** Demonstration freedom from disease using multiple complex data sources for highly pathogenic avian influenza in New Zealand. Error bar plot showing the median posterior probability of HPAI freedom (and associated 95% credible intervals) for the baseline surveillance scenario and alternative scenarios related to changes in between-farm prevalence probability (scenarios 8 and 9).

8.4   Discussion

Decision makers in animal health require an objective, structured and repeatable process for assessing the ongoing sensitivity of surveillance systems to decide on alternative options that might be applied to increase surveillance efficiency (Campbell et al. 2007). This paper combines two decision making processes to achieve this goal: a geographical risk assessment of disease incursion and spread risk and secondly, a scenario tree model to quantify surveillance system performance. The focus of this work is the development of a methodology for surveillance system assessment rather than the evaluation of the current passive surveillance system for HPAI in New Zealand. This paper represents the first of two steps in methodology development, the second of which is the process of information elicitation from local experts to ensure a more robust and relevant input values for HPAI surveillance in this country. Current examples in the literature have used spatial risk assessment (Snow et al. 2007) and scenario trees modeling (Martin, Cameron, Barfod, Sergeant & Greiner 2007, Martin 2008) separately. To the best of our knowledge this is the first time the two methods have been combined to assess the performance of a surveillance system.

The spatial risk assessment approach used data on animal and human demographics, road networks and ecology to describe the geographical distribution of avian influenza introduction and spread. These input factors were modeled as binary variables affecting disease occurrence to obtain a semi-quantitative estimate of the distribution of risk throughout New Zealand. For this model to be of practical use to animal health authorities a more robust process for ranking individual risks is required. This may be achieved by firstly improving the definition of the risk factors, and secondly by weighting factors according to their importance as perceived by subject matter experts. Risk model approaches use a variety of methods for expressing or defining risk which can include simple presence or absence as used in this paper, a scale of values expressed as whole numbers as in Snow et al. (2007) or probabilities to express incremental values of risk. Snow et al. (2007) used a number of scoring methods to the express the risk posed by different wild bird species and poultry farms. To define risk posed by wild birds, abundance scores in the range of 0 − 5 were assigned to each species for each month of the year on the basis of observed abundance in each of 10 square kilometre grids across the United Kingdom. For

defining the risk areas due to commercial poultry holdings, each holding was scored on five holding-level factors: holding size, farm classification as free range, the presence of ducks and geese in outdoor production, and production type. Risk of incursion due to holding size was scored as the natural log of the number of birds, whilst the remaining factors were scored as present or absent (0's or 1's).

Weighting of each of the risk factors in terms of importance is another method for improving the approach. This can be achieved via multidisciplinary forum of local experts such as a Delphi conference (Elliott et al. 2005). A Delphi conference involves a structured group communication to allow groups of individuals, as a whole, to deal with a complex problem. The group could be comprised of biosecurity experts, ornithologists, and poultry veterinarians with knowledge of the epidemiological situation of the country. These experts could then be asked to rank each of the factors in terms of risk.

Estimates used in the scenario tree also require validation using actual surveillance data and expert or interest groups to inform the input of each component of the model. This process represents the most difficult and resource intensive part of the development process as various groups and organisations will need to be contacted, brought together and surveyed. These should include farmers, veterinarians, laboratories involved in poultry diagnostics, and biosecurity and poultry industry officials. An expert panel organised to elicit data on the potential incursion of six exotic animal diseases into The Netherlands in 1998 brought together a group of 43 individuals to obtain data which would be used for informing a simulation model for assessing the impact of a number of strategies to reduce the risk of disease incursion (Horst et al. 1998). Acknowledging the potential biases that may be associated with elicitation of opinions, the authors concluded that in the absence of data, this may be the best option. Use of structured elicitation methods together with sensitivity analyses to assess uncertainty in data derived in this way provides a method for assessing the importance of data uncertainty.

Some or all of the components of the model described in this paper may be of use to animal health officials. For example, the outcome from the geographical risk component identified areas of the country with a relatively high risk of incursion and spread (mostly where both wild birds and poultry units are co-located). Knowledge of these areas allows animal health authorities to monitor more closely reports from these identified areas in order to determine when targeted activities are required to improve passive reporting by

farmers. This could be achieved through measures such as awareness campaigns, facilitated by the media or industry meetings. It may also be used by authorities to plan targeted surveillance in high risk areas to ensure best use of limited resources in order to increase the chances of detection.

The scenario tree on its own may be used as an evaluation tool to assess the detection capacity of individual surveillance systems (passive *versus* active) or to compare the usefulness of proposed alternative strategies. As a tool for evaluating a passive surveillance system, it allows animal health authorities to assess the effect of varying input parameters on the sensitivity of the system thereby allowing for identification of influential parameters which may be targeted for improvement. For example, if the probability of a farmer detecting clinical signs was low, then efforts at improving farmer detection based on distribution of educational materials could be implemented to improve sensitivity of the system as a whole. The results from the baseline model show that the estimated median sensitivities for each of the 12 months of surveillance were consistently low with the highest value of 0.18 estimated for the sixth month of the study period. According to the model the surveillance system at most is likely to detect infections if it is present with a 0.18 probability at the defined design prevalence. The associated estimates of probability of disease freedom increased in small intervals of 0.02 from month 1 to month 12 with a final estimate of 0.84. The small increase in confidence over the 12 months period implies that the level of reporting is not sufficient to ensure that an incursion is detected and extra focus should be placed on increasing farmer reports. As the data used in this model was simulated, these analyses need to be repeated using actual data collected by the state veterinary service.

A limitation of this study is that we focused on the likelihood of HPAI virus introduction and spread in domestic poultry via wild birds and trade and not the emergence of HPAI from endemic LPAI strains circulating in wild birds. Given the relative isolation of New Zealand and strict biosecurity measures at ports of entry, it may be argued that influenza surveillance in this country should be focused on the second scenario, whereby HPAI might emerge in domestic poultry via the interaction between wild birds and back yard/outdoor poultry. These are two distinct surveillance approaches requiring very different scenario trees. Surveillance for HPAI strains, by necessity, relies on surveillance for clinical signs of disease while surveillance for LPAI relies on serological (active) surveil-

lance and would require distinct inputs. Development of a scenario tree to assess evaluate the active surveillance component is recommended.

The ability to detect disease incursion early requires all potential risks and limitations present in a surveillance system to be identified and addressed. A geographic risk model, used in conjunction with a scenario tree model, provides a means to achieve both these goals. Further evaluation of the approach is required to ensure more robust outcomes reflecting the actual situation in New Zealand. Scenario tree models to evaluate the passive surveillance system provides a potentially powerful tool to explicitly examine and quantify each component of the system. This provides the opportunity to determine factors affecting surveillance system sensitivity and, by extension, confidence in disease freedom. In situations of uncertainly, particularly in countries where NAI is not present and passive surveillance system is the primary means for early detection, the ability to periodically evaluate the system will prove to be an important tool.

CHAPTER 9

General discussion

Surveillance systems for animal diseases have multiple objectives that are increasingly challenged by changing national and global conditions. These multiple objectives relate to the ability to accurately describe endemic disease conditions, promptly detect disease incursions, demonstrate freedom from disease to trading partners, and the ability to assess eradication and control programmes (Anonymous 2007*b*). Increasing threats due to emerging diseases, changing requirements for demonstrating disease freedom at the international level, and a reduction in animal health infrastructure investment at the national level are factors that conspire against effective disease surveillance.

The spread of animal diseases to new geographic regions is often associated with many severe and unwanted consequences. Substantial economic losses are associated with epidemics due to loss in trade (James & Rushton 2002), costs associated with control programmes (Webster et al. 2006), as well as threats to food security (McLeod et al. 2004), human health, animal welfare, and tourism (Thompson et al. 2002). The recent emergence and spread of highly pathogenic avian influenza due the H5N1 virus to new areas across the globe is but one manifestation of the increasing trend in the appearance and spread of emerging diseases in livestock populations. This trend has been potentiated by trade globalisation, intensification in animal production systems, poor veterinary infrastructure in many countries, poor biosecurity, climate change, bioterrorism, and urbanisation (Morse 2004). These problems are predicted to continue well into the future. Of the numerous emerging diseases that have affected livestock around the globe, the epidemics of FMD in the United Kingdom, Taiwan, Uruguay, and Argentina from 2000 – 2001 (McLaws & Ribble 2007), BSE in the United Kingdom, Europe, Canada and the USA from 1986, and outbreaks of highly pathogenic avian influenza due to H7N3 in Belgium (Berg & Houdart

2008), H7N7 in The Netherlands (Elbers et al. 2004) and H5N1 in Southeast Asia (Sims et al. 2005, Sims 2006) have highlighted a number of problems with early detection of known and emerging disease incursions. These factors relate to poor information infrastructures to support effective surveillance strategies, lack of knowledge of the distribution of factors that might increase the risk of disease introduction and spread, and factors related to disease manifestation that are likely to impact upon time to detection.

In this thesis, the epidemiological features of the HPAI H5N1 epidemic that occurred in the Republic of Vietnam between December 2003 and February 2004 have been described (Chapters 4 and 5), the results of which were then used to inform a series of studies aimed at developing effective surveillance strategies for HPAI in New Zealand. Acknowledging the importance of enumerating animal populations at risk, this thesis provides a methodological approach for enumerating backyard poultry populations (Chapter 6). In addition to outlining a means to better enumerate the domestic poultry population at risk this thesis also examined the spatial distribution of other at-risk avian populations, in particular wild migratory birds (Chapter 8). Acknowledging that the act of movement might also be highly influential in determining the distribution of disease Chapter 7 provides a description of movement patterns within the New Zealand commercial poultry industry. Drawing these elements together, Chapter 8 presents a scenario tree model to quantify the effectiveness of New Zealand's passive surveillance system for HPAI. It should be noted that in Chapter 7 key data elements to inform the scenario tree model (in particular, the number of reports of suspected HPAI cases reported per month) were not available at the time of writing, so it is stressed that Chapter 8 provides a methodological approach rather than an absolute estimate of New Zealand's surveillance HPAI surveillance efficiency *per se*.

9.1   Lessons learned about HPAI epidemiology

The analyses conducted in Chapters 4 and 5 were undertaken to elucidate epidemiological features influencing the distribution and spread of HPAI H5N1 during the 2003 – 2004 outbreaks in Vietnam. Chapter 4 focused purely on descriptive analyses (as a means for hypothesis generation) whereas Chapter 5 was concerned with quantifying the effect of a number of environmental and population-level risk factors on the spatial distribution of disease. In Chapter 4 examination of the spatial and temporal pattern of outbreaks allowed

broad scale patterns in disease incidence to be identified. The descriptive analyses of the number of affected HPAI H5N1 communes showed that, overall, 87% of all provinces reported the presence of disease, indicating that infection was widespread throughout the country. The outbreak was characteristic of a point source epidemic with disease simultaneously seeded in the south and north of the country. The results shown in Chapter 4 lend support to the hypothesis that once HPAI enters a naïve population, the presence of high densities of susceptible species as well as complex animal trading patterns contribute to rapid and wide scale disease dissemination (McLaws & Ribble 2007). The use of a mixed effects model to impute the number of outbreaks in areas for which no data existed allowed for uncertainties in case reporting to be accounted for by borrowing strength from neighbouring areas. This approach was particularly useful for estimating disease frequencies in the presence of missing data (Berke 2001). Whereas the compilation of complete and accurate data sets should always be the goal for any state veterinary service managing an outbreak response, this is not always possible for a variety of reasons. The methodology described in Chapter 4 demonstrates one approach for dealing with missing and/or incomplete data — allowing better use to be made of existing, albeit imperfect, information.

To test the hypothesis of the possible involvement of risk factors in the epidemiology of the outbreaks in Vietnam, a Bayesian zero-inflated Poisson model was used to examine the effect of a variety of environmental and population-level risk factors on the number of reported cases of HPAI across Vietnam. The analyses showed that in areas where disease was reported, the presence of irrigated land areas increased the risk of outbreaks whereas higher elevations were associated with a decrease in risk. Once these risk factors were accounted-for, a single large region of elevated risk of disease was identified in the Red River Delta area. We can only speculate on the reason(s) for this area of elevated risk, suffice to say that its presence would be consistent with regional similarities in the likelihood of reporting disease and/or the presence of factors increasing the likelihood of disease transmission (e.g. animal movement patterns).

The methodological approach taken in Chapter 5 also showed that satellite data can be used to help explain the spatial distribution of disease, particularly in countries where detailed risk factor information is sparse. The success of this approach will depend on, of course, the disease of interest and the type and resolution of the satellite data being

used. The analyses presented in Chapter 5 suggest that environmental data (e.g. land use, elevation, vegetation index) — because it is slow to change over time — provides a more robust set of explanatory variables, compared with data sets enumerating human and animal population densities.

9.2 The population at risk

Countries with densely populated populated poultry areas (Capua, Marangon, dalla Pozza, Terregino & Cattoli 2003, Elbers et al. 2004, Stegeman et al. 2004, Garske et al. 2007) and large backyard poultry populations (Alexander 2007, Epprecht et al. 2007) that are located along wild bird migratory pathways (Anonymous 2008*e*) are vulnerable to outbreaks of NAI. Thus the distribution of NAI outbreaks within countries is likely to show regional variation dependent on the distribution of the population at risk, environmental, and management factors. Amongst these factors are the type of species present (Capua & Marangon 2004, Ellis et al. 2004, Sturm-Ramirez et al. 2004), the type of housing (influencing the degree of contact with wild birds), the number of birds present, and biosecurity level.

Given the relatively limited knowledge of the distribution of backyard poultry populations in New Zealand and the role backyard poultry might play in establishing NAI in the commercial poultry sector, Chapter 6 provides a simple methodology for quantifying the distribution of backyard poultry. Backyard poultry ownership was not common in the two areas selected for study, but varied according to land classification. The relatively low density of backyard poultry (approximately 1 bird per square kilometre) implies that density dependent spread of disease is unlikely, unless disease is able to spread to other areas via direct and/or indirect means (Halvorson et al. 1980, Webster et al. 1992, Sawabe et al. 2006, Sievert et al. 2006). This contrasts with countries like The Netherlands where the density of backyard poultry is relatively high (Stegeman et al. 2004). Despite the low risk posed by low bird densities, the prevalent practice of allowing birds to free range, increases the likelihood of exposure to wild birds. As part of epidemic contingency planning effort should be applied to educate backyard poultry owners regarding the risks that wild birds might pose to domestic poultry in terms of disease transmission (Muller et al. 1999). There was no evidence to support a relationship between the commercial sec-

tor and the backyard bird premises in the two study areas. This may not always be the case as movements between non-commercial and commercial poultry enterprises have, in other countries, been associated with widespread dissemination of disease (Panigrahy et al. 2002, Garber et al. 2007).

Our study found no association between the presence of backyard poultry and socio-economic deprivation. Further studies to investigate the relationships between (say) ethnicity and the likelihood of bird ownership in other areas of the country, particularly in and around larger cities (characterised by higher densities of ethnically diverse populations) would provide a means for investigating these relationships in greater detail. Studies of this type would allow factors associated with backyard poultry ownership such as population density, distance from urban centres, land parcel area, and ethnicity to be more precisely defined. This would provide the means for predicting the distribution of backyard poultry (on the basis of data routinely recorded for other purposes) rather than attempting to enumerate animal numbers via cross-sectional surveys. Moreover, the point could be made that complete enumeration of animal populations is virtually impossible, and simulation modelling on the basis of identified 'risk factors' for animal ownership should be used as a means for augmenting census data — providing authorities with the best possible estimate of the spatial distribution of an animal population at risk.

9.3   Movement patterns

It is well acknowledged that movements that occur within animal industries have important implications for farm-to-farm spread of disease, through direct and indirect contact (Gibbens et al. 2001, Woolhouse et al. 2005, Févre et al. 2006). Moreover, knowledge of movement patterns and how they vary by season, geographical region and enterprise type are useful in terms of identifying high risk periods and locations that are likely to disperse disease, in the event that it enters an animal population (Christley et al. 2005, Kiss et al. 2006, León et al. 2006). With knowledge of these risks, more focused and cost effective surveillance approaches can be applied.

Given the lack of a national-level source of movement data within the poultry industry, a cross-sectional survey was used to quantify the different types of contacts within the commercial poultry sector in order to evaluate how these might contribute to disease

spread (Chapter 7). The movements examined included contacts mediated through feed, live birds and hatching eggs, table eggs and poultry product, and waste litter and manure. Two broad categories of network structures were identified: the first was a 'hub and spoke' type arrangement with small numbers of network hubs (e.g. feed suppliers and hatcheries) providing goods and services to larger numbers of client farms. In addition to the hubs acting as the predominant source of material moving onto farms, smaller numbers of intermediary (high betweenness score) enterprises were identified. In the event of an infectious disease outbreak, these hubs and intermediaries would facilitate the spread of disease throughout the network. The second network category was comprised of the manure and waste litter contacts and was characterised by individual enterprises having many contacts. The potential for disease transmission in this category was not was great as for the first ('hub and spoke') category.

The importance of each movement type in terms of influencing transmission of infectious disease throughout the network will vary, with direct contact thought to be the most efficient means for disease spread. As observed in a number of avian influenza outbreaks, indirect contact via humans is also an important route (Thomas et al. 2005). Since this study did not explicitly address movements mediated only by humans, it is difficult to determine what role this type of movement would play in disease spread in New Zealand. A logical extension to the study described in Chapter 7 would be to quantify the frequency and nature of human movements on- and off- individual poultry enterprises. Additionally, the importance of movement type is likely to vary with the type of disease under consideration. For example, feed would be the most important mechanism for spreading contaminants such as dioxin compared with, for example, the movement of live birds.

Because movement patterns are highly dynamic, and in the absence of a dedicated traceability system, repeated cross-sectional surveys to characterise movement patterns are recommended. Additionally, further analyses to examine how disease would spread within the contact networks will serve to better inform surveillance strategies. Possible approaches include model-based approaches such as that developed by Truscott et al. (2007) and Sharkey et al. (2008). Regression analyses (Ribbens et al. 2008) can be used to examine the influence of factors such as enterprise type on network level characteristics (e.g. betweeness scores). This information is useful, since it allows 'profiles' of risky enterprises to be developed. Disease control authorities can then target surveillance interven-

tions towards enterprises assessed to be of high risk on the basis of profiling, rather than having to work off the results of one-off cross-sectional studies of movement patterns.

9.4 Risk based surveillance

Surveillance for emerging diseases is associated with a number of uncertainties. The first relates to questions surrounding when and where a disease incursion is likely to occur. The second uncertainty relates to the level and type of surveillance required to provide the most sensitive means for detecting incursions in a cost effective manner. This is of foremost importance to animal health authorities since early detection of disease is closely associated with a country's ability to demonstrate freedom of disease (Baldock 1998). To address these issues Chapter 8 combines two decision support tools: a geographic risk assessment model and a scenario tree model. The geographic risk model incorporated a number of data sources detailing animal and human population demographics, wild birds, land use and the distribution of road networks. The quality of the data available for this analysis was high in terms of detail and coverage. This allowed development of a detailed geographic risk model, providing a further example of the value that can be derived from these data sets. To ensure continued benefit is derived from such data sets it is critical that sufficient funds are made available to to continue their ongoing development and maintenance.

To address the uncertainty surrounding whether the current passive surveillance system in New Zealand is likely to detect an avian influenza incursion, the scenario tree model developed in Chapter 8 can be used to evaluate the system sensitivity as well provide an estimate of the probability that New Zealand is free of disease given the sensitivity of the system as a whole. In conjunction with the geographic risk model, it can be used to by animal health authorities to modify surveillance strategies on the basis of risk. The value of this approach is that it provides a simple, quantitative approach for evaluating data from multiple sources that is structured, scientific and repeatable. As a decision making tool, the model on its own may be used as an evaluation tool to assess the detection capacity of passive surveillance *versus* an alternative (e.g. active surveillance). As a tool for evaluating a passive surveillance system, it allows animal health authorities to assess the effect of varying input parameters on the sensitivity of the system allowing influential

parameters to be identified.

9.5 Further research

The studies described in this thesis have identified a number of factors that are important to consider in the design of an HPAI surveillance strategy for New Zealand. With respect to factors that must be considered in the design of an effective surveillance system, a number of recommendations can be made with regards to backyard poultry populations and movement data. Although the study presented in Chapter 6 provided no evidence to support a biosecurity risk to the commercial poultry sector arising from backyard poultry, the results cannot be interpolated to other areas of the country. Similar studies in other areas of the country need to be carried out to characterise these populations with greater certainty. The data from these surveys could then be used to validate the simulation model to estimate the distribution of backyard poultry described in Chapter 8.

Soliciting information from farmers via cross-sectional surveys can be difficult and prone to poor response rates. For this reason there is therefore a need to develop a system to capture movement event information in real time. To capture data at the farm level possible approaches might include the use of simple spreadsheet programs which can then be compiled at the national level on a periodic basis. Other — longer term — solutions include the implementation of computerised traceability systems (for example Anonymous 2008*c*). In this case cross-sectional surveys could then be reserved for recording movement of personnel such as catching crews, and staff or used to validate data from captured by the traceability system.

Given that notifiable avian influenza has not been detected in New Zealand, a possible approach to improve the current surveillance programme for wild birds and domestic poultry would be to target areas and species most at risk and during higher risk periods. To facilitate this process I propose that the approach described in Chapter 8 be used as a tool to design a fully risk based surveillance strategy (Stärk et al. 2006). The geographical risk component of the model can be used to focus sampling on both wild and domestic birds to ensure early detection. Data gathered from these surveillance can be incorporated into the spatial model to better inform areas at risk.

9.6 Conclusion

This thesis presents a number of methodological approaches that are sufficiently generic to be used to inform the design of surveillance strategies for a variety of animal diseases, not just those of poultry. Examination of past epidemics, as exemplified by the epidemic of HPAI in Vietnam described in this thesis, provide insight into the epidemiological features of, and risk factors for, disease. This information then provides the basis for gathering knowledge about animal populations at risk, clarifying their distribution and patterns of contact. Finally, the design of a surveillance model capable of identifying critical performance points and identifying critical control points for preventing spread are logical next steps. Although epidemiology, as a discipline, is well equipped with a vast range of analytical techniques that can be used to enhance the understanding of factors influencing the spread of disease among animal populations, the quality of data used to support these techniques is often lacking. The challenge in the years ahead, for both developed and developing countries, is to set in place the appropriate infrastructures to collect details of animal populations consistent in quality over time and place to allow insightful analyses to be realised when and where they are required.

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Appendix 1

Epicentre, Massey University Questionnaire to

Describe the Backyard Poultry Sector in Palmerston North

Thank you for agreeing to participate in our project. One of the aims of this project is to quantify key aspects of the New Zealand poultry industry in an effort to provide the industry with information that will allow disease monitoring and surveillance activities to be more effectively targeted.

The objectives of this part of the project are to:

- Characterise the extent and nature of the informal (free-range and backyard) sector of the poultry industry.

- Characterise network patterns that exist within the informal sector and identify potential cross-over points between the informal and formal sectors with a view to identifying areas of vulnerability whereby diseases established in the informal sector might gain entry and establish themselves in the formal sector.

This project is funded by the Pacific Vet funds administered by IVABS, Massey University. The project is implemented through the Epicentre, Massey University and is supported by the Ministry of Agriculture and Fisheries of New Zealand.

Confidentiality
All information will be treated confidentially. No individual property details will be reported to any party.

LAND PARCEL INFORMATION

Date	
Name	
Address	
Phone (home)	
Phone (work)	
Location	Easting		Northing	

2.1. Property status	Tick	Tick only one box
Owned		
Rented		
Lease		

3. DOMESTIC BIRD OWNERHIP

3.1. Do you keep domestic poultry on your property?	Tick	Tick only one box
Yes		Go to question 3.2.
No		End questionnaire.

3.2. What is the major type of domestic poultry kept?	Tick	Tick only one box
Production for home use		
Hobby		
Commercial production		
Domestic pets		

3.3. Why do you keep domestic poultry?	Score	1 = most important; 6 = least important
Food		Production for meat, eggs, and/or feathers.
Feeding scraps		
Extra Income		
Pleasure		
Aviculture club		
Manure		
Other (specify)		

3.4. How long have you kept domestic poultry on this property?		years

3.5. Do you or someone in your household work in the commercial poultry industry?	Tick	Tick only one box
Yes		Go to question 3.6.
No		Go to question 3.7.

3.6. If yes, which sector?	Tick	Tick only one box
Processing facility		
Breeder Farm		
Broiler farm		
Layer farm		
Hatchery		

3.7. Do you belong to an aviculture club or association?	Tick	Tick only one box
Yes		Go to question 3.8.
No		Go to section 4.

3.8. If yes, what is (are) the name(s) of the club(s) or association(s)?	

4. DOMESTIC BIRDS PRESENT AT TIME OF SURVEY

4.1. Please indicate the number and type of domestic poultry present on the property on the day of the survey.	Number
Aviculture	
Ducks	
Geese	
Guinea fowl	
Ostriches	
Pet/caged birds	
Pheasants	
Pigeons	
Poultry for eggs	
Poultry for meat	
Swans	
Turkeys	
Other(specify)	

4.2. Please indicate the type and numbers of other animals present on the property on the day of the survey.	Number
Cats	
Cattle	
Dogs	
Goats	
Sheep	
Other (specify)	

5. HOUSING

5.1. Where are your domestic poultry kept?	Tick	Tick only one box
Inside a shed or coop		Go to question 5.2
Free range within the property		Go to section 6.
Free range crossing property boundary		Go to section 6.

5.2. If domestic poultry are kept inside pens or coops, are they allowed to free range outside?	Tick	Tick only one box
Yes		Go to question 5.3
No		Go to question 6.1

5.3. For approximately how long are domestic poultry allowed to remain outside each day?		hours

6. ANIMAL AND WILD BIRD CONTACTS

6.1. In the last month, have you noticed wild birds in the immediate area where your domestic poultry are kept?	Tick	Tick only one box
Yes		Go to question 6.2.
No		Go to question 6.4.

6.2. In the last month, on how many times have you sighted wild birds in the immediate area to where your domestic poultry are kept?		days

6.3. List the type(s) of wild birds seen on your property during the last month (refer to Annex 1 for details).

6.4. Are there any ponds or water bodies on or near your property?	Tick	Tick only one box
Yes		Go to question 6.5.
No		Go to question 6.6.

6.5. In the last month, have you noticed waterfowls in ponds or water bodies on your property?	Tick	Tick only one box
Yes		
No		

6.6. Do you have wild bird feeders on your property?	Tick	Tick only one box
Yes		
No		

7. BIOSECURITY

7.1. Do you have any special requirements for persons entering the area where poultry are kept?	Tick	Tick only one box
Yes		Go to question 7.2.
No		Go to section 8.

7.2. If yes, specify these requirements

8. CARCASS AND LITTER DISPOSAL

8.1. Approximately how many deaths occurred in your domestic poultry flock over the last 12 months?(For reasons other than slaughter)		deaths

8.2. What is the main method of disposal of dead birds?	Tick	Tick more than one box if necessary
Incinerate		
Bury on premises		
Compost		
Council rubbish dump		
Fed to other animals		
Rubbish can		
Renderer		
Other (specify)		

8.3. What is the most common method of litter/manure disposal?	Tick	Tick more than one box if necessary
Do not have enough		
Rubbish dump		
Outdoor pile		
Manure shed or compost		
Sell		
Spread on garden		
Other methods (specify)		

9. FEED

9.1. What is the main type of feed offered?	Tick	Tick only one box
Purchased feed		Go to question 9.2
Kitchen scrap		Go to question 10.1
Other (specify)		Go to question 10.1

9.2. What is the main source of purchased feed?	Tick	Tick only one box
Feed mill		
Store		
Other (specify)		

10. WATER

10.1. What is the main source of water for domestic poultry?	Tick	Tick only one box
Town supply		
River		
Bore		
Other (specify)		

11. BIRD AND PRODUCT MOVEMENT

11.1. Over the last 12 months, please specify the quantity of fertile eggs, and birds that were <u>brought onto</u> your property	Quantity	Source (company and town)
Eggs		
Day old chicks		
Pullets		
Adult birds		

11.2. Over the last 12 months, please specify the quantity of eggs, and birds that <u>left</u> your property	Quantity	Destination (company and town)
Eggs		
Day old chicks		
Pullets		
Adult birds		

12. SHOW BIRDS

12.1. Have you publicly exhibited birds over the last 12 months?	Tick	Tick only one box
Yes		Go to question 12.2.
No		Go to section 13.

12.2. If yes, how many times during the last 12 months?		occasions

12.3. If yes, how many times during the last 3 months?		occasions

12.4. Where were birds taken?		
Name of show	Month	Location

13. MOVEMENT

13.1. Have you visited a location with birds during the last 3 months?	Tick	Tick only one box
Yes		Go to question 13.2.
No		End questionnaire.

13.2. If yes, specify the location and number of times visited during the period			
Location	Contact	Number of visits	Month
Market			
Feed/farm store			
Farmer market			
Neighbours backyard			
Other(specify)			

Name of interviewer	
Date	

Answer refusal	99
Don't know	88
Biased or guess	55

Appendix 2

Contact Structures in the New Zealand Poultry Industry
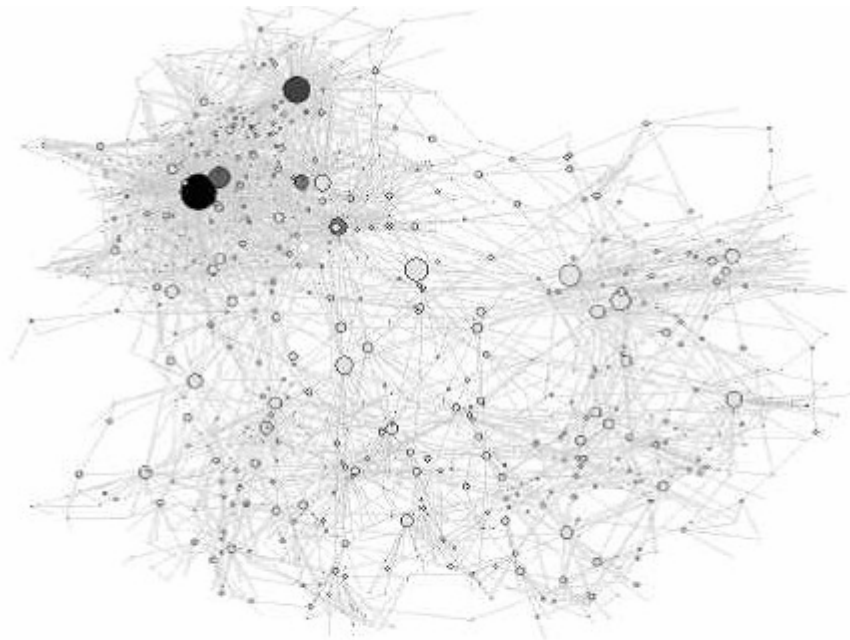
Key Contacts:

Caryl Lockhart, Epicentre, Massey University, (06) 350 5855
Natalie Gerber, Poultry association of New Zealand, (09) 520 43 00

Contact Structures in the New Zealand Poultry Industry

The objectives of this survey are to describe the extent and nature of contact structures in the intensive and semi-intensive sectors of the New Zealand poultry industry.

Why are we conducting this survey?

This survey will help us define the extent and nature of contacts that occur between people and companies that interact with your farm. Specifically we're interested in contacts made through the sale of feed, transportation of poultry and related products, regular visits made by industry personnel, and the movement of waste products such as manure, litter and dead birds.

What will this survey tell us?

Contacts are an important means by which disease syndromes can be transmitted from farm to farm. This survey will give us a better idea of the activities which pose the greatest risk of spreading a disease. This information will be used to refine and optimise surveillance aimed to protect your livelihood.

Please help

This project has been funded by Biosecurity New Zealand (within the Ministry of Agriculture and Forestry) and is endorsed by the Poultry Industry Association of New Zealand and the Egg Producers Federation. The study will only be useful if **all** producers take part and we request that you help us by sparing some of your valuable time to complete this questionnaire. This project is implemented through researchers at the EpiCentre, Massey University.

Confidentiality

All information will be treated confidentially. No individual property details will be reported to any party.

If you have any questions or concerns about completing the questionnaire or about being in this study, you may contact either:

Caryl Lockhart
Tel: (06) 350 5855
Email: c.lockhart@massey.ac.nz.

Natalie Gerber
Tel: (09) 520 43 00
Email: natalie@pianz.org.nz

Filling in this questionnaire

In this questionnaire we'd like you to think about individuals and companies that move to and from your farm throughout the year. Each section follows the same general format.

In the first part we want you to list the companies and individuals that have moved onto or off the farm over the **last 12 months**.

In the second part we want you to give us an idea of the number of movements that occurred during the **last complete month**.

In the third part, we'd like you to tell us how the **numbers of movements that occur at other times of the year compare with what happened in the last month** (using the graph or table provided).

If you're filling in this questionnaire on 15th May, the last complete month would be April. If you provided details for 10 movements that occurred in April and you estimate that there will be the same number in May, and twice as many (i.e. 20 movements) in June, July, and August and half the number (i.e. 5 movements) for the remainder of the year your graph would be filled in as follows:

	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
Number	one half	one half	one half	⊗	same	double	double	double	one half	one half	one half	one half
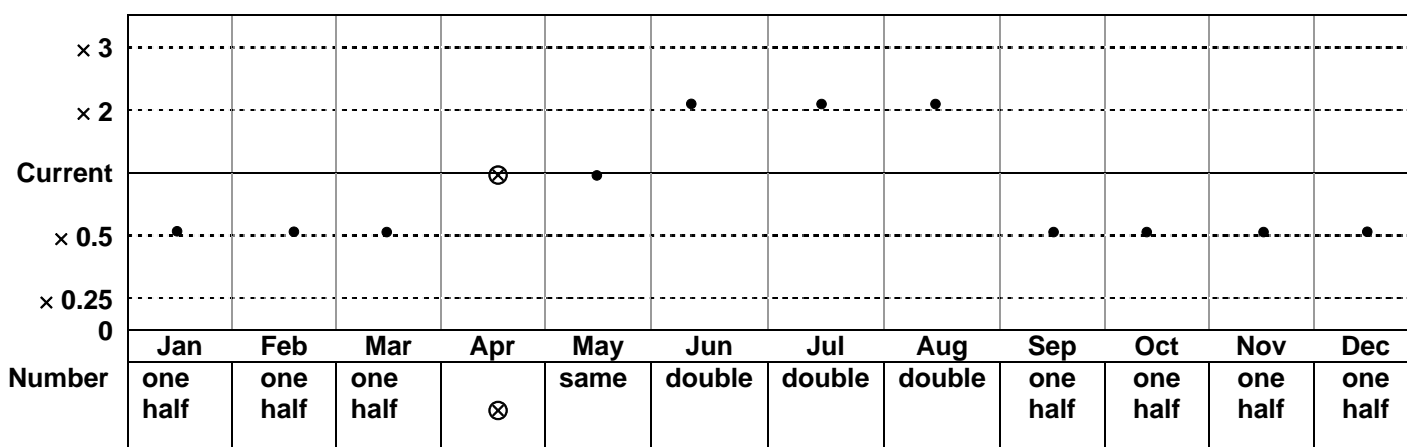
Use the ⊗ symbol to indicate the month your complete record relates to. If you are filling out the bottom part of the graph, it should be filled as above. You might opt to fill in both parts of the graph.

Please enter details for the whole year. Specify NA if a section or question is not applicable.

Returning the questionnaire

Please use the prepaid, addressed envelope provided.

2

1. ENTERPRISE AND FARM DETAILS

In this questionnaire, we use the term **farm** to refer to facilities where birds (or eggs) are kept under a common system of management. In most situations a farm will be a single physical location. Sometimes a farm may be made up of several distinct physical locations in close proximity (which we call **sites**).

1.1. Details of the person filling in this questionnaire	
Name	
Position	

1.2. Farm contact details	
Name	
Street or PO Box number	
Town	
Phone (business)	
Phone (home)	
Phone (mobile)	
Facsimile	
Email	
Parent company (if applicable) [a]	

[a] A parent company refers to the organisation that owns birds that are raised on one or more farms. Tegel Foods Limited, for example, would be referred to as a parent company.

1.3. Farm location details	Address (town or city only)
Main site (1)	
Other site (2)	
Other site (3)	
Other site (4)	
Other site (5)	

1.4. What type of farm do you run?	Number	Number 1 to 6, in order of importance(refers to the farm type that provides your largest production output)
Commercial poultry – breeder		
Commercial poultry – layer hens		
Commercial poultry – pullets		
Commercial poultry – broilers		
Commercial poultry – turkeys		
Commercial poultry – hatchery		
Commercial poultry – ducks		
Commercial free range - broilers		
Other - specify		

1.5. Indicate the number and type of birds (or eggs for hatcheries) present on the farm on the day of the survey.

Species	Approximate number	Total shed capacity
2.1. Layers		
2.2. Pullets		
2.3. Hatchery only (give fertile egg numbers)		
2.4. Broilers		
2.5. Turkeys		
2.6. Ducks		
2.7 Other (e.g. caged, pet birds, geese)		

1.6. How is this farm managed?	Tick	You may tick more than one box
Shed or barn raised		
Free range		
Caged		

4

2. TRANSPORT

In this question we are interested in knowing the companies and/or individuals that have conveyed poultry or poultry-related product (including feed, manure and dead birds) onto or off your farm.

In each case, please indicate the town or city of origin of the transporter. For example, if Company A transported poultry from your farm to a processing plant and the company's depot was in Wanganui, list Wanganui as the address of origin of the transporter.

ONTO FARM:

2.1. List the name and location details of individuals or companies that transported poultry or poultry-related product <u>ONTO</u> this farm over the last 12 months, in order of importance. Use additional lines if necessary.			
Code	**Name**	**Category**	**Origin address (town or city only)**
SRC-A			
SRC-B			
SRC-C			
SRC-D			
SRC-E			

Categories include those who transport:

(1) Feed.

(2) Hatching eggs.

(3) Day old chicks, pullets, and adult birds.

(4) Table eggs.

(5) Poultry product.

(6) Manure and litter.

(7) Dead birds.

OFF FARM:

2.2. List the name and location details of individuals or companies that transported poultry or poultry-related product <u>OFF</u> this farm over the last 12 months, in order of importance. Use additional lines if necessary.			
Code	**Name**	**Category**	**Destination address (town or city only)**
DES-A			
DES-B			
DES-C			
DES-D			
DES-E			

Categories include those who transport:

(1) Feed.

(2) Hatching eggs.

(3) Day old chicks, pullets, and adult birds.

(4) Table eggs.

(5) Poultry product.

(6) Manure and litter.

(7) Dead birds.

3. FEED

In this question we are interested in the origin of feed that is used on your farm and the destination of feed that might be sent from your farm to another location. In the majority of cases there will be a one-way flow of feed onto a farm. In some situations feed might be sold or returned to a distributor. If these cases exist, we'd like to know about them.

In each case, please indicate the town or city of origin (or destination) of the feed. For example, if you purchased feed from Company B whose depot was in Napier give Napier as the address of the feed supplier.

SOURCE:

3.1. List the name and location details of individuals or companies that feed was <u>SOURCED FROM</u> over the last 12 months, in order of importance. Use additional codes if necessary.			
Code	**Name**	**Category**	**Origin address (town or city only)**
SRC-A			
SRC-B			
SRC-C			
SRC-D			
SRC-E			

Categories include::

(1)   Milled feed.

(2)   Bagged feed.

(3)   Home mix.

(4)   Combination of bought in and home mixed feed.

(5)   Other.

DESTINATION:

3.2. List the name and location details of <u>DESTINATION</u> individuals or companies you sent feed <u>TO</u> over the last 12 months, in order of importance. Use additional codes if necessary.			
Code	**Name**	**Category**	**Destination address (town or city only)**
DES-A			
DES-B			
DES-C			
DES-D			
DES-E			

Categories include::

(1)   Milled feed.

(2)   Bagged feed.

(3)   Home mix.

(4)   Combination of bought in and home mixed feed.

(5)   Other.

3.3. Using the codes listed in Question 3.1 and 3.2 indicate the <u>SOURCE</u> and approximate quantity of feed brought onto this farm and the <u>DESTINATION</u> and approximate quantity of feed sent off this farm over the <u>LAST COMPLETE MONTH</u>.

Month	

Category	Source (e.g. purchases)			Destination (e.g. sales)		
	Code	Number of movements on	Quantity (specify units)	Code	Number of movements off	Quantity (specify units)
Milled feed						
Bagged feed						
Home mix						
Other						

3.5. In Question 3.3 you provided details of feed-related movements that occurred in the last month. Use the graph below to indicate how the number of movements that occurred at other times of the year compare with what happened in the last month.

Please indicate the relative frequency of movement events for the <u>entire</u> year.

	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
× 3												
× 2												
Current												
× 0.5												
× 0.25												
0												
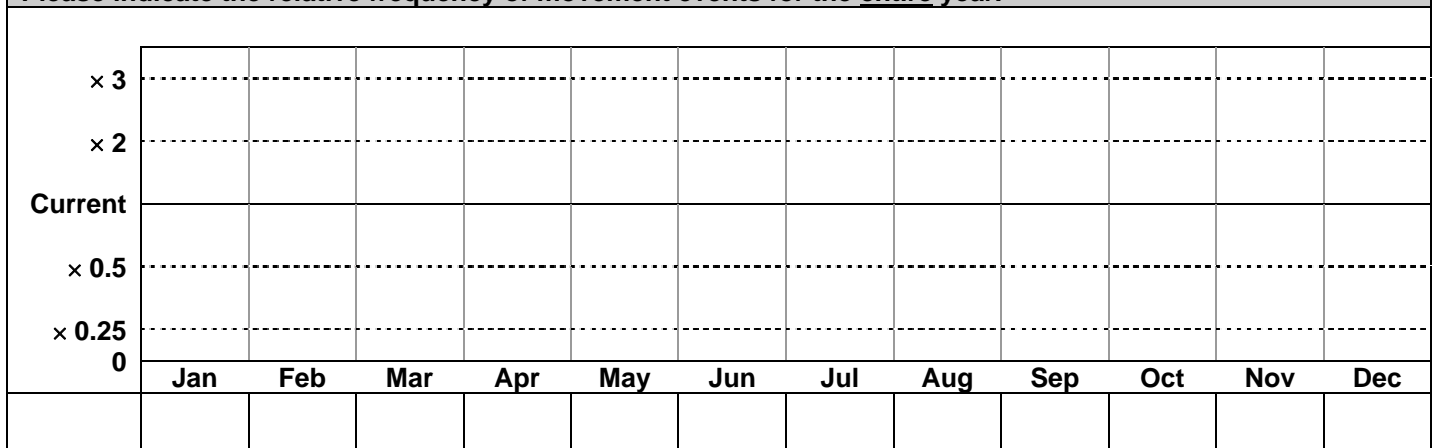
4. LIVE BIRDS AND HATCHING EGGS

In this question we are interested in the origin of live birds and/or hatching eggs that came onto your farm and the destination of live birds (including broilers for processing) and/or hatching eggs were sent from your farm to another location.

ONTO FARM:

	4.1. List the name and details of individuals or companies that you <u>SOURCED</u> live birds and/or hatching eggs <u>FROM</u> over the last 12 months, in order of importance. Use additional codes if necessary.		
Code	**Name**	**Category**	**Origin address (town or city only)**
SRC-A			
SRC-B			
SRC-C			
SRC-D			
SRC-E			

Categories include::

(1)   Hatching eggs.

(2)   Day old chicks.

(3)   Pullets.

(4)   Adult birds.

OFF FARM:

	4.2. List the name and details of <u>DESTINATION</u> individuals or companies that you sent live birds and/or hatching eggs <u>TO</u> over the last 12 months, in order of importance. Use additional codes if necessary.		
Code	**Name**	**Category**	**Destination address (town or city only)**
DES-A			
DES-B			
DES-C			
DES-D			
DES-E			

Categories include::

(1)   Hatching eggs.

(2)   Day old chicks.

(3)   Pullets.

(4)   Adult birds.

4.3. Using the codes listed in Questions 4.1 and 4.2 indicate the <u>SOURCE</u> and quantity of live birds and/or hatching eggs brought onto this farm and the <u>DESTINATION</u> and quantity of live birds and/or hatching eggs sent off this farm over the last month.

Month	

Category	Source (e.g. purchases)			Destination (e.g. sales)		
	Code	Number of movements on	Quantity (specify units)	Code	Number of movements off	Quantity (specify units)
Hatching eggs						
Day old chicks						
Pullets						
Adult birds						

4.4. In Question 4.3 you provided details of live birds and/or hatching egg movements that occurred in the last month. Use the graph below to indicate how the number of movements that occurred at other times of the year compare with what happened in the last month.

Please indicate the relative frequency of movement events for the <u>entire</u> year.

	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
× 3												
× 2												
Current												
× 0.5												
× 0.25												
0												
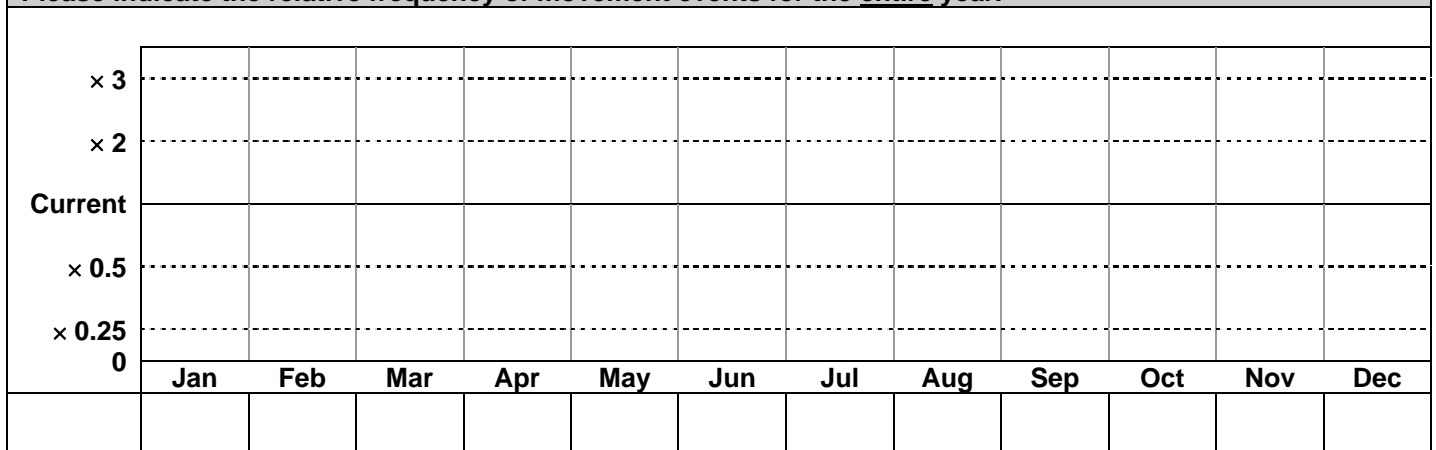
5. TABLE EGGS AND POULTRY PRODUCT

In this question we are interested in the origin of table eggs and/or poultry product (e.g. dressed chickens) that came onto your farm and the destination of table eggs and/or poultry product that was sent from your farm to another location.

ONTO FARM:

5.1. List the name and details of individuals or companies that you <u>SOURCED</u> table eggs and/or poultry product <u>FROM</u> over the last 12 months, in order of importance. Use additional codes if necessary.

Code	Name	Category	Origin address (town or city only)
SRC-A			
SRC-B			
SRC-C			
SRC-D			
SRC-E			

Categories include:

(1)   Table eggs.

(2)   Poultry product.

(3)   Feathers and/or offal.

OFF FARM:

5.2. List the name and details of <u>DESTINATION</u> individuals or companies that you sent table eggs and/or poultry product <u>TO</u> over the last 12 months, in order of importance. Use additional codes if necessary.

Code	Name	Category	Destination address (town or city only)
DES-A			
DES-B			
DES-C			
DES-D			
DES-E			

Categories include:

(1)   Table eggs.

(2)   Poultry product.

(3)   Feathers and/or offal.

5.3. Using the codes listed in Questions 5.1 and 5.2 indicate the <u>SOURCE</u> and quantity of table eggs and/or poultry product brought onto this farm and the <u>DESTINATION</u> and quantity of table eggs and/or poultry product sent off this farm over the last month.						
Month						
Category	**Source (e.g. purchases)**			**Destination (e.g. sales)**		
	Code	**Number of movements on**	**Quantity (specify units)**	**Code**	**Number of movements off**	**Quantity (specify units)**
Table eggs						
Poultry product						
Feathers and/or offal						

5.4. In Question 5.3 you provided details of table eggs and/or poultry product movements that occurred in the last month. Use the graph below to indicate how the number of movements that occurred at other times of the year compared with what happened in the last month.

Please indicate the relative frequency of movement events for the <u>entire</u> year.

	× 3	× 2	Current	× 0.5	× 0.25	0

	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
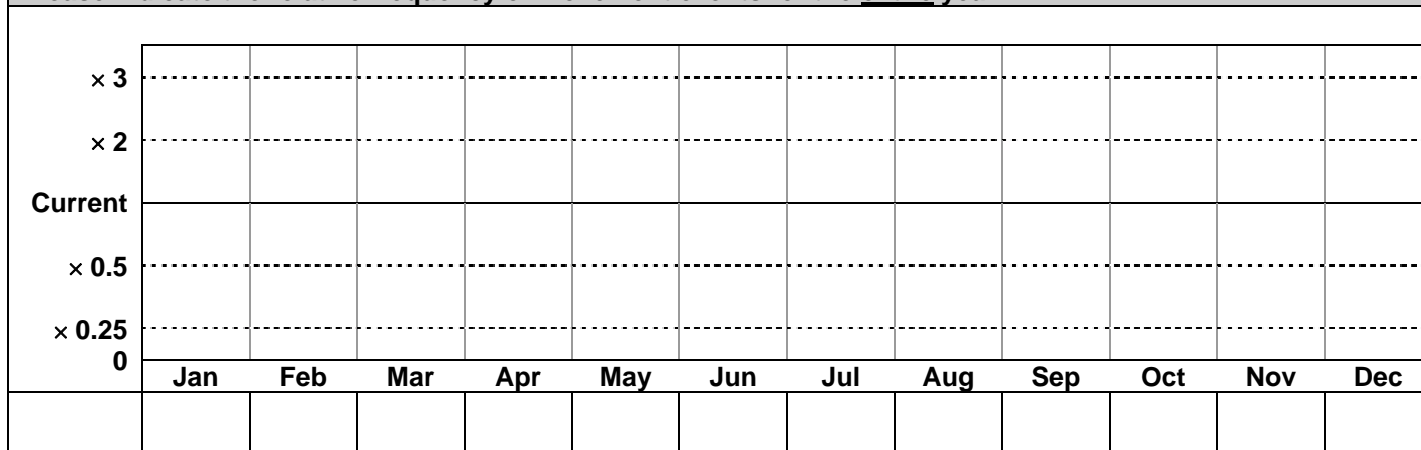
6. REGULAR MOVEMENTS OF PERSONNEL

In this question we are interested in the movement of people associated with the poultry industry onto your farm and the destination of permanent members of staff to other locations where poultry are present.

In this question we're not interested in details of every single movement, only those that occur on a regular basis (e.g. routine visits by advisors, contractors, and personnel from other premises where poultry are kept).

ONTO FARM:

Code	Name	Category	Origin address (town or city only)
6.1. List the name and details of individuals who made regular <u>ON FARM</u> visit over the last 12 months, in order of importance. Use additional codes if necessary.			
SRC-A			
SRC-B			
SRC-C			
SRC-D			
SRC-E			

Categories include:

(1) Veterinarians, advisors, industry representatives.

(2) Contractors (those having direct contact with poultry sheds or equipment (e.g. cleaning and maintenance crews).

(3) Individuals from premises where commercial poultry are kept.

(4) Individuals from premises where non-commercial poultry are kept.

OFF FARM:

Code	Name	Category	Destination address (town or city only)
6.2. List the name and details of those permanent staff members who made an <u>OFF FARM</u> visit to other locations where poultry were present over the last 3 MONTHS, in order of importance. Use additional codes if necessary.			
DES-A			
DES-B			
DES-C			
DES-D			
DES-E			

Categories include:

(1) Locations where commercial poultry are kept.

(2) Locations where non-commercial poultry are kept.

6.3. Using the codes listed in Questions 6.1 and 6.2 indicate the origin and number of times individuals associated with the poultry industry made <u>ON FARM</u> or <u>OFF FARM</u> visits over the last month.				

Month				
Category	**On farm visits**		**Off farm visits** 13	
	Code	**Approximate number on**	**Code**	**Approximate number off**
Veterinarian Advisor Industry representatives				
Contractors				
Commercial				
Non-commercial				

6.4. In Question 6.3 you provided details of personnel movements that occurred in the last month. Use the graph below to indicate how the number of movements that occurred at other times of the year compared with what happened in the last month.

Please indicate the relative frequency of movement events for the <u>entire</u> year.

	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
× 3												
× 2												
Current												
× 0.5												
× 0.25												
0												
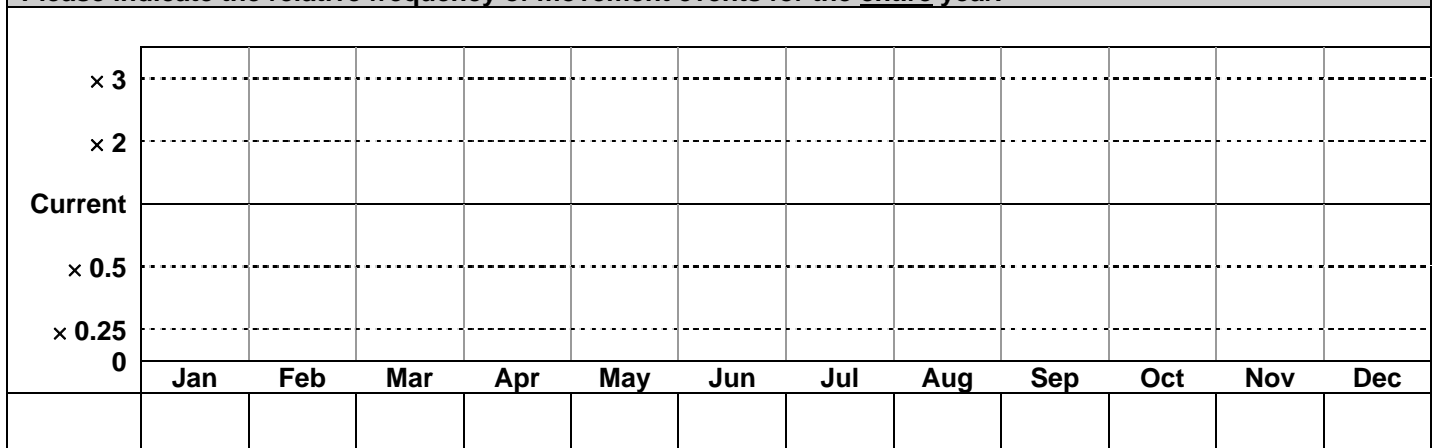
7. MANURE, LITTER, AND DEAD BIRDS

In this question we'd like to know the movement of manure, litter, and dead birds to and from your farm. In the majority of cases there will be a one-way flow of manure, litter, and dead birds off the farm. In this case leave Question 7.1 blank.

In this question we use the term "dead birds" to refer to those birds that have died on site.

ONTO FARM:

7.1. List the name and details of individuals or companies that manure, litter, or dead birds were <u>SOURCED FROM</u> over the last 12 months, in order of importance. Use additional codes if necessary.			
Code	**Name**	**Category**	**Address (town or city only)**
SRC-A			
SRC-B			
SRC-C			
SRC-D			
SRC-E			

Categories include:

(1)   Birds.

(2)   Manure and litter.

OFF FARM:

7.2. List the name and details of <u>DESTINATION</u> individuals or companies who you sent manure, litter, or dead birds <u>TO</u> over the last 12 months, in order of importance. Use additional codes if necessary.			
Code	**Name**	**Category**	**Destination address (town or city only)**
DES-A			
DES-B			
DES-C			
DES-D			
DES-E			

Categories include:

(1)   Birds.

(2)   Manure and litter.

7.3. Using the codes listed in Questions 7.1 and 7.2 indicate the SOURCE and quantity of manure, litter, or dead birds brought onto this farm and the DESTINATION and quantity of manure, litter, or dead birds sent off this farm over the last month.

Month	

Category	Source (e.g. purchases)			Destination (e.g. sales) ¹⁵		
	Code	Number of movements on	Quantity (specify units)	Code	Number of movements off	Quantity (specify units)
Birds						
Manure and litter						

7.4. In Question 7.3 you provided details of manure, litter, and dead bird movements that occurred in the last month. Use the graph below to indicate how the number of movements that occurred at other times of the year compared with what happened in the last month.

Please indicate the relative frequency of movement events for the entire year.

	× 3	× 2	Current	× 0.5	× 0.25	0

Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec