Project no. 310806

Providing a new generation of methodologies and tools for cost-effective risk-based animal health surveillance systems for the benefit of livestock producers, decision makers and consumers

KBBE
Collaborative Project
FP7-KBBE-2012-6

http://www.fp7-risksur.eu

Deliverable No. D4.14

Systematic review of surveillance systems for endemic disease, including information on the extent of multi-objective surveillance activities

WP 4 – Prevalence estimation and case detection for endemic disease

Authors: Arianna Comin (SVA)
Fernanda Dórea (SVA)
Thomas Rosendal (SVA)
Timothee Vergne (RVC)
Jenny Frössling (SVA)
Maria Nöremark (SVA)
Helene Wahlström (SVA)
Ann Lindberg (SVA)

Lead participant: SVA

Date: 20 September 2013
Type: Deliverable

TABLE OF CONTENTS

1 Abstract

The planning, implementation and evaluation of actions against animal diseases in general, and against diseases continuously present in the population in particular, are important to reduce the impact of diseases on animal production and welfare, and on public health. In order to encourage the adoption of currently available surveillance methodologies, and guide the further development of these tools, a literature review was performed. The review targeted publications describing existing approaches for surveillance of endemic diseases. After initial retrieval of 2163 articles, and two rounds of screening, 69 papers were included in the review. These were grouped into five major groups: methodological papers (7 publications); validation of new data sources for surveillance (4); surveillance design (23), critical evaluations of implemented surveillance (13), and descriptions of surveillance results with focus on disease frequency estimates (22).

Methodological papers addressed mainly risk-based surveillance approaches (6 out of 7), suggesting new methods to classify subpopulations according to risk, methods for risk-based sampling design, or the challenge of population inference from risk-based surveillance data. Data validation publications aimed at presenting alternative data sources which can provide surveillance information with lower cost, greater completeness or faster availability.

Publications on surveillance design brought up the discussion about the need for outcome-based surveillance regulations, and harmonisation of activities among countries. This issue was also extensively explored in the publications classified in the group “surveillance evaluation”.

Another common theme on surveillance design was the need to increase participation of stakeholders on surveillance, through disease monitoring networks or participatory epidemiology methods. Sampling designs for wildlife disease surveillance and the challenge of understanding vector-borne disease transmission were other reviewed themes.

Publications providing disease frequency estimations were centred on two main goals: development of methods for population inference from case detection data, especially in the case of imperfect data collection; or methods to correct apparent prevalence from field investigations in order to account for test imperfections, time from evidence, and other available information such as expert opinion.

A total of 30 (out of 69) publications dealt with risk-based surveillance strategies. The issue was reflected in different ways: addressing the design and incorporation of risk-based strategies into existing surveillance; presentation of analytical methods that allow correction of bias in data from risk-based sampling, which can then be used for epidemiological inference; and evaluating the use of new methods to define risk, such as animal movement evaluated through network analysis, biosecurity, and production type.

Considering the number of different methodologies highlighted by this review, there is a clear need for guidance to establish which of those methods are most appropriate for which diseases, as well as a need to develop tools that can help surveillance designers to reduce the gap between theory and practice. These challenges can be addressed in the scope of RISKSUR.

2 Introduction

Disease *surveillance* is defined as an active system to describe health hazard occurrence involving some kind of directed action (interventions) against the occurrence of diseases or infection, which may be triggered when a defined threshold of prevalence or incidence is reached (Salman, 2003). *Monitoring* also describes health hazard occurrence, however without any predefined risk mitigation plans.

This document focuses on surveillance aimed at *prevalence estimation and case detection for endemic diseases/infections*. These terms have been used according to the following definitions:

> *"Surveillance: The systematic, continuous or repeated, measurement, collection, collation, analysis, interpretation and timely dissemination of animal health and welfare related data from defined populations, essential for describing health hazard occurrence and to contribute to the planning, implementation, and evaluation of risk mitigation measure"* (Hoinville, 2012; Hoinville et al., 2013).
>
> *"Endemic diseases: diseases known to be present in the population"* (Hoinville et al., 2009).

It is worth noting that the most recent terminology review for surveillance, quoted above, has replaced the terms "disease occurrence" and "disease control measures" with the terms "health hazard occurrence" and "risk mitigation measures", respectively, in comparison to the definition adopted in an earlier workshop (Hoinville et al., 2009). In the present document the term "disease" is used in a general sense to mean both disease and infection, irrespective of clinical signs. Moreover, the health hazard discussed can sometimes refer to general clinical syndromes, such as "respiratory diseases", in which case the term disease does not refer to one specific pathogenic process.

2.1 Why is surveillance for endemic diseases important

Animal diseases can threaten humans by direct transmission through contact or as foodborne zoonoses. They can also affect human populations indirectly through the reduction in food supply, impediment of trade, and other forms of economical loss associated with the spread of diseases in animal populations (Hoinville et al., 2013; Kellar, 2012). Estimated productivity losses due to endemic diseases have been reported to reach 17% in the United Kingdom and up to 50% in developing countries (Flint and Woolliams, n.d.). Moreover, the value of animal populations is not restricted to animal products and by-products, but also related to the use of animals as pets, for sports, work or research (Häsler et al., 2011). Diseases permanently present in a country or region reduce the gain derived from resources committed to animals fulfilling all these roles, in additional to animal production (Häsler et al., 2011). Surveillance against animal diseases, therefore, aims at protecting the health of the animal populations, but also at protecting public health (Hoinville et al., 2013).

The planning, implementation and evaluation of actions against animal diseases in general, and against diseases continuously present in the population in particular, are therefore important to "reduce the impact of diseases on animal production and welfare and on public health" and "ensure that confidence in the health status of animals moving between countries is maintained and [...] trade barriers are justified" (Hoinville et al., 2013). The adoption of such actions necessarily depends on information regarding disease distribution in the population (Christensen, 2001; Hoinville et al., 2013; Häsler and Howe, 2012), that is, disease frequency estimation (measurement of the level of disease presence/force of infection) and case detection (identifying individual cases of a specified condition in order to implement some response).

These two surveillance goals – disease frequency estimation and case detection – can be expanded into the following surveillance purposes: describe the baseline level, distribution and impact of

specified health hazards; describe changes in the health of the population, including changes in the occurrence of health indicators or specified diseases; describe changes that may threaten the health of the population, such as changes in the population structure or its exposure to risk factors; and detect cases to facilitate control (Hoinville, 2012; Hoinville et al., 2013).

In the context of surveillance as defined above, it is implied that the continuous collection of data regarding the health status of the animal population is part of a strategy to reduce the negative effects of diseases (Hoinville et al., 2013). The actions that endemic diseases trigger can be aimed at control, as so defined "the efforts directed toward reducing the frequency of existing disease to levels biologically and/or economically justifiable or otherwise of little consequence", or when possible, aimed at eradication, which "describes the efforts to eliminate selected organisms from a defined population" (Christensen, 2001).

Discussions can arise regarding whether it is worth carrying out surveillance for control and/or eradication of endemic low threat hazards (low impact), especially those non-zoonotic and which do not have an acute impact on animal production (Hoinville et al., 2009). However, surveillance information is important in guiding disease prioritisation and the decisions regarding which hazards to target, and it can also inform the adoption of measures that maximize the benefits of resources invested in surveillance (Drewe et al., 2012). More importantly, multi-objective surveillance programs can be implemented in order to allow health improvement through the control of several hazards. Two main reasons justify the surveillance of endemic diseases, even in low threat settings. First, it can identify changes in the incidence of such hazard. When surveillance is in place, major changes in the incidence can be detected and trigger interventions to mitigate the risks associated with the hazard. Second, it has been pointed out that "surveillance for endemic disease provides a baseline against which new (emerging) diseases may be detected" (Hoinville et al., 2009).

The issues regarding early detection of diseases has gained much attention in the last decade, especially due to the emergence of new diseases, increase in trade and movement of people, and bioterrorism threats (Dórea et al., 2011). Surveillance aimed at case finding is usually directed at areas where disease is believed to have low prevalence or be eradicated, with the aim of detecting and responding to cases as early as possible. It can therefore also be considered as "surveillance for early disease detection". However the latter term has been used more commonly to express measures to protect against the incursion of new diseases (emerging or not previously present in a territory). Continuous surveillance for endemic hazards may provide relevant information regarding the structure and health of animal populations, enabling the design of surveillance for emerging diseases and disease freedom demonstration. The information collected through surveillance activities developed in response to an endemic threat will also help to inform the allocation of resources among all these different strategies of disease control (Häsler et al., 2011).

2.2 Shortcoming of conventional methods

The environment in which surveillance is applied is subject to constant changes in the patterns of animal populations and their management, emerging diseases, and increasing international trade. Technology and methodologies evolve at fast pace, and the sources of data available continue to increase. Surveillance methods must comply with these continuous changes, striving towards measures that are "affordable, sustainable, effective and adapted" (Doherr et al., 2012).

During a workshop organized during the International Symposium on Veterinary Epidemiology and Economics in Durban, South Africa, in 2009, the development and application of methods for effective surveillance (in livestock populations) were discussed (Hoinville et al., 2009). Areas in which the efficiency of current surveillance systems still could improve were highlighted, including: "the location of data collection, the sampling strategy, combining surveillance for multiple pathogens, using multiple

surveillance strands[1] for specific diseases, and using this to validate cheaper options and the use of social network analysis" (Hoinville et al., 2009).

Conventional surveillance methods explore only a limited amount of data sources (Doherr et al., 2012), which most of the time can only be accessed late in the disease continuum (Dórea et al., 2011). Even routinely collected data, such as abattoir condemnation records, which have high area coverage, are still largely underused (Doherr et al., 2012). Much of the analytical methods available to inform epidemiological decisions assume the availability of information derived from active collection, conducted scientifically to guarantee representative coverage of the population (Kellar, 2012). However this active information gathering is expensive (Kellar, 2012), and methods are needed in order to make use of the much available "dirty data" (Hoinville et al., 2009).

The improvement in data access needs to be accompanied by an improvement in the analytical methods and incorporation of new technologies (Dórea et al., 2011; Kellar, 2012). Current analytical challenges include for instance the integration of multiple data sources, an issue that has been addressed for surveillance components aiming at disease freedom demonstration (Martin et al., 2007), but remains underexplored for ongoing surveillance of endemic diseases. Combining multiple data sources is particularly challenging when the surveillance components are designed using different strategies, such as risk-based or even non-probabilistic sampling (Stärk et al., 2006).

Technical developments need to be incorporated into practical tools in order to be made accessible to surveillance designers. In the case of risk-based surveillance for instance, the identification of subpopulations needs to be supported by tools that allow accurate and quick assessment of epidemiological parameters that contribute to the risk classification (Cannon, 2009). Moreover, these methods still have limited, if any, integration into surveillance systems aimed at disease frequency estimation. While risk-based sampling has been gaining popularity in the design of surveys to demonstrate freedom of disease, methods to allow population inference from data collected through risk-based surveillance, though developed (Wells et al., 2009; Williams et al., 2009a), have not yet been acknowledged and integrated in surveillance planning. Surveillance for endemic diseases aimed at case detection, on the other hand, lacks tools and standardised measures for objective performance comparison.

Faced with a plethora of available methods, surveillance designers usually lack tools that allow them to choose the best methods for specific scenarios. Due maybe to the lack of standard methods to evaluate surveillance systems (Drewe et al., 2012), or the costs associated with this task, documentation on the evaluation of animal surveillance systems are lacking, especially explicit economic evaluations (Drewe et al., 2012). Surveillance components are expected to vary in sensitivity and population coverage, but surveillance designers often need to make an economic decision based on the cost per case found. The lack of tools to achieve such an assessment, coupled with the gap between scientists and decision makers, results in the latter lacking clarification regarding the most appropriate surveillance methods for different disease types (Hoinville et al., 2009).

The need to develop quality measures is also essential to assure comparability of surveillance results among countries. Transparent and repeatable processes to evaluate and report surveillance results are needed in order to achieve output-based surveillance standards (Cameron, 2012). In the case of endemic diseases, for instance, an assessment of system sensitivity would allow comparability of the number of cases or prevalence estimates reported by different countries.

[1] The most recent terminology review uses the term "surveillance component" (Hoinville, 2012).

2.3 Brief summary of recent developments of new methods and how they approach these challenges

Considering the two goals of endemic disease surveillance outlined previously – disease frequency estimation and case detection – the different methodological improvements will necessarily aim at: increasing the accuracy of estimation or reduce the cost to achieve the target accuracy, in the case of frequency estimation; and increase case detection capacity (sensitivity and coverage of case detection) or reduce the cost to achieve the target capacity when the goal is case detection. These goals have partly been addressed with the use of new and cheaper data sources, use of mathematical simulations to replace the need for data collection, and prioritisation of strategies based on risk.

2.3.1 Validation of new data sources

The focus on early disease detection (which as previously noted is related to case detection) has stimulated the search for new data sources, which can contain signatures of disease spread in a population even before diagnosis (Dórea et al., 2011). This type of surveillance has been coined ***syndromic surveillance*** due to its initial focus on pre-diagnostic data which cannot be monitored for a specific disease, but can be grouped into clinical syndromes. The development of analytical methods that allow automated, real or near-real time monitoring of a data stream has ultimately lead to the exploitation of many other sources of data which were under-explored earlier, such as mortality data (Perrin et al., 2012) and abattoir data (Dupuy et al., 2013b).The continued monitoring of these data streams has been demonstrated useful also for the surveillance of endemic diseases (Dórea et al., 2011).

Participatory epidemiology is used for "harvesting qualitative epidemiological intelligence contained within community observations, existing veterinary knowledge and traditional oral history" (Ali et al., 2006). Methods of participatory epidemiology are therefore also a new form of data collection, which allows surveillance planning to incorporate the field knowledge of farmers and other animal stakeholders.

2.3.2 Risk-based surveillance

Risk-based surveillance uses knowledge concerning the animal population and the disease dynamics in order to allocate resources effectively, increasing the efficacy of surveillance methods. By concentrating higher efforts in the population strata subjected to higher risk, or allocating resources according to the risk mitigation potential of different measures, risk-based surveillance is expected to increase the benefit-cost ratio of resources applied to animal health surveillance or risk mitigation (Stärk et al., 2006). The purposeful targeting of specific population strata, however, creates a challenge to the use of epidemiological information collected from the population, and to analyze performance (Willeberg et al., 2012).

2.4 Introduction of the project aims and aim of the review

The introduction outlined above shows how recent methodological advances have increased the number of data sources that can be used for surveillance, improved the analytical methods that can be applied to those data, and ultimately improved the quantity and quality of information that can be available for decision in animal surveillance. RISKSUR is a project involving 12 partners from 10 European countries, which objective is well summarized by the project title "Providing a new generation of methodologies and tools for cost-effective risk-based animal health surveillance systems for the benefit of livestock producers, decision makers and consumers". In other words, the project aims at incorporating available, novel scientific methods into frameworks and integrated tools that allow the design and implementation of economically optimized animal health surveillance systems.

The main surveillance objectives covered by the scope of the project are: 1) early detection of animal disease, 2) demonstration of freedom from animal disease, and 3) determination of disease frequency and detection of cases of endemic animal disease.

The aim of this systematic review is to identify and examine existing frameworks for surveillance of ***endemic diseases***, with particular emphasis on surveillance designs and/or methods (either operational or statistical) addressed to case detection or frequency (prevalence and/or incidence) estimation.

3 Material and methods

3.1 Literature sources and search strategy

Two sources were searched on 21st January 2013: CabAbstract and Scopus. These two databases cover around 91% of journals related to veterinary topics (Grindlay et al., 2012). A list of keywords was drafted and conveniently combined into a Boolean query to identify the topics of this review, namely: *animal disease surveillance*, *endemic diseases,* and *case finding*/*prevalence estimates* (Table 1).

Table 1. *Boolean query applied to identify the topics of the present review. Asterisks represent wildcards (searches for any word that includes the stem presented).*

Topic	Search terms
Animal disease surveillance	surveillance OR monitor* AND animal* OR livestock OR veterinar* OR fish* OR wildlife OR "food system*" OR herd* OR farm* OR cattle OR cow* OR bovine OR ruminant* OR pig* OR porcine OR swine OR sheep OR goat* OR poultry OR bird* OR avian OR horse OR equine OR cat* OR dog* AND disease* OR health OR infection* OR outbreak
	AND
Endemic diseases	endemic OR enzootic
	AND
Case finding or frequency estimates	"case detection" OR "case finding" OR eradicat* OR (estimat* AND (prevalence OR incidence))

These terms were searched for in the title and abstract. The use of wildcards (*) ensured that articles containing any variation of each of the search terms were identified. The literature search was restricted to articles written in English (for reviewing convenience) and published in the last 20 years (i.e. 1993-2013).

3.2 Definitions

In this report, as for the RISKSUR project in general, the terminology adopted was that defined in the report of a workshop held to discuss the terminology used in animal health surveillance with the aim of standardizing the information between research groups, stakeholders and decision-makers (Hoinville, 2012; Hoinville et al., 2013).

Threat: the hazard or infectious disease which can potentially affect a susceptible population and spread between individuals and herds. Depending on the spread of the hazard along populations, the health and economic consequences are variable.

Endemic disease: a disease that is known to be present in the population of interest.

Surveillance: the systematic (continuous or repeated) measurement, collection, collation, analysis, interpretation and timely dissemination of animal health and welfare related data from defined populations, essential for describing health hazard occurrence and to contribute to the planning, implementation, and evaluation of risk mitigation measures.

Active (proactive) surveillance: Investigator-initiated collection of animal health related data through actions scheduled in advance using a defined protocol. Decisions about whether information is collected, and what information should be collected from which animals is made by the investigator.

Passive (reactive) surveillance: Observer-initiated provision of animal health related data (e.g. voluntary notification of suspect disease) or the use of existing data for surveillance. Decisions about whether information is provided, and what information is provided from which animals is made by the data provider.

Risk-based surveillance: use of information about the probability of occurrence and the magnitude of the biological and/or economic consequence of health hazards to plan, design or interpret the results obtained from surveillance systems. Risk-based surveillance can include one or several of the following four approaches:

- Risk-based prioritisation: determining which hazards should be selected for surveillance based on information about the probability of their occurrence and the extent of biologic and/or economic consequence of their occurrence.
- Risk-based requirement: use of prior or additional information about the probability of hazard occurrence to revise the surveillance intensity required to achieve the stated surveillance purpose.
- Risk-based sampling: designing a sampling strategy to reduce the cost or enhance the accuracy of surveillance by preferentially sampling strata (e.g. age groups or geographical areas) within the target population that are more likely to be exposed, affected, detected, become affected, transmit infection or cause other consequences (e.g. large economic losses or trade restrictions).
- Risk-based analysis: use of prior or additional information about the probability of hazard occurrence, including contextual information and prior likelihood of disease, in the analysis of surveillance data to revise conclusions about disease status.

3.3 Study selection and data extraction

After application of the query described in Table 1, a list of articles was outlined. Repeated items and items not published in SCI[2] journals were removed. From the remaining, 100 papers were randomly selected and their titles and abstracts were read individually by two reviewers, who selected/discarded them applying a list of primary exclusion criteria. The **primary exclusion criteria were**:

- The paper is not related to surveillance programs;
- The paper reports results of surveillance without description of surveillance methods;
- The paper presents case reports/outbreak investigations;
- The paper presents experimental infections;
- The paper presents the results of field surveys not based on a systematic data collection, or a single study of prevalence estimation;
- The paper is focused on diseases that are not endemic in the study area;
- The paper is focused on surveillance of human diseases exclusively;
- The paper is focused on the evaluations of diagnostic tests/methods;
- The paper is focused on intervention measures rather than on surveillance (for instance assessment of the impact of vaccination strategy);
- The paper is focused on surveillance systems that do not aim at detecting cases or estimating frequency of endemic diseases;
- The paper describes a pilot or an evaluation of a surveillance system but without fully describing surveillance methods;

[2] Science Citation Information, available at http://www.sci-thomsonreuters.org/.

- The paper is focused on the evaluations of vaccine efficacy;
- The paper is focused on the molecular characterizations of pathogens;
- The paper is a review of an animal disease;
- The paper is a pure theoretical study, or focuses on statistical methods or tools development without clear link to surveillance application;
- The paper presents a risk analysis.

The agreement between the two reviewers was then assessed by computing the Cohen's Kappa coefficient; the main discrepancies were discussed in order to improve the agreement until it reached at least 80%. After that, the two reviewers screened individually half of the remaining papers each, deciding whether to include them or not in the review. The full-text version of all selected papers was downloaded, either via internet or asking the corresponding authors, and the secondary exclusion criteria applied. The secondary screening step was conducted in parallel by three reviewers, and the articles finally included in the review were those deemed worth of inclusion by at least two of the three of them. The **secondary exclusion criteria** were:

- Unavailability of full-text version;
- The paper provides insufficient information to allow the evaluation of described methods;
- The paper does not describe any surveillance design/methods;
- The paper presents a primary exclusion criterion that was not apparent from reading the titles and abstracts only.

Articles were included in this review if they presented a comprehensive description of the surveillance design or the method to estimate presence/prevalence of endemic diseases.

The list of variables to be extracted from each paper was agreed in close collaboration with the teams responsible for WP 1, 2 and 4. Data extracted from the selected articles included: surveillance system evaluated, location, threat discussed, disease status, species involved, data collected/analysed, collection method, measure of disease occurrence, analysis performed, surveillance evaluation method and eventual improvements proposed. A full list of the variables extracted is provided in Annex II.

4 Results

4.1 General features of the papers included in the review

The primary search returned a total of 3099 items. Removal of duplicates and articles not published in SCI journals (such as books or reports) resulted in the selection of 2163 articles for screening. The application of the primary exclusion criteria resulted in 354 papers for retrieval of full-text. The process is detailed in Figure 1. Table 2 lists a summary of the screening process based on full-text retrieval and evaluation, which resulted in 69 articles being included in the review. As shown in Figure 1, the 69 articles selected were divided into five main groups according to the goal of the study: presentation of a new methodology for surveillance design or analysis of results, validation of a data generation process which could aid surveillance, surveillance design description, critical evaluation of a surveillance system or its components, and lastly disease frequency estimation based on the results of a surveillance activity. These groups are discussed in details further below.

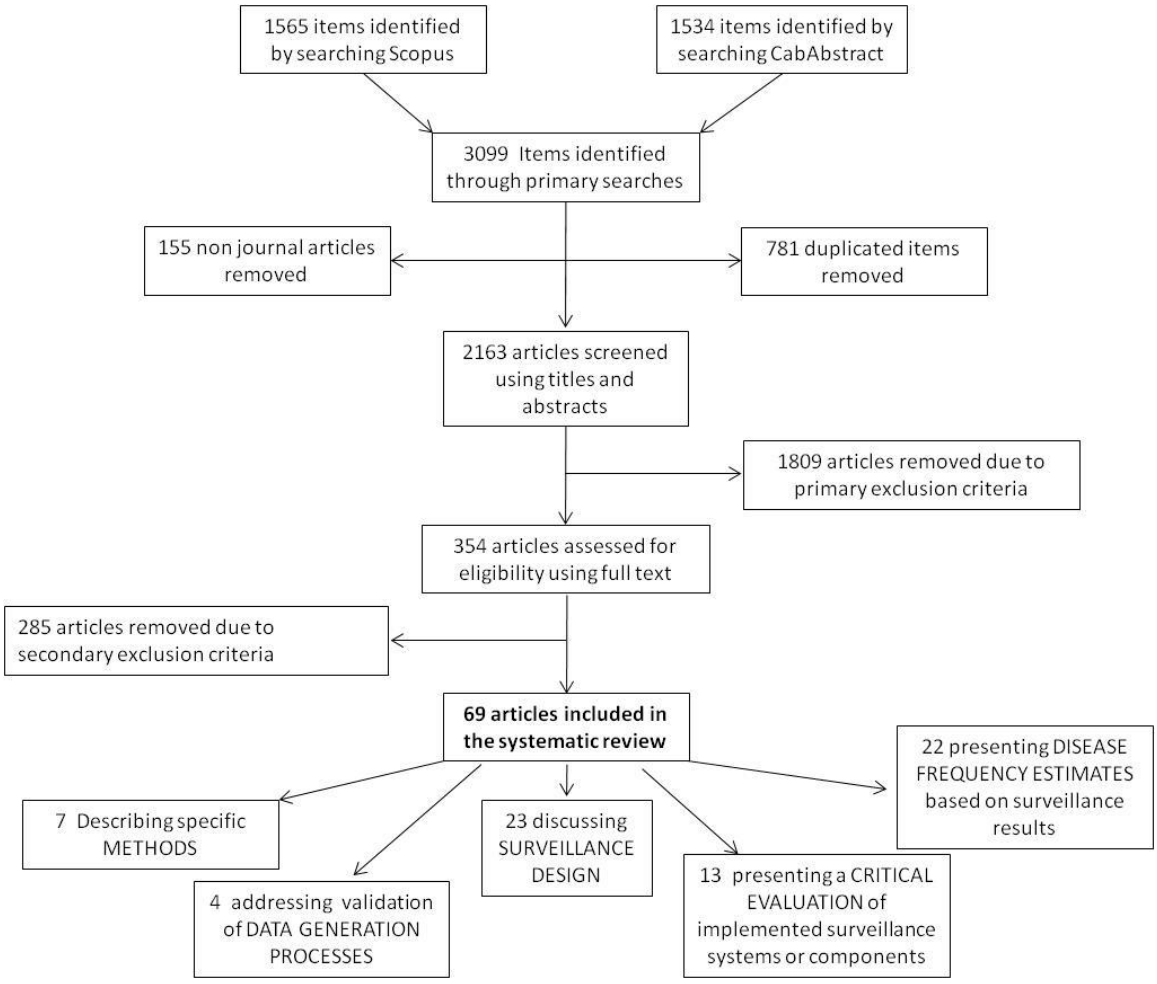

***Figure 1**. Flow chart documenting the process of literature retrieval and screening, in order to perform the systematic review of surveillance systems for case detection or prevalence estimation of endemic diseases.*

Table 2. *Summarised reasons for exclusion in the secondary screening.*

Reason	Frequency
Non-availability of full-text	50
Field surveys not based on a systematic data collection	45
Insufficient information provided to allow characterization of surveillance methods	38
Diseases not endemic in the study area	23
Risk analysis/ risk factors assessments	17
Classified as a purely theoretical study	17
Evaluations of diagnostic tests/methods	13
Reviews of animal diseases	13
Characterization of pathogens or disease study	10
Not focused on animal health (human health)	11
Only reporting the results of surveillance without description of surveillance methods	14
Focus on intervention measures rather than surveillance	9
Not related to surveillance programs	6
Single study of prevalence estimation	6
Focus on statistical methods or tools development without clear link to surveillance application	5
Case reports/outbreak investigations	3
Evaluation study which did not fully describe surveillance methods	3
Pilot studies	2

All selected articles were further classified regarding the application of risk-based surveillance strategies. Figure 2 summarizes the number of articles selected by year of publication, detailing the classification regarding the use of risk-based methods. Table 3 presents all the 69 selected publications, according to their primary purpose and application of risk-based methods.

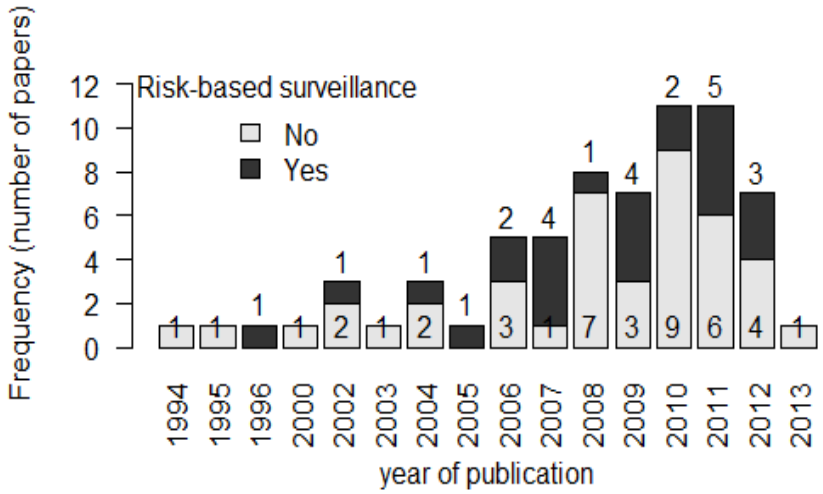

Figure 2*. Number. of publications by year (total = 69), stratified by application of risk-based methods.*

Table 3. *Publications selected for the review by primary purpose and application of risk-based methods.*

Primary purpose	Not risk-based		Risk-based		Total
	No.	References	No.	References	
Methodological articles					
	1	(Christensen, 1996)	6	(Frössling et al., 2012; Prattley et al., 2007; Wells et al., 2009; Willeberg et al., 2012; Williams et al., 2009a, 2009b)	7
Validate a data generation process					
	4	(Bartlett et al., 2010; Gulliksen et al., 2009; Holt et al., 2011; Smith et al., 2011)	0	-	4
Surveillance design					
For disease frequency estimation	4	(Ali et al., 2006; Christensen et al., 1994; Cotilla et al., 2010; Driotl et al., 2011)	3	(EFSA, 2011, 2009a, 2009b)	7
For case detection	11	(Allworth and Kennedy, 2000; Azhar et al., 2010; Bustamante and Lord, 2010; Carver et al., 2010; Chazel et al., 2010; Diefenbach et al., 2004; Kaneene et al., 2006; Lee et al., 2009; Mulatti et al., 2012; Nusser et al., 2008; Presi and Heim, 2010)	5	(Alban et al., 2011; Alexandrovl et al., 2011; de Koeijer et al., 2002; Radunz, 2006; Walsh and Miller, 2010)	16
Evaluation of surveillance (all focused on case detection)					
	5	(Kluiters et al., 2008; Martinez et al., 2008; Nielsen and Rattenborg, 2011; Pearce et al., 2008; Warnick et al., 2006)	8	(Del Rio Vilas et al., 2007; Giovannini et al., 2004; Gonzales et al., 2010; Lynn et al., 2007; Sala and Ru, 2009; Sala et al., 2009; Walker et al., 2012; Willeberg et al., 2011)	13
Disease frequency estimates					
From case detection surveillance	7	(Ebel et al., 2008; Enøe et al., 2003; Ersbøll and Nielsen, 2011; Gonzales-Barron et al., 2008; Mweu et al., 2012; Nielsen et al., 2011; Sergeant and Baldock, 2002)	8	(Greineri et al., 2011; Gubbins, 2008; Häusermann et al., 2010; Sugiura, 2006; Supervie and Costagliola, 2007; Supervie and Ostagliola, 2004; Vergne et al., 2012a, 2012b)	15
From prevalence investigations	7	(Elbers et al., 1995; Lombard et al., 2013; Miró et al., 2007; O'Brien et al., 2002, 2008, 2004; Santman-Berends et al., 2010)	0	-	7
Total	39		30		69

The 69 selected articles dealt with 32 different threats: 26 specific infectious diseases (12 viral, 9 bacterial, 3 prionic and 2 parasitic) and 6 generic disease conditions (Table 4). Two articles investigated two different diseases at the same time (Frössling et al., 2012; Häusermann et al., 2010) whereas the others considered just one threat. Among specific threats, 12/26 (46.2%) were caused by zoonotic agents.

Table 4. *Threats investigated in the selected articles*

Threat	Frequency	Zoonosis	References
Bovine Spongiform Encephalitis	11	YES	(de Koeijer et al., 2002; Giovannini et al., 2005; Greineri et al., 2011; Häusermann et al., 2010; Prattley et al., 2007; Sala and Ru, 2009; Sala et al., 2009; Sugiura, 2006; Supervie and Costagliola, 2007; Supervie and Ostagliola, 2004; Willeberg et al., 2011)
Salmonella	7	YES	(Ersbøll and Nielsen, 2011; Gonzales-Barron et al., 2008; Nielsen and Rattenborg, 2011; Nielsen et al., 2011; Smith et al., 2011; Warnick et al., 2006; Willeberg et al., 2012)
Scrapie	6	NO	(Del Rio Vilas et al., 2007; Gubbins, 2008; Häusermann et al., 2010; Lynn et al., 2007; Vergne et al., 2012a; Williams et al., 2009b)
Bovine Tuberculosis	5	YES	(Kaneene et al., 2006; O'Brien et al., 2002, 2008, 2004; Radunz, 2006)
Avian Influenza	4	YES	(Azhar et al., 2010; Gonzales et al., 2010; Martinez et al., 2008; Walker et al., 2012)
Paratuberculosis	4	NO	(Allworth and Kennedy, 2000; Lombard et al., 2013; Pearce et al., 2008; Sergeant and Baldock, 2002)
Bluetongue	3	NO	(EFSA, 2011; Kluiters et al., 2008; Santman-Berends et al., 2010)
Bovine brucellosis	2	YES	(Ebel et al., 2008; Lee et al., 2009)
Chronic Wasting Disease	2	NO	(Diefenbach et al., 2004; Walsh and Miller, 2010)
Arboviruses	1	YES	(Bustamante and Lord, 2010)
Aujeszky's disease	1	NO	(Elbers et al., 2000)
Bovine Calicivirus	1	NO	(Frössling et al., 2012)
Bovine Respiratory Syncitial Virus	1	NO	(Frössling et al., 2012)
Bovine Viral Diarrhea	1	NO	(Presi and Heim, 2010)
Classical Swine Fever	1	NO	(Alexandrovl et al., 2011)
Foot and Mouth Disease	1	NO	(Vergne et al., 2012b)
Hantaviruses	1	YES	(Carver et al., 2010)
Heartwater infection	1	NO	(Driotl et al., 2011)
Leishmaniosis	1	YES	(Miró et al., 2007)
Mycoplasmoses	1	NO	(Chazel et al., 2010)
Rabbit hemorrhagic disease	1	NO	(Cotilla et al., 2010)
Streptococcus agalactie	1	NO	(Mweu et al., 2012)
Trichinella	1	YES	(Alban et al., 2011)
West Nile Virus	1	YES	(Mulatti et al., 2012)
Wildlife diseases (generic)	1	-	(Nusser et al., 2008)
VTEC O157	1	YES	(EFSA, 2009a)
Yersinia enterocolitica	1	YES	(EFSA, 2009b)
Transmissible animal diseases (generic)	3	-	(Ali et al., 2006; Wells et al., 2009; Williams et al., 2009a)
Pig diseases (generic)	2	-	(Christensen, 1996; Christensen et al., 1994)
Pig respiratory diseases (generic)	2	-	(Enøe et al., 2003; Holt et al., 2011)
Calf diseases (generic)	1	-	(Gulliksen et al., 2009)
Dog and cat diseases (generic)	1	-	(Bartlett et al., 2010)

Cattle were the most frequent subject of the animal surveillance systems included in the present review, followed by small ruminants and pigs (Figure 6). Nine systems (13.4%) monitored more than one species at the same time: seven due to the inclusion of multiple ruminant species (Chazel et al., 2010; Driotl et al., 2011; EFSA, 2011, 2009a; Häusermann et al., 2010; Kaneene et al., 2006; Kluiters

et al., 2008), one considering multiple West Nile Virus hosts (Mulatti et al., 2012), and one including pigs, horses and wild boars (Alban et al., 2011). The remaining 58 (86.6%) focused on one species only.

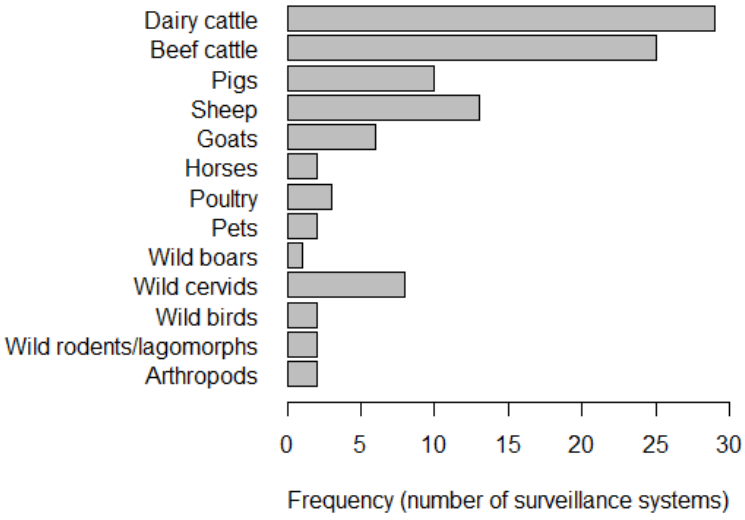

Figure 3. *Species that were targeted by the surveillances presented in the papers included in the review.*

The papers included in this review referred to surveillance systems located unevenly across the globe and dominated by Europe and the United States (Table 5). One article compared two surveillance systems in two countries (Sala and Ru, 2009) and 5 papers did not refer to any particular country.

Table 5. *Locations where the surveillance systems included in this review were implemented/ proposed.*

Threat	Frequency	References
USA	14	(Bartlett et al., 2010; Carver et al., 2010; Diefenbach et al., 2004; Ebel et al., 2008; Kaneene et al., 2006; Lombard et al., 2013; Lynn et al., 2007; Nusser et al., 2008; O'Brien et al., 2004, 2002, 2008; Pearce et al., 2008; Walsh and Miller, 2010; Wells et al., 2009)
Denmark	9	(Christensen, 1996; Christensen et al., 1994; Enøe et al., 2003; Ersbøll and Nielsen, 2011; Mweu et al., 2012; Nielsen and Rattenborg, 2011; Vergne et al., 2012b; Willeberg et al., 2012, 2011)
European Union	7	(Alban et al., 2011; Del Rio Vilas et al., 2007; EFSA, 2011, 2009a; Giovannini et al., 2005; Gonzales et al., 2010; Martinez et al., 2008)
France	6	(Chazel et al., 2010; Sala and Ru, 2009; Sala et al., 2009; Supervie and Costagliola, 2007; Supervie and Ostagliola, 2004; Vergne et al., 2012a)
Australia	3	(Allworth and Kennedy, 2000; Radunz, 2006; Sergeant and Baldock, 2002)
Netherlands	3	(de Koeijer et al., 2002; Elbers et al., 2000; Santman-Berends et al., 2010)
Switzerland	3	(Häusermann et al., 2010; Kluiters et al., 2008; Presi and Heim, 2010)
United Kingdom	3	(Gubbins, 2008; Holt et al., 2011; Smith et al., 2011)
Italy	2	(Mulatti et al., 2012; Sala and Ru, 2009)
Spain	2	(Cotilla et al., 2010; Miró et al., 2007)
Bulgaria	1	(Alexandrovl et al., 2011)
Cambodia	1	(Vergne et al., 2012b)
Caribbean	1	(Driotl et al., 2011)
Germany	1	(Greineri et al., 2011)

Indonesia	1	(Azhar et al., 2010)
Ireland	1	(Gonzales-Barron et al., 2008)
Japan	1	(Sugiura, 2006)
Korea	1	(Lee et al., 2009)
Norway	1	(Gulliksen et al., 2009)
Pakistan	1	(Ali et al., 2006)
Sweden	1	(Frössling et al., 2012)
Thailand	1	(Walker et al., 2012)
No specific country	5	(Bustamante and Lord, 2010; Prattley et al., 2007; Wells et al., 2009; Williams et al., 2009a, 2009b)

4.2 Summary or article methodologies

4.2.1 Methodological articles

Christensen (1996) presented a method based on change-point analyses to detect single or multiple points of inflexion in the trends of disease incidence rate. While the application of this method to risk-based surveillance is not discussed in the article, the method has potential for evaluation of the impact of interventions and review of surveillance strategies, that is, to inform risk-based requirement.

All other six papers explicitly addressed risk-based surveillance. Frössling *et al*. (2012) proposed the use of network analysis methods (such as “in-degree” and “ingoing infection chain” to identify risk subpopulations when designing risk-based sampling.

Williams *et al.* (2009b) and Willeberg *et al.* (2012) discussed risk-based sampling design. Williams *et al.* (2009b) developed an adaptation of Poisson sampling for use in animal surveys, demonstrating that the use of this method allows population estimates to be made from the results of the surveillance activity carried out, despite the biased sampling strategy. Willeberg *et al.* (2012) demonstrated that the design of risk-based sampling using adjusted relative risks can result in unpredictable effects in the estimation of system sensitivity, and that crude risks should be used instead, when designing risk-based sampling.

The next three papers addressed the issue of population inference from risk-based surveillance data. Prattley *et al.* (2007) developed a spreadsheet that allows the estimation of BSE prevalence in a national herd taking into account population characteristics, results of surveillance testing (targeted at specific risk categories), and characteristics of the disease. Williams *et al.* (2009a) presented the mathematical development of estimators for disease detection and prevalence estimation when risk-based surveillance is used. Wells *et al.* (2009) used stochastic simulation and compared the case detection performance and prevalence estimations when using random sampling in comparison to targeted (risk-based).

The papers are summarized in Table 6.

4.2.2 Validation of Data Generation Processes

Four papers described specific data generation processes and their value for surveillance. All sources of data are passive and not risk-based.

Bartlett *et al.* (2010) evaluated the potential of a veterinary medical database, which is fed by North American veterinary schools, as a source of disease surveillance information in companion animals. Comparing the apparent prevalence in the regions closest to the hospitals to the prevalence in areas

outside a 5 miles radius, they concluded that this geographical dichotomization can reduce referral bias.

The remaining three papers were associated with monitoring programs already implemented, and aimed at validating their utility by assessing their completeness (Gulliksen et al., 2009) or their accuracy in identifying cases in comparison to valid diagnostic methods (Holt et al., 2011; Smith et al., 2011).

Gulliksen *et al.* (2009) evaluated a self-reporting source of data, the Norwegian cattle Health Recording System for dairy herds. The final estimation of underreporting was of around 40%.

Holte *et al.* (2011) used linear and logistic regression to investigate the association between recorded gross pathological lesions recording during slaughter and the results of serology in the herd of origin. The study found statistical associations between slaughter findings (namely recorded pleurism) and serological findings, but concluded that more research is needed to validate the data collection scheme.

Smith *et al.* (2011) used logistic regression to investigate the association between gross pathological lesions recorded at slaughter in pigs in three different voluntary health monitoring programs, and positive serology for individual animals, accounting for animal clustering and seasonality. The results showed positive associations between *Salmonella* positive serology and the occurrence of several gross pathological lesions.

Results are summarized in Table 7.

4.2.3 Surveillance design

Design of surveillance to monitor health indicators and/or estimate disease frequency

Seven papers that were included in the review discussed ongoing monitoring methods to assess the burden of disease in a population, contributing to the implementation of control measures.

Cotilla *et al.* (2010) described a seroprevalence survey in rabbits in Spain which was coupled with a survey of population abundance. The authors concluded that the high population abundance during hunting season makes this an ideal period to survey prevalence.

Ali *et al.* (2006) discussed the use of participatory surveillance to harvest epidemiological information from a community of livestock farmers in Pakistan, concluding on the usefulness of the data collected to establish control and eradication strategies. The authors used proportional piling to estimate the relative prevalence of several livestock diseases, and matrix scoring in order to assess their impact on livelihood.

Two authors discussed the establishment of continuous monitoring systems based on direct farm involvement. Christensen *et al.* (1994) presented a three year pilot of the “Health and Production Surveillance System” aimed at providing producers and other industry stakeholders with information about production performance, disease occurrence and the impact of disease at the herd and national levels. Driotl *et al.* (2011) focused on one specific disease – heartwater – in an area of high tick infestation and high prevalence. The surveillance described was based on establishing a network of livestock stakeholders, supported by the veterinary services, and which relies on farmer notification of nervous cases followed by molecular diagnostics.

Three of the surveillance designs reviewed were risk-based. The technical specifications for the monitoring and reporting of verotoxigenic *Escherichia coli* (VTEC) (EFSA, 2009a) proposed a cost-effective surveillance plan harmonised across European Union member states (MS), focusing on

animals slaughtered young (3-24 months). Harmonised, risk-based surveys were also proposed for *Yersinia enterocolotica* in pigs (EFSA, 2009b). The scientific opinion on bluetongue monitoring and surveillance (EFSA, 2011) discussed targeting regions with higher risk of disease introduction, and reviewed the appropriate size of geographical units for the purpose of monitoring.

Results are summarized in Table 8.

Design of surveillance to detect cases

Six papers focused on the selection of animals to include in the investigation. Nusser *et al.* (2008) and Diefenbach *et al.* (2004) discussed the problems associated with convenience sampling in wildlife, using simulations that took into account the heterogeneity in landscape and population habits and distribution. The other four papers included risk-based strategies. Walsh and Miller (2010) also considered convenience sampling in wildlife, but suggested a weighting system that takes into account animal health, sex, age, source and probability of inclusion. The authors provided a cost-analysis for the method. De Koeijer *et al.* (2002) used mathematical simulations to evaluate the factors that influence the age distribution of BSE cases, and suggest sampling designs targeting ages of higher relative incidence in a given country. Alexandrovl *et al.* (2011) suggested considering the biosecurity level of different pig herds in order to design a risk-based control of CSF, and proposed that this approach allows countries with a high proportion of non-professional pig herds to meet EU standards. Standardised surveillance across MS of the EU using output-based surveillance was also defended by Alban *et al.* (2011). The authors discussed the use of risk-based approaches to review the current surveillance against *Trichinella*. The calculation of risk would take into account characteristics of the pig population in each country, and the sensitivity of the surveillance in place.

Three publications presented a description of surveillance systems and discussed the choice of surveillance components. Azhar *et al.* (2010) presented the strengthening of surveillance to control HPAI in Indonesia with the inclusion of community information through participatory epidemiology. Kaneene *et al.* (2006) described the USA experience with abattoir surveillance and some improvements such as a reward program to encourage veterinarians to search for granulomas in abbatoirs, and the use of animal identification. Allworth and Kennedy (2000) described four components included in the Australian surveillance system against Johne's disease in ovine.

Three authors complemented their description of the surveillance design with the presentation of results. Mulatti *et al.* (2012) presented a strategy for the surveillance of West Nile Virus in North-Eastern Italy which combines passive surveillance, and serological surveys in both horses and mosquito vectors. Results from 2011 are presented. Lee *et al.* (2009) presented results of the surveillance program against bovine brucellosis in the Republic of Korea from 2000 to 2006. The reasons for prolonged disease episodes were evaluated. Finally, Chazel *et al.* (2010) presented the results of the national surveillance network for monitoring of mycoplasmosis in France.

Two publications documented successful strategies to eradicate diseases. Radunz (2006) focused on tuberculosis eradication in Australia, which was supported by industry participation, stable funding and strong technical base. In the final stages herds were targeted for testing based on the history of occurrence of disease, with previously infected herds being considered of higher risk. Presi and Heim (2010) demonstrated how the eradication of BVD in Switzerland was carried out in a one-year time frame through the adoption of strong measures, such as testing the whole cattle population for viral detection (without serological screening).

We also included here two publications which discussed the role of vector population dynamics in the design of surveillance against vector-borne diseases. Bustamante and Lord (2010) used mathematical models to show that the infectiousness of mosquitoes (with virus such as arboviruses) is not always a direct proportion of the prevalence of infection, and recommended that vector population

characteristics must be considered when designing surveillance for vector-borne diseases. Carver *et al.* (2010) recommended the same after study of several sampling schemes for detection of hantaviruses infection in mice.

Details of the 16 publications are given in Table 9.

4.2.4 Critical evaluation of surveillance

This review excluded publications which specifically focused on developing metrics for the evaluation of surveillance systems (methods for evaluation). However, 13 papers were found which presented and discussed an existing surveillance system, fitting the purpose of this review, but additionally presented a critical evaluation of surveillance design or outputs, and often suggested improvements. Details are given below and summarized in Table 10.

Four publications compared the implementation of European Union surveillance regulations among various member states. Gonzales *et al.* (2010) and Martinzes *et al.* (2008) focused on avian influenza, the first authors on low-pathogenic and the latter on H5N1 HPAI. Gonzales *et al.* (2010) showed that countries sampling more than that recommended by the EU had a significantly higher probability of detection, and recommended refining surveillance. The authors also recommended risk-based sampling, showing that the design prevalence can be increased for certain production types. Martinzes *et al.* (2008) also demonstrated a positive relationship between sampling and probability of detection.

Giovannini *et al.* (2005) and Del Rio Vilas *et al.* (2007) discussed TSE surveillance across the European Union. Del Rio Vilas *et al.* (2007) explored the reasons for heterogeneity in scrapie surveillance using a meta-regression approach, finding that the proportion of adult sheep population samples as fallen stock can partly explain the differences in the detection of cases in this group over abattoir sampling. Giovannini *et al.* (2005) compared BSE prevalence estimates across several countries to investigate the ability of sampling procedures to detect the presence of infection. Specifically, the authors investigated the probability to miss the infection by sampling only risk animals, and the precision of prevalence estimates using results from the sampling of risk- and healthy animals.

Lynn *et al.* (2007) provided a qualitative evaluation of scrapie surveillance in the US in comparison to targets set in the surveillance design. Warnick *et al.* (2006) evaluated the efficacy of *Salmonella* surveillance in Denmark by estimating its sensitivity, specificity and predictive values, based on simulation models. Mathematical simulations were also used by Willeberg *et al.* (2011) to compare multiple surveillance scenarios, and demonstrated how sample size could be reduced while keeping surveillance sensitivity.

Pearce *et al.* (2008) compared three surveillance designs against Johne's disease based on the prevalence estimation provided by each, and investigated spatial autocorrelation among the proportion of positive cases in different locations. Kluiters *et al.* (2008) also used spatial statistics to investigate the spatial distribution of surveillance efforts against bluetongue in Switzerland.

Four articles discussed the evaluation of surveillance based on its impact on reducing disease burden. Walker *et al.* (2012) evaluated the infection-to-report distribution before and after adoption of an "X-Ray" surveillance against H5N1 in Thailand; Sala and Ru (2009) and Sala *et al.* (2009) performed evaluations of BSE trends in order to investigate the effect of specific control measures in reducing incidence; and Nielsen and Rattenborg (2011) investigated several risk factors that could be associated with the occurrence of *Salmonella* Dublin in cattle herds in Denmark, concluding that the introduction of surveillance was the most significant factor.

4.2.5 Disease frequency estimates

Disease frequency estimation from the results of ongoing case detection surveillance

Results of continuous monitoring programs for *Salmonella* in bovine herds were used to evaluate temporal and geographical changes in disease burden in Denmark by Ersbøll and Nielse (2011) and Mweu *et al.* (2012). In both cases the effect of surveillance activities in reducing disease burden was also assessed (evaluation of the impact of surveillance, which was however not considered to be the main focus of the article).

Nielsen *et al.* (2011), Sergeant and Baldock (2002), Enøe *et al.* (2003) and Ebel *et al.* (2008) provided Bayesian estimations of the true prevalence from apparent prevalence, correcting for test sensitivity, specificity, and uncertainties in the values of these parameters. The evaluation performed by Enøe *et al.* (2003) also included a trend analysis, assessing changes in prevalence that are corrected for the changes in the diagnostic test performance along time. Ebel *et al.* (2008) also evaluated multiple years, allowing evidence from each year to contribute to the prevalence estimation in the following ones (priors). The latter strategy was also employed by two other publications: Gonzales-Baron *et al.* (2008) and Häausermann *et al.* (2010). The latter authors used data from BSE and scrapie surveillance, the only risk-based surveillance design considered among the studies listed above.

On the subject of making use of BSE surveillance data, four studies provided estimation of true prevalence accounting for different risk-subpopulations targeted for sampling. Greineri *et al.* (2011) used a Bayesian model to adjust apparent prevalence accounting for varied test sensitivity in different age groups. Sugiura (2006) accounted for differences in incidence risk among sub-populations using a maximum likelihood estimate of the number of cases as a Poisson distributed variable. Supervie and Costagliola (2004) used a non-parametric maximum likelihood estimation in order to take into account age and year specific incidence rates of BSE. The method was later applied Supervie and Costagliola (2007) also accounting for additional evidence provided by screening tests.

Three publications dealt with the use of data collected through multiple surveillance components, which in all cases involved at least one risk-based approach. Gubbins (2008) assumed these multiple components to be independent. Vergne *et al.* (2012a) used Bayesian based regression models (zero-truncated Poisson and negative-binomial) to estimate the total number of scrapie infected holdings in France based on results of various surveillance components, understood to represent capture-recapture data. In Cambodia. Vergne *et al.* (2012b) used participatory protocols in order to gather additional data to complement imperfect surveillance data available, and estimate the true number of villages infected with FMD.

Details are given in Table 11.

Disease frequency estimation based on surveillance specifically carried out with this aim

This review excluded publications which simply reported results from prevalence surveys, without description of surveillance methods. Seven papers were found which presented disease frequency estimations as part of an ongoing surveillance strategy.

Elbers *et al.* (2000) described the design of surveys to investigate the seroprevalence of pseudorabies in swine, presenting sample size calculations based on design prevalence (within and between-herds), and desired precision and confidence. The steps for a 2-stage sampling survey (selection of herds and then animals within herd) is described.

O'Briend *et al.* (2004 and 2008) presented the results of *Mycoplasma bovis* seroprevalence surveys in wildlife, estimating true prevalence from apparent prevalence based on direct application of formulas

to correct for test sensitivity and specificity at the animal level. Lombard *et al.* (2013) presented the results of a prevalence study for *Mycobacterium avium* in US dairy herds, and used Bayesian estimation for the correction based on herd sensitivity (estimated from previous evidence) and herd specificivty (from expert opinion).

O'Briend *et al.* (2012), Santman-Berend *et al.* (2010) and Miró *et al.* (2007) used the results of cross-sectional studies to investigate the contribution of various risk factors to the occurrence of disease, such as animal characteristics, management practices and geographical area.

Details from these publications are given in Table 12. None of the publications in this group used risk-based surveillance approaches.

4.2.6 Risk-based approaches

Thirty of the publications detailed above involved the use of risk-based approach. Twenty-eight addressed risk-based sampling, one risk-based requirement (Alban et al., 2011), and one publication addressed both (Giovannini et al., 2005). Table 13 provides a summary of the risk definitions used, which were detailed in Tables 6 through 12 for each paper individually. The table excludes two papers which were theoretical discussions regarding the design of risk-based sampling, rather than application to a concrete example (Wells et al., 2009; Williams et al., 2009a).

Table 6. *Summary of the publications focusing on presenting new methodologies.*

Citation	Overall goal of method	RB[1]	Applied example	Input	Methods used	Output
(Christensen, 1996)	Monitor population health over time	No (R)	Danish pig health and production monitoring system (preweaning mortality and respiratory diseases)	Daily recordings of disease or syndrome occurrence	Change-point analysis: for continuous variables (based on the Anderson-Darling uniformity statistic); and for discrete time monitoring (based on likelihood ratios and the Pearson chi-square test)	Situational awareness regarding disease burden and changes
(Frössling et al., 2012)	Classify subpopulations according to risk	S	Bovine Coronavirus and Bovine Respiratory Syncytial virus serologies in Sweden	Movement data	Network analysis (estimate "in-degree" and "ingoing infection chain") Logistic regression (test association of network measures to seropositive herds)	Definition of subpopulations with higher disease risk
(Williams et al., 2009b)	Risk-based sampling design	S	Demonstrated through mathematical simulations	Population strata and relative risks	Poisson sampling	Cost-effective sampling design to detect disease and population inference
(Willeberg et al., 2012)		S	Danish surveillance data: *Salmonella* surveillance in dairy cattle; *Trichinella* surveillance in slaughtered pigs	Measures of disease frequency in different population strata	Logistic regression (calculate crude and adjusted odds-ratio)	Relative risks for use in risk-based sampling
(Prattley et al., 2007)	Population inference (prevalence) from risk-based surveillance data	S	BSE surveillance in several countries	Number of animals sampled and positive in different population strata	Maximum likelihood estimation of probabilities	Prevalence estimates from data generated through risk-based sampling
(Williams et al., 2009a)		S	Demonstrated through mathematical simulations		Mathematical demonstration of estimator formulas	
(Wells et al., 2009)		S	Demonstrated through mathematical simulations			

1- Risk-based: R= Risk-based requirement, S=Risk-based sampling

Table 7. *Summary of the publications focusing on validating (passive) data generation processes.*

Citation	Threat monitored	No. of years	Epidem. unit	Surv[1]	Cov[2]	Data source evaluated	Methods used	Attributes evaluated	Conclusions
(Bartlett et al., 2010)	Several, SNOMED coded	1	Companion animals, animal	No	C	Veterinary hospitals database	Apparent prevalence comparison between two areas	Bias	Referral bias can be corrected, but sustainability problem
(Gulliksen et al., 2009)	Syndromes (diarrhoea and respiratory)	1	Dairy cattle, herd	Yes	C	Norwegian cattle Health Recording System (self-reported)	Cox proportional hazards; simple percentage comparison	Completeness	Severe underreporting (around 40%)
(Holt et al., 2011)	Syndromes (post-weaning multi-systemic, respiratory)	1	Pigs, herd	Yes	C	Gross pathological lesions at abattoir	Principal components analysis, linear and logistic regression (measure association to a validate diagnostic method)	Sensitivty	Significant association with herd health status, but more validation is needed
(Smith et al., 2011)	*Salmonella sp.*	5	Pigs, animal	Yes	C	Gross pathological lesions at abattoir	Logistic regression with robust standard errors (measure association to a validate diagnostic method)	Sensitivty	Significant association with true health status

1-Associated to an ongoing surveillance.

2- Coverage of the data source – C= Country.

Table 8. *Summary of the publications focusing on surveillance design to monitor health indicators and/or estimate disease frequency.*

Citation	Threat	Cov[1]	Y[2]	RB[3]	RB definition	Epid. unit	SC[4]	Data generated	Proposed methods/activities	Quantitative methods used
(Cotilla et al., 2010)	Rabbit Hemorrhagic disease	R		No	-	Rabbit, animal	A	Population density estimates; serology coupled with hunting season	Consider population abundance when surveying wild populations	Mathematical model of disease spread
(Ali et al., 2006)	Various livestock diseases	R	2002	No	-	Herd	Ptc	Information gathered in meetings with the community	Participatory epidemiology to estimate disease burden and impact	Proportional piling and matrix scoring
(Christensen et al., 1994)	Various syndromes	C	1989	No	-	Herd	P	Daily number of cases	Network of health monitoring involving farmers and veterinary services	Instantaneous incidence rate calculation and trend
(Driotl et al., 2011)	Heartwater	R	2003	No	-	Cattle, animal	P	Reported clinical cases		-
(EFSA, 2009a)	VTEC	EU	-	S	Age	Cattle, animal	A	VTEC detection in hides at slaughter	Sampling a minimum number of animals in the risk category per year	Sample size calculation
(EFSA, 2009b)	*Yersinia enterocolotica*	EU	-	S	Weight at slaughter	Pig, animal	A	Detection in tonsils at slaughter		Sample size calculation
(EFSA, 2011)	Bluetongue	EU	-	S	Geograph-ical area	Various livestock, animal	A+ P	Suspicion reports and active serology	Recommends assessment of surveillance using mathematical simulations	- (based on literature review)

1-Coverage of the surveillance program: R=Regional; C=Country; EU = European Unnion.
2-Year activities started
3-Risk-based: S= sampling
4- Surveillance component: A = active, P=passive, Ptc=Participatory

Table 9. *Summary of the publications focusing on surveillance design to detect cases.*

Citation	Threat	Cov [1]	Y [2]	RB [3]	RB definition	Epid. unit	SC [4]	Data generated	Proposed methods/activities	Quantitative methods used
(Nusser et al., 2008)	CWD	R	-	No	-	Wild cervids, animal	A	Diagnostic tests applied to animals harvested by hunters	Complement convenience sampling with other methods, and take into account population and landscape information	Landscape-based simulations(explore properties of estimators from convenience samples in relation to probabilistic sampling)
(Diefenbach et al., 2004)	CWD	R	2002	No	-	Wild cervids, animal	A			Mathematical simulations (estimate the probability of detection of CWD based on sampling design)
(Walsh and Miller, 2010)	CWD	R	2003	S	Age, health and sex	Wild cervids, animal	A		Assign weights to sampling based on hunters harvest, based on their probability of being clinical cases	Estimate inclusion probability and relative risk for animals based on health, sex and age
(de Koeijer et al., 2002)	BSE	Various	-	S	Age	Cattle, animal	A	Active testing of animals during slaughter	Determine age group with the highest relative incidence.	Age-structure mathematical modelling
(Alexandrovl et al., 2011)	CSF	C	2007	S	Biosecurity level	Pig, farm	A	Information regarding management characteristics of the farm; active serology	Categorization of pig holdings, and adjustment of the active serological investigations according to risk	-
(Alban et al., 2011)	Trichinellosis	EU	-	R	Production, system sensitivity	Pig, animal	A	Active testing of animals during slaughter	Categorize MS into 3 subclasses based on the confidence that *Trichinella* can be considered absent and pig population characteristics. Use output-based surveillance	Estimation of sample size based on desired system sensitivity and considering sub-populations with differential risk
(Azhar et al., 2010)	HPAI	C	2004	No	-	Poultry, flock	A+ Ptc	Disease burden information collected on the field	Visit to farms, control of outbreaks and participatory epidemiology	-
(Kaneene et al., 2006)	Tuberculosis	C	1950's	No	-	Cattle, animal	A	Gross pathological investigation during slaughter	Reward programs for granuloma finding and examination of wild ruminants	-
(Allworth and Kennedy, 2000)	Johne's disease	C	1997	No	-	Sheep/ goats, flock	A+ P	Various components (active and passive)	Four initiatives described, including voluntary certification programs and risk zoning.	-

(Mulatti et al., 2012)	WNV	R	2011	No	-	Horses/ mosquito	A+ P	Active serological investigation in horses and mosquitos (trapping) and passive surveillance of wild birds	Combine passive surveillance with active testing; reduce costs by testing sera from horses collected for other surveillance purpose; consider dynamics of the vector population.	-
(Lee et al., 2009)	Brucellosis	C	2000	No	-	Cattle, herd	A	Various, including mandatory herd testing and abattoir surveillance	Use two measures of disease control: episode duration and time to re-restriction. Investigate their association to risk factors	Generalized estimating equation model (identify risk factors for episode duration); Cox's proportional hazard model (risk factors to time to re-restriction)
(Chazel et al., 2010)	Mycoplas-moses	C	2003	No	-	Ruminant s, animal	P	Mycoplasma isolates sent for typing	Centralized network to identify mycoplasmas and store clinical information	-
(Radunz, 2006)	TB	C	1970	S	History of infection	Cattle, herd	A	Gross pathological investigation during slaughter, active serology	Compelement abattoir surveillance with active testing of risk hers, depopulation in case of detection	-
(Presi and Heim, 2010)	BVD	C	2008	No	-	Cattle, animal	A	Active virus detection testing	Slaughter all positive animals	-
(Bustamante and Lord, 2010)	Arboviruses	-	-	No	-	Mosquito , individual	A	Mosquito trapping and testing	Account for vector population dynamics when designing sampling	Mathematical model (study the relationship between prevalence of infected mosquitoes and infection rate)
(Carver et al., 2010)	Hantaviruse s	R	1995	No	-	Mouse, individual	A	Mice trapping and testing	Account for host population dynamics when designing sampling	Evaluated the prevalence estimation errors associated with several sampling strategies

1-Coverage of the surveillance program: R=Regional; C=Country; EU = European Union

2-Year activities started

3-Risk-based: S= sampling, R= Requirement

4- Surveillance component: A = active, P=passive, Ptc=Participatory

Table 10. *Summary of the publications presenting a critical evaluation of surveillance.*

Citation	Threat	Cov[1]	Y[2]	RB[3]	RB definition	Epid. unit	SC[4]	Attribute evaluated	Quantitative methods	Suggested improvements
(Gonzales et al., 2010)	LPAI	EU	2003	S	Production type	Poultry, flock	A	Compliance (to EU recommended sample size)	Logistic regression (probability of finding positive holdings versus sampling ratio); Poisson regression (relative risks for production types)	Review surveillance requirement; consider risk-based sampling according to production types
(Martinez et al., 2008)	HPAI	EU	2005	No	-	Wild birds, animal	P	Ratio between probability of sampling and probability of infection	Probability co-kriging (estimate incidence conditional to distance between cases and spatial distribution of population at risk)	-
(Del Rio Vilas et al., 2007)	Scrapie	EU	2002	S	Age, cohort[5]	Sheep, animal	A+ P	Consistency (of same protocol across countries)	Meta-regression with random effects(OR of sampling fallen stock to abattoir animals on prob. of detection); Bayesian estimation of the number of events in both groups (binomial prob. dist.)	-
(Giovannini et al., 2005)	BSE	EU	2001	S+ R	Age, cohort[5]	Cattle, animal	A+ P	True-positives, false-positives, false-negatives sensitivity and specificity	Bayesian inference (calculate prevalence accounting for test Se, Sp and uncertainty);	Classification of countries into only two risk categories: low and high. Adopt risk-based requirement
(Lynn et al., 2007)	Scrapie	C	Not give n	S	genetic, clinical signs	Sheep, animal	A+ P	Effectiveness of sampling, sensitivity, representativeness,	-	Revision of definition of clinical animals; improve training; further validate the sampling methodology.
(Warnick et al., 2006)	*Salmonella*	C	2002	No	-	Cattle, herd	A	Accuracy and predictive values	Mathematical simulations based on a scenario diagram (estimate surveillance sensitivity, specificity and predictive values)	-
(Willeberg et al., 2011)	BSE	C	2001	S	Age	Cattle, animal	A	Sampling efficacy	Mathematical simulations (compare several surveillance scenarios, optimizing sample size for a given sensitivity)	Raising the age limit for testing animals (as it would reduce the sample size but not the sensitivity of detection)
(Pearce et al., 2008)	Johne's	R	-	No	-	Cattle, animal	A	Prevalence estimates	Chi-square test (comparison of proportion detected by three surveillance methods); trend assessment; spatial autocorrelation using Cuzick and Edwars test (proportion of positives per area)	Adopt risk-based sampling (based on clinical signs) to increase the probability of detecting cases.
(Kluiters et	Bluetongue	C	2007	No	-	Cattle,	A+	Coverage	Spatial scan statistic and Moran's I	Spatial variation in surveillance

al., 2008)						animal	P	(geographical)	statistic (test for clustering of surveillance data); Bayesian estimation of prevalence	data (not only disease burden) should be considered when analysing case detection on a national scale.
(Walker et al., 2012)	Avian influenza	R	2004	S	Production type	Poultry, sub-district	A	Impact	Spatio-temporal model of disease spread (fit to outbreak data and used to estimate the probability of infection for each production type); risk maps (calculate reproduction rate per tambon); gamma distribution fitting (to compare outbreak reporting before and after application of X-ray surveillance)	Strengthen active surveillance especially directed at production types of higher risk
(Sala et al., 2009)	BSE	C	1990	S	Age, cohort[5]	Cattle, animal	A+P	Impact	Restricted cubic regression splines (determine effect of control measures while accounting for the non-linear effects of age at screening, birth cohort and date of diagnostic)	Use of the methodology should guide the (re)design of BASE surveillance
(Sala and Ru, 2009)	BSE	C	2001	S	Age, cohort[5]	Cattle, animal	A+P	Impact		
(Nielsen and Rattenborg, 2011)	*Salmonella*	C	2002	No	-	Cattle, herd	A	Impact	Logistic regression (to investigate risk factors for disease occurrence, such as season, management factors and time on the surveillance program)	-

1-Coverage of the surveillance program: R=Regional; C=Country; EU = European Union

2-Year activities started

3-Risk-based: S= sampling, R= Requirement

4- Surveillance component: A = active, P=passive, Ptc=Participatory

5- General TSE surveillance based on age at slaughter and risk cohort (clinical signs, fallen stock, emergency slaughter)

Table 11. *Summary of the publications presenting disease frequency estimation from case detection surveillance.*

Citation	Threat	Cov[1]	Y[2]	RB[3]	RB definition	Epid. unit	SC[4]	Data Generation Process	Disease frequency measure	Quantitative methods
(Ersbøll and Nielsen, 2011)	*Salmonella* Dublin	R	2002	No	-	Cattle, herd	A	Bulk-tank milk testing in all dairy herds in the study area	Apparent herd prevalence	Logistic regression (evaluate risk factors and effect of control on changes in prevalence); Spatial scan statistics and standardized morbidity ratio (evaluate spatial clustering of cases);
(Mweu et al., 2012)	*Streptococcus agalactie*	C	1950	No	-	Cattle, herd	A	Mandatory bulk milk testing	Apparent herd prevalence (95% exact binomial CI); annual incidence, entry, exit, recovery and transmission rates	Poisson regression (compare incidence rates before and after control measures), infectious disease spread model (estimate transmission rate)
(Nielsen et al., 2011)	*Salmonella sp.*	C	2006	No	-	Cattle, herd	A	Survey of herds at slaughter, bacterial culture and serology testing	True prevalence of herds and within herds	Bayesian estimation of true prevalence accounting for test Se and Sp
(Sergeant and Baldock, 2002)	*Johne's*	C	1999	No	-	Sheep, flock	A	Active testing during slaughter	True herd prevalence	Bayesian estimation of true prevalence accounting for test Se and Sp, and uncertainty of those parameters
(Enøe et al., 2003)	Chronic pleuritis	C	1993	No	-	Pigs, animal	A	Gross pathological investigation during slaughter	True prevalence	Bayesian estimation (using latent class models implemented with Gibbs sampling) of true prevalence accounting for test Se and Sp; logistic regression to investigate time trends on the prevalence
(Ebel et al., 2008)	Brucelosis	C	1934	No	-	Cattle, herd	A	Gross pathological investigation during slaughter	True herd prevalence	Bayesian inference (link process model – used to estimate prevalence based on slaughter data, accumulating evidence along years, and accounting for number of animals tested per herd and test Se and Sp)
(Gonzales-Barron et al., 2008)	*Salmonella sp.*	C	2005	No	-	Pigs, animal	A	Meat juice serology	Seroprevalence per herd category (low, medium, high prevalence herd)	Bayesian estimation accounting for evidence from previous year
(Häusermann et al., 2010)	Scrapie /BSE	C	1990	S	Age-cohort[5]	Sheep/ goats, animal	A	Active testing during slaughter	Prevalence of herds and within herds	Bayesian estimation accounting for evidence from previous year

(Greineri et al., 2011)	BSE	C	1997	S	Age-cohort[5]	Cattle, animal	A	Active testing during slaughter	Prevalence per birth cohort and ratio of undetected to detected cases	Bayesian estimation of true prevalence accounting for age dependent sensitivity
(Sugiura, 2006)	BSE	C	1996	S	Age-cohort[5]	Cattle, animal	A+P	Active testing during slaughter; diagnostic in fallen stock and notified suspicions	Prevalence and incidence risk by risk population	Maximum likelihood estimate of the number of cases, modelled as a Poisson distributed variable
(Supervie and Ostagliola, 2004)	BSE	C	1990	S	Age-cohort[5]	Cattle, animal	A+P		Annual incidence	Non-parametric maximum likelihood estimation of incidence rates taking into account the effect of age
(Supervie and Costagliola, 2007)	BSE	C	2001	S	Age-cohort[5]	Cattle, animal	A+P		Annual incidence	Non-parametric maximum likelihood estimation of incidence rates taking into account the effect of age, and also evidence provided by previous testing
(Gubbins, 2008)	Scrapie	C	2002	S	Age-cohort[5]	Sheep, animal	A+P		Prevalence and relative risk of infection per PrP genotype	Mathematical modelling (to estimate the true prevalence accounting for survivorship, death before clinical manifestation, and underreporting); and maximum likelihood estimation (number of cases as a Poisson distributed variable)
(Vergne et al., 2012a)	Scrapie	C	1996	S	Age-cohort[5]	Pigs, farm	A+P		Number of holdings with at least one infected animal	Bayesian zero-truncated Poisson and negative binomial models (estimate number of cases using capture-recapture data from surveillance)
(Vergne et al., 2012b)	FMD	R	2009	S	Purchase of animals	Cattle, village	A+Ptc	Serological survey; information collected from the community	Number of infected villages	Capture-recapture methods to incorporate evidence from participatory epidemiology

1-Coverage of the surveillance program: R=Regional; C=Country

2-Year surveillance program started (or if not specified, the year the data generation process utilized by the work started)

3-Risk-based: S= sampling, R= Requirement

4- Surveillance component: A = active, P=passive, Ptc=Participatory

5- General TSE surveillance based on age at slaughter and risk cohort (clinical signs, fallen stock, emergency slaughter)

Table 12. *Summary of the publications presenting disease frequency estimation from studies designed with this goal.*

Citation	Threat	Cov [1]	Y [2]	Epid. unit	SC [3]	Sampling scheme	Disease frequency measure	Quantitative methods
(Elbers et al., 2000)	Aujeszky's	C	1993	Pigs, animal	A	Two-stage sampling	Seroprevalence (95%CI) of pig population stratified by region and type (sows vs fattening pigs)	Sample size calculations accounting for clustering
(O'Brien et al., 2008)	Tuberculosis	R	1998	Wild cervids, animal	A	Voluntary submission by hunters	True prevalence	Apparent prevalence corrected using point values of test Se and Sp
(O'Brien et al., 2004)	Tuberculosis	R	1995	Wild cervids, animal	A	Voluntary submission by hunters	True prevalence	Apparent prevalence corrected using point values of test Se and Sp
(Lombard et al., 2013)	Johne's	C	1996	Cattle,	A	Collect environmental fecal samples from 6 different locations on each herd	True prevalence	Bayesian estimation of true prevalence accounting for test Se and Sp
(O'Brien et al., 2002)	Tuberculosis	R	1995	Wild cervids, animal	A	Voluntary submission by hunters, road-kills and found dead, and small survey in 18 private hunting clubs	Apparent prevalence	Logistic regression (evaluation of association with risk factors: age, sex, survey method and geographical area)
(Santman-Berends et al., 2010)	Bluetongue	C	2007	Cattle,	A	Montly testing of 15-25 lactating cows in 14 herds per compartment	Apparent prevalence	Logistic regression (evaluation of association with risk factors related to management)
(Miró et al., 2007)	Leishmaniosis	R	1996	Companion animals, individual	A	Collect blood and feces from 100 dogs from 13 shelters twice a year	Mean increase in seroprevalence per herd, compartment and region	Chi-square tests (association with age, sex, breed and intestinal parasite seroprevalence)

1-Coverage of the surveillance program: R=Regional; C=Country

2-Year activities started

3- Surveillance component: A = active, P=passive, Ptc=Participatory

Table 13. *Risk definitions in the risk-based surveillance systems described in the papers included in the review (total=28).*

	Risk group	Frequency
Animal-level risk factors	Age	8
	Age and clinical signs/death	7
	Clinical signs/death	2
	Weight at slaughter	1
	Genetic traits	1
Herd-level risk factors	Animal Production type	3
	Animal movement	3
	Biosecurity of herds	1
	Geographic location	1
	History of risk (exposure)	1

5 Discussion

Recent international workshops gathering animal veterinary epidemiologists from several countries have discussed the development and application of effective surveillance methods (Hoinville, 2012; Hoinville et al., 2009). Scientists have highlighted the areas where further technical development is needed, but there is also an understanding that many of the recent developments in surveillance methods have not yet been incorporated into operating animal surveillance programs. This might be due to the gap in communication between scientists and surveillance designers (Doherr et al., 2012; Hoinville et al., 2009).

In order to encourage the adoption of currently available surveillance methodologies, and guide the further development of these tools, this work aimed at reviewing the current literature describing existing approaches for surveillance of endemic diseases. Previous reviews have summarized the development of specific surveillance tools, such as syndromic surveillance (Dórea et al., 2011; Dupuy et al., 2013a), and risk-based methods (Oidtmann et al., 2013; Stärk et al., 2006), or focused on surveillance evaluation (Drewe et al., 2012). This work tried to include any surveillance strategies proposed or implemented to provide disease frequency estimation or case detection of endemic diseases in a given animal population.

A large number of papers were retrieved (2163) and 354 met the primary exclusion criteria, reflecting the intensity of development and implementation of animal surveillance methods. When higher scrutiny was applied, and papers with insufficient information regarding the described methods were removed (38), only 69 papers remained and were included in this review (Figure 1). From these, 42 of the papers referred to studies carried out in European countries, and 14 in the USA (Table 5). Many implemented surveillance systems, even in developed countries, were not captured in this review likely because they are only published in national journals in their native language. Most of these systems were national, but this may reflect publication bias against smaller, local systems.

The most frequent infectious diseases addressed were zoonotic, except for scrapie (Table 4). The high number of papers describing scrapie surveillance represents the overall high representation of transmissible spongiform encephalopathies (TSE) in the studies included in this review – 17 in total. The spread of BSE has caused a concomitant increase in the interest for scrapie due to public health concerns, after the successful experimental transmission of BSE to sheep in 2001 (Del Rio Vilas et al., 2007). The long incubation period for BSE and the difficulty to detect infected animals are reasons that can help explain the intensity of the research related to this disease, focused on developing efficient methods to detect and mitigate the risks associated with the presence of TSE in food animals after the sudden emergence of BSE in the late 1980's. The sudden emergence of the disease and the initial uncertainties regarding the mode of transmission, especially whether transmission to humans was possible, also resulted in high policy concerns, and a consequent large effort to ensure that decision were science-based.

Despite the higher number of studies focusing on zoonotic threats (35 papers focusing on zoonotic agents as compared to 25 papers focusing on non-zoonotic agents), 14 out of the 26 specific infectious diseases addressed were non-zoonotic. Besides the two non-zoonotic TSEs (scrapie and chronic wasting disease - CWD), the non-zoonotic diseases reviewed can have a high impact in animal production due to fast transmission and negative effect on trade, as for instance foot-and-mouth disease (FMD), classical swine fever (CSF) and bluetongue; or cause economic losses due to chronic persistence in the herd, such as Bovine Viral Diarrhea (BVD) and paratuberculosis. Only two wildlife diseases of non-zoonotic potential were considered – CWD (a TSE) and rabbit hemorrhagic fever.

Cattle were the most frequent animal species surveyed (Figure 6). This is likely to be due to the higher number of surveillance components designed around this animal group, though the high representation of BSE in the review must also be borne in mind here.

Because animals are clustered in herds or flocks, the epidemiological unit generally considered in epidemiological analyses is often the herd. However, among the papers reviewed, almost 3 times more papers considered the epidemiological unit to be the animal, as opposed to the herd or flock (Tables 6-12). This reflects the high representation of TSEs, but also the availability of analytical methods capable of dealing with the effects of animal clustering, and providing unbiased inferences for animal populations. Additionally, some papers dealt with animals not organized in herds, such as companion animals (Bartlett et al., 2010) and wildlife (Carver et al., 2010; Cotilla et al., 2010; Nusser et al., 2008; O'Brien et al., 2002, 2008, 2004).

Kellar (2012) discussed the challenges of animal health surveillance implementation and pointed out the need for surveillance programs to benefit from technological developments that reduce the amount of intervention needed to carry out disease control (Kellar, 2012). The author discussed how the efficiency of population level diagnostics can be increased not only by improving the accuracy of laboratory tests, but also by using "complementary assessments and innovative epidemiological concepts". Six of the seven articles presenting new methods – all published in the past five years – suggested risk-based approaches to increase the efficiency of the surveillance design, or to maximize the amount of information that can be generated from data collected after targeting risk-subpopulations. While risk-based surveillance approaches are not new, the methodologies to allow population inference represent a new development, which seems to start to be incorporated into epidemiological studies. None of the publications classified as aiming to estimate disease frequency in a population, using prevalence studies, used risk-based approaches. In contrast, seven papers discussed the retrospective analysis of risk-based case detection surveillance to detect TSEs, in order to draw population inference. The approaches were mostly based on Bayesian estimation of the actual number of cases, but some authors also used maximum likelihood estimators.

Most of the data sources explored were traditional surveillance data (Tables 6-12), such as serological surveys, number of cases detected by active or passive surveillance components, and prevalence of positive animals/herds in active investigations. Four publications investigated the surveillance value of alternative sources of data. These publications addressed the need to explore data which is already centralized and computerized – such as veterinary hospitals databases, or health management information; and also underexplored data such as abattoir inspection records. Bias and completeness were measured when assessing the databases, and the sensitivity was evaluated for the abattoir gross pathological investigation.

The need to consider alternatives to traditional structured surveys, previously pointed out by scientists involved with surveillance design (Hoinville et al., 2009), were also discussed by the papers included in this review. Improvements in sampling strategy (besides the risk-based strategies discussed above) and surveillance components were presented. Those were usually not focusing on incorporation of a specific analytical tool, but advice regarding the refocusing of sampling strategies, incorporation of new surveillance components, use of sentinel populations, and more careful consideration of external sources of variation in the disease-population dynamics, such as for instance vector dynamics. In the workshop to discuss livestock surveillance in 2009 it was documented that, with respect to vector-borne diseases, "more innovation was required to identify and source alternative information" (Hoinville et al., 2009). The two papers included in this review which address this specific issue (Bustamante and Lord, 2010; Carver et al., 2010) were published since then, in 2010.

The inclusion of information gathered directly from farmers and the community, through participatory approaches, was described in three papers: (Ali et al., 2006) discussed it as a method to estimate disease

burden in a population; (Azhar et al., 2010) reported its importance in strengthening HPAI outbreak control efforts in Indonesia; and (Vergne et al., 2012b) used this information to complement information from a serological survey to detect FMD infection in Cambodia.

The use of surveillance data for multiple disease programs was also discussed. Only (Mulatti et al., 2012) explicitly indicated the use of sera collected as part of the surveillance program for other equine diseases, for serological testing aiming at investigating the presence of West Nile virus circulation. However, several of the surveillance programs listed in Tables 8 through 12 are addressed against multiple threats, especially monitoring programs aimed at the control of unspecific clinical syndromes that compromise animal production in pigs and cattle.

Harmonisation of surveillance strategies was discussed mainly in the context of European Union regulations, as for instance in (EFSA, 2009a) and (EFSA, 2009b). The surveillance designs proposed in these two publications make use of risk-based strategies to increase the efficacy of sampling, but propose an input-based standard, with the minimum number of sample per country set *a priori*. In contrast, (Alban et al., 2011) defended that countries should be evaluated based on their risk with the goal of setting output-based standards, that is, using an epidemiological design that allows countries to achieve the same final sensitivity or confidence, taking into account the epidemiological situation and information available. (Alexandrovl et al., 2011) also discussed the use of risk-based approaches in order to allow countries with different production realities to meet standards set out for all European Union member states (MS). (Gonzales et al., 2010), (Martinez et al., 2008) and (Del Rio Vilas et al., 2007), evaluated implementation of input-based EU regulations across several member states, showing a lack of compliance of consistency that results in outputs that may be hard or impossible to compare.

Kellar (2012) pointed out the need for surveillance designers to prove that interventions are rational and cost-effective and to justify their decisions to the higher levels responsible for allocating money, and also to those in the field implementing or being targeted by the surveillance actions. The publications reviewed reflect efforts to continuously seek improvement of already implemented surveillance systems. Moreover, 13 publications reviewed explicitly assessed and discussed the performance of surveillance systems and their features, based on attributes such as compliance, accuracy, efficacy or impact. In contrast, only one paper (which main goal was actually surveillance design, not evaluation) explicitly included a cost analysis (Walsh and Miller, 2010). The scarce incorporation of economic evaluation into surveillance evaluation has been previously noted in a systematic review of animal and public health system evaluations (Drewe et al., 2012).

When estimating disease frequency in a population, the most common issue was correcting apparent prevalence to estimate true prevalence, taking into account mainly test diagnostic characteristics, but also correcting for an imperfect data collection process (such as biases from risk-based sampling, underreporting or convenience sampling). Bayesian estimators and maximum likelihood methods were the quantitative methods most used in these cases.

This review highlighted the widespread use of risk-based surveillance. The number of papers discussing risk-based surveillance seemed to follow the overall number of papers per year included in the review, demonstrating that the idea of risk-based surveillance is not new. Among the papers which discussed risk-based surveillance, the majority of risk definitions were based on age and clinical signs, which reflects the high proportion of papers discussing TSEs surveillance. The European Commission has mandated risk-based surveillance for BSE in cattle since 2000 (Giovannini et al., 2005), based on the age of animals being slaughtered, the type of slaughter, and focusing also on animals dead on farm. All of the surveillance systems discussed for TSE were classified as risk-based.

The review also showed that scientists continue to search for methods to define and assess risk. The issue of risk-based surveillance was reflected in different ways: addressing the design and incorporation of risk-based strategies into existing surveillance (Alban et al., 2011; Alexandrovl et al., 2011; de Koeijer et al., 2002; Frössling et al., 2012; Giovannini et al., 2005; Sugiura, 2006; Walker et al., 2012; Walsh and Miller, 2010; Willeberg et al., 2012); presentation of analytical methods that allow correction of bias in data from risk-based sampling, which can then be used for epidemiological inference (Wells et al., 2009; Williams et al., 2009a); and evaluating the use of new methods to define risk, such as animal movement evaluated through network analysis (Frössling et al., 2012), biosecurity (Alexandrovl et al., 2011), and production type (Alban et al., 2011; Gonzales et al., 2010). The spatial distribution of risk or surveillance activities was also discussed (Ersbøll and Nielsen, 2011; Kluiters et al., 2008). Fourteen authors suggested that risk-based sampling could improve currently employed surveillance strategies for the systems described.

Known drawbacks of risk-based surveillance were acknowledged, especially the difficulty in making population inferences from data collected based on purposeful targeting of specific population strata (Wells et al., 2009; Williams et al., 2009a). But developments are still needed to provide quality standards to evaluate and compare surveillance results, including cost-benefit analysis.

Considering the number of different methodologies highlighted by this review, three challenges can be pointed out for the design and implementation of new (or revised) surveillance components. First, there is a need to incorporate new epidemiological approaches into readily available tools, which would allow surveillance designers and decision-makers to apply the analytical methods proposed by research. Second, a surveillance designer may find it difficult to establishing which of those methods are most appropriate for which diseases, especially in different settings such as varying disease status (endemic or not for instance) and resources availability (developed versus developing countries). And lastly, there is a need for prioritisation strategies that allow decision-makers to determine how to distribute resources available among various surveillance components, for various diseases.

Despite the developments in surveillance, the gap between scientists and decision-makers is still reflected in a large gap between theory and practical application of the surveillance design, analysis and evaluation tools. Moreover, several of the discussions presented in the reviewed papers underlined the struggle to incorporate some innovative methods into surveillance, due to the current legal requirements. The use of output-based standards would facilitate the creation of frameworks where some of the methodologies proposed could be incorporated to substitute or complement existing surveillance components.

These challenges can be addressed in the scope of RISKSUR by the development of guidelines that help surveillance designers and decision-makers make sense of the great number of surveillance methods proposed (which surveillance components are needed, and how to design and implement them), as well as “ready-to-use” tools that make the current analytical developments accessible (how to analyse the data generated by such surveillance components).

6 References

Alban, L., Pozio, E., Boes, J., Boireau, P., Boué, F., Claes, M., Cook, a J.C., Dorny, P., Enemark, H.L., van der Giessen, J., Hunt, K.R., Howell, M., Kirjusina, M., Nöckler, K., Rossi, P., Smith, G.C., Snow, L., Taylor, M. a, Theodoropoulos, G., Vallée, I., Viera-Pinto, M.M., Zimmer, I. a, 2011. Towards a standardised surveillance for Trichinella in the European Union. Preventive veterinary medicine 99, 148–60.

Alexandrovl, T., Kamenovi, P., Depner, K., 2011. Surveillance and control of classical swine fever in Bulgaria , a country with a high proportion of non-professional pig holdings 140–142.

Ali, S.N., Asif, M., Rehman, A., Jat, L.A., Ali, Q., Hussain, M., 2006. Participatory Surveillance of Livestock Diseases in District Karachi – Pakistan. Internation Journal of Agriculture and Biology 8, 652–656.

Allworth, M.B., Kennedy, D.J., 2000. Progress in national control and assurance programs for ovine Johne' s disease in Australia 77, 415–422.

Azhar, M., Lubis, A.S., Siregar, E.S., Alders, R.G., Brum, E., McGrane, J., Morgan, I., Roeder, P., 2010. Participatory disease surveillance and response in Indonesia: strengthening veterinary services and empowering communities to prevent and control highly pathogenic avian influenza. Avian diseases 54, 749–53.

Bartlett, P.C., van Buren, J.W., Neterer, M., Zhou, C., 2010. Disease surveillance and referral bias in the veterinary medical database. Preventive veterinary medicine 94, 264–71.

Bustamante, D.M., Lord, C.C., 2010. Sources of error in the estimation of mosquito infection rates used to assess risk of arbovirus transmission. The American journal of tropical medicine and hygiene 82, 1172–84.

Cameron, A.R., 2012. The consequences of risk-based surveillance: Developing output-based standards for surveillance to demonstrate freedom from disease. Preventive veterinary medicine 105, 280–6.

Cannon, R.M., 2009. Inspecting and monitoring on a restricted budget--where best to look? Preventive veterinary medicine 92, 163–74.

Carver, S., Mills, J.N., Kuenzi, A., Flietstra, T., Douglass, R., 2010. Sampling frequency differentially influences interpretation of zoonotic pathogen and host dynamics: Sin Nombre virus and deer mice. Vector borne and zoonotic diseases (Larchmont, N.Y.) 10, 575–83.

Chazel, M., Tardy, F., Le Grand, D., Calavas, D., Poumarat, F., 2010. Mycoplasmoses of ruminants in France: recent data from the national surveillance network. BMC veterinary research 6, 32.

Christensen, J., 1996. Multiple change-point analysis of disease incidence rates 99, 53–76.

Christensen, J., 2001. Epidemiological concepts regarding disease monitoring and surveillance. Acta veterinaria Scandinavica. Supplementum 94, 11–16.

Christensen, J., Ellegaarda, B., Petersen, B.K., Willeberg, P., 1994. Pig health and production surveillance in Denmark : sampling design , data recording , and measures of disease frequency 5877.

Cotilla, I., Delibes-Mateos, M., Ramírez, E., Castro, F., Cooke, B.D., Villafuerte, R., 2010. Establishing a serological surveillance protocol for rabbit hemorrhagic disease by combining mathematical models and field data: implication for rabbit conservation. European Journal of Wildlife Research 56, 725–733.

De Koeijer, A., Schreuder, B., Bouma, A., 2002. Factors that influence the age distribution of BSE cases : potentials for age targeting in surveillance 76, 223–233.

Del Rio Vilas, V.J., Hopp, P., Nunes, T., Ru, G., Sivam, K., Ortiz-Pelaez, A., 2007. Explaining the heterogeneous scrapie surveillance figures across Europe: a meta-regression approach. BMC veterinary research 3, 13.

Diefenbach, D.R., Rosenberry, C.S., Boyd, R.C., 2004. From the Field : Efficacy of detecting Chronic Wasting Disease via sampling hunter-killed white-tailed deer 32, 267–272.

Doherr, M.G., Calavas, D., Cameron, A., Dufour, B., Greiner, M., Gustafson, L., Hoinville, L., Knopf, L., Roger, F., Stärk, K.D.C., Salman, M.D., 2012. First international conference on animal health surveillance (ICAHS). Preventive veterinary medicine 105, 165–8.

Dórea, F.C., Sanchez, J., Revie, C.W., 2011. Veterinary syndromic surveillance: Current initiatives and potential for development. Preventive veterinary medicine 101, 1–17.

Drewe, J. a, Hoinville, L.J., Cook, a J.C., Floyd, T., Stärk, K.D.C., 2012. Evaluation of animal and public health surveillance systems: a systematic review. Epidemiology and infection 140, 575–90.

Driotl, C., Pradel, J., Teissier, R., Redon, J.M., Vachiery, N., Gerbieri, G., Lefrancois, T., 2011. Establishment of Heartwater surveillance in an enzootic situation : Example in Guadeloupe , French West Indies . Guadeloupe Franoe 431–433.

Dupuy, C., Bronner, A., Watson, E., Wuyckhuise-Sjouke, L., Reist, M., Fouillet, A., Calavas, D., Hendrikx, P., Perrin, J.-B., 2013a. Inventory of veterinary syndromic surveillance initiatives in Europe (Triple-S project): Current situation and perspectives. Preventive veterinary medicine 111, 220–9.

Dupuy, C., Morignat, E., Maugey, X., Vinard, J.-L., Hendrikx, P., Ducrot, C., Calavas, D., Gay, E., 2013b. Defining syndromes using cattle meat inspection data for syndromic surveillance purposes: a statistical approach with the 2005-2010 data from ten French slaughterhouses. BMC veterinary research 9, 88.

Ebel, E.D., Williams, M.S., Tomlinson, S.M., 2008. Estimating herd prevalence of bovine brucellosis in 46 USA states using slaughter surveillance. Preventive veterinary medicine 85, 295–316.

EFSA, 2009a. SCIENTIFIC REPORT OF EFSA Technical specifications for the monitoring and reporting of verotoxigenic Escherichia coli (VTEC) on animals and food (VTEC surveys on animals and food) 1 7, 1–43.

EFSA, 2009b. Technical specifications for harmonised national surveys on Yersinia enterocolitica in slaughter pigs 1 7, 1–43.

EFSA, 2011. Scientific Opinion on bluetongue monitoring and surveillance 1 9.

Elbers, A.R.W., Dekkers, L.J.M., van der Giessen, J.W.B., 2000. Sero-surveillance of wild boar in the Netherlands, 1996-1999. Rev.sci.tech.Off.int.Epiz. 19, 848–854.

Elbers, A.R.W., Stegeman, J.A., Jong, M.F. De, Lambers, J.H., Koning, R. De, 1995. Estimating sample sizes for a two-stage sampling survey of seroprevalence of pseudorabies virus (PRV)-infected swine at a regional level in the Netherlands. Veterinary Quartely 17, 92–95.

Enøe, C., Christensen, G., Andersen, S., Willeberg, P., 2003. The need for built-in validation of surveillance data so that changes in diagnostic performance of post-mortem meat inspection can be detected. Preventive Veterinary Medicine 57, 117–125.

Ersbøll, A.K., Nielsen, L.R., 2011. Spatial patterns in surveillance data during control of Salmonella Dublin in bovine dairy herds in Jutland, Denmark 2003-2009. Spatial and spatio-temporal epidemiology 2, 195–204.

Flint, A.P.F., Woolliams, J.A., n.d. Precision animal breeding. Philos.Trans.R.Sco.Lond.B 360, 2067-2083. In: Souza Monteiro, D.M.; Roman Carrasco, L.; Joe Moffitt, L.; Cook, A.J.C. Robust surveillance of animal diseases: An application to the detection of bluetongue disease. Preventive Vete.

Frössling, J., Ohlson, A., Björkman, C., Håkansson, N., Nöremark, M., 2012. Application of network analysis parameters in risk-based surveillance - examples based on cattle trade data and bovine infections in Sweden. Preventive veterinary medicine 105, 202–8.

Giovannini, a, Calistri, P., Conte, a, Savini, L., Nannini, D., Patta, C., Santucci, U., Caporale, V., 2004. Bluetongue virus surveillance in a newly infected area. Veterinaria italiana 40, 188–97.

Giovannini, A., Savini, L., Conte, A., Fiore, G.L., 2005. Comparison of BSE prevalence estimates from EU countries for the period July to December 2001 to the OIE and EU GBR classifications. Journal of veterinary medicine. B, Infectious diseases and veterinary public health 52, 262–71.

Gonzales, J.L., Elbers, A.R.W., Bouma, A., Koch, G., de Wit, J.J., Stegeman, J.A., 2010. Low-pathogenic notifiable avian influenza serosurveillance and the risk of infection in poultry - a critical review of the European Union active surveillance programme (2005-2007). Influenza and other respiratory viruses 4, 91–9.

Gonzales-Barron, U., Soumpasis, I., Butler, F., Prendergast, D., Duffy, G., 2008. Prevalence of Salmonella in caecal contents of slaughter pigs in Ireland as estimated from meat juice serology data, in: CIGR - International Conference of Agricultural Engineering.

Greineri, M., Selhorst, T., Johnson, W.O., Doherr, M., 2011. Sensitivity-adjusted BSE Prevalence can be Estimated Using Surveillance Data Without External Information on Incubation Time and Age at Infection 314–315.

Grindlay, D.J.C., Brennan, M.L., Dean, R.S., 2012. Searching the veterinary literature: a comparison of the coverage of veterinary journals by nine bibliographic databases. Journal of veterinary medical education 39, 404–12.

Gubbins, S., 2008. Prevalence of sheep infected with classical scrapie in Great Britain: integrating multiple sources of surveillance data for 2002. Journal of the Royal Society, Interface / the Royal Society 5, 1343–51.

Gulliksen, S.M., Lie, K.I., Østerås, O., 2009. Calf health monitoring in Norwegian dairy herds. Journal of dairy science 92, 1660–9.

Hoinville, L., 2012. Animal Health Surveillance Terminology Final Report from Pre-ICAHS Workshop October 2012.

Hoinville, L., Ellis-Iversen, J., Vink, D., Watson, E., Snow, L., Gibbens, J., 2009. Discussing the Development and Application of Methods for Effective Surveillance in Livestock Populations. Report of a Workshop held prior to the ISVEE conference. Durban, South Africa.

Hoinville, L.J., Alban, L., Drewe, J.A., Gibbens, J.C., Gustafson, L., Häsler, B., Saegerman, C., Salman, M., Stärk, K.D.C., 2013. Proposed terms and concepts for describing and evaluating animal-health surveillance systems. Preventive veterinary medicine null.

Holt, H.R., Alarcon, P., Velasova, M., Pfeiffer, D.U., Wieland, B., 2011. BPEX Pig Health Scheme: a useful monitoring system for respiratory disease control in pig farms? BMC veterinary research 7, 82.

Häsler, B., Howe, K., 2012. Evaluating the Role of Surveillance in National Policies for Animal Health Évaluer le rôle de la surveillance dans les politiques nationales de santé animale Evaluation der Bedeutung der Kontrolle staatlicher Politikmaßnahmen zur Sicherung der Tiergesun. EuroChoices 11, 39–44.

Häsler, B., Howe, K.S., Stärk, K.D.C., 2011. Conceptualising the technical relationship of animal disease surveillance to intervention and mitigation as a basis for economic analysis. BMC health services research 11, 225.

Häusermann, C., Schwermer, H., Oevermann, A., Nentwig, A., Zurbriggen, A., Heim, D., Seuberlich, T., 2010. Surveillance and simulation of bovine spongiform encephalopathy and scrapie in small ruminants in Switzerland. BMC veterinary research 6, 20.

Kaneene, J.B., Miller, R., Meyer, R.M., 2006. Abattoir surveillance: The U.S. experience 112, 273–282.

Kellar, J.A., 2012. Animal health surveillance: navigation amidst the flotsam of human frailty and fiscal inertia. Preventive veterinary medicine 105, 169–75.

Kluiters, G., Chaignat, V., Schwermer, H., 2008. Spatial distribution of bluetongue surveillance and cases in Switzerland. Schweizer Archiv für Tierheilkunde 150, 543–52.

Lee, B.Y., Higgins, I.M., Moon, O.K., Clegg, T.A., McGrath, G., Collins, D.M., Park, J.Y., Yoon, H.C., Lee, S.J., More, S.J., 2009. Surveillance and control of bovine brucellosis in the Republic of Korea during 2000-2006. Preventive veterinary medicine 90, 66–79.

Lombard, J.E., Gardner, I.A., Jafarzadeh, S.R., Fossler, C.P., Harris, B., Capsel, R.T., Wagner, B.A., Johnson, W.O., 2013. Herd-level prevalence of Mycobacterium avium subsp. paratuberculosis infection in United States dairy herds in 2007. Preventive veterinary medicine 108, 234–8.

Lynn, T., Grannis, J., Williams, M., Marshall, K., Miller, R., Bush, E., Bruntz, S., 2007. An evaluation of scrapie surveillance in the United States. Preventive veterinary medicine 81, 70–9.

Martin, P.A.J., Cameron, A.R., Greiner, M., 2007. Demonstrating freedom from disease using multiple complex data sources 1: a new methodology based on scenario trees. Preventive veterinary medicine 79, 71–97.

Martinez, M., Perez, A.M., de la Torre, A., Iglesias, I., Muñoz, M.J., 2008. Association between number of wild birds sampled for identification of H5N1 avian influenza virus and incidence of the disease in the European Union. Transboundary and emerging diseases 55, 393–403.

Miró, G., Montoya, A., Mateo, M., Alonso, A., García, S., García, A., Caballero, M.J., Molina, R., 2007. A leishmaniosis surveillance system among stray dogs in the region of Madrid: ten years of serodiagnosis (1996-2006). Parasitology research 101, 253–7.

Mulatti, P., Bonfanti, L., Capelli, G., Capello, K., Lorenzetto, M., Terregino, C., Monaco, F., Ferri, G., Marangon, S., 2012. West Nile Virus in North-Eastern Italy, 2011: Entomological and Equine IgM-Based Surveillance to Detect Active Virus Circulation. Zoonoses and public health 1–8.

Mweu, M.M., Nielsen, S.S., Halasa, T., Toft, N., 2012. Annual incidence, prevalence and transmission characteristics of Streptococcus agalactiae in Danish dairy herds. Preventive veterinary medicine 106, 244–50.

Nielsen, L.R., Rattenborg, E., 2011. Active Surveillance and Control Programme for Salmonella Dublin in Cattle: Alternatives to Acceptance of Endemic Infection with Poor Control Options 210–212.

Nielsen, T.D., Nielsen, L.R., Toft, N., 2011. Bayesian estimation of true between-herd and within-herd prevalence of Salmonella in Danish veal calves. Preventive veterinary medicine 100, 155–62.

Nusser, S.M., Clark, W.R., Otis, D.L., Huang, L., 2008. Sampling Considerations for Disease Surveillance in Wildlife Populations. Journal of Wildlife Management 72, 52–60.

O'Brien, D., Schmitt, S.M., Fierke, J.S., Hogle, S.A., Winterstein, S.R., Cooley, T.M., Moritz, W.E., Diegel, K.L., Fitzgerald, S.D., Berry, D.E., Kaneene, J.B., 2002. Epidemiology of Mycobacterium bovis 54, 47–63.

O'Brien, D.J., Schmitt, S.M., Berry, D.E., Fitzgerald, S.D., Lyon, T.J., Vanneste, J.R., Cooley, T.M., Hogle, S. a, Fierke, J.S., 2008. Estimating the true prevalence of Mycobacterium bovis in free-ranging elk in Michigan. Journal of wildlife diseases 44, 802–10.

O'Brien, D.J., Schmitt, S.M., Berry, D.E., Fitzgerald, S.D., Vanneste, J.R., Lyon, T.J., Magsig, D., Fierke, J.S., Cooley, T.M., Zwick, L.S., Thomsen, B. V, 2004. Estimating the true prevalence of Mycobacterium bovis in hunter-harvested white-tailed deer in Michigan. Journal of wildlife diseases 40, 42–52.

Oidtmann, B., Peeler, E., Lyngstad, T., Brun, E., Bang Jensen, B., Stärk, K.D.C., 2013. Risk-based methods for fish and terrestrial animal disease surveillance. Preventive Veterinary Medicine null.

Pearce, B.H., Fosgate, G.T., Ward, M.P., Roussel, A.J., Norby, B., Tavornpanich, S., Ellis, D., 2008. Comparison of three methods of surveillance with application to the detection of Johne's disease seropositivity in Texas cattle. Preventive veterinary medicine 86, 1–7.

Perrin, J.-B., Ducrot, C., Vinard, J.-L., Morignat, E., Calavas, D., Hendrikx, P., 2012. Assessment of the utility of routinely collected cattle census and disposal data for syndromic surveillance. Preventive veterinary medicine 105, 244–52.

Prattley, D.J., Cannon, R.M., Wilesmith, J.W., Morris, R.S., Stevenson, M.A., 2007. A model (BSurvE) for estimating the prevalence of bovine spongiform encephalopathy in a national herd. Preventive veterinary medicine 80, 330–43.

Presi, P., Heim, D., 2010. BVD eradication in Switzerland--a new approach. Veterinary microbiology 142, 137–42.

Radunz, B., 2006. Surveillance and risk management during the latter stages of eradication: experiences from Australia. Veterinary microbiology 112, 283–90.

Sala, C., Morignat, E., Ducrot, C., Calavas, D., 2009. Modelling the trend of bovine spongiform encephalopathy prevalence in France: Use of restricted cubic spline regression in age-period-cohort models to estimate the efficiency of control measures. Preventive veterinary medicine 90, 90–101.

Sala, C., Ru, G., 2009. Time trends in exposure of cattle to bovine spongiform encephalopathy and cohort effect in France and Italy: value of the classical Age-Period-Cohort approach. BMC veterinary research 5, 34.

Salman, M.D. (Ed.), 2003. Animal Disease Surveillance and Survey Systems, 1st ed. Iowa State Press, Iowa.

Santman-Berends, I.M.G. a, Bartels, C.J.M., van Schaik, G., Stegeman, J. a, Vellema, P., 2010. The increase in seroprevalence of bluetongue virus (BTV) serotype 8 infections and associated risk factors in Dutch dairy herds, in 2007. Veterinary microbiology 142, 268–75.

Sergeant, E.S.G., Baldock, F.C., 2002. The estimated prevalence of Johne's disease infected sheep flocks in Australia. Australian Veterinary Journal 80, 762–768.

Smith, R.P., Sanchez-Vazquez, M.J., Cook, A.J.C., Edwards, S. a, 2011. Abattoir-based study investigating the association between gross pathological lesions and serological tests for Salmonella infection in pigs. The Veterinary record 168, 240.

Stärk, K.D.C., Regula, G., Hernandez, J., Knopf, L., Fuchs, K., Morris, R.S., Davies, P., 2006. Concepts for risk-based surveillance in the field of veterinary medicine and veterinary public health: review of current approaches. BMC health services research 6, 20.

Sugiura, K., 2006. Adjusted incidence risks of BSE in risk subpopulations of cattle in Japan. Preventive veterinary medicine 75, 163–76.

Supervie, V., Costagliola, D., 2007. Estimating incidence of the French BSE infection using a joint analysis of both asymptomatic and clinical BSE surveillance data. Mathematical biosciences 209, 90–107.

Supervie, V., Ostagliola, D.C., 2004. The unrecognised French BSE epidemic 35, 349–362.

Walker, P., Cauchemez, S., Hartemink, N., Tiensin, T., Ghani, A.C., 2012. Outbreaks of H5N1 in poultry in Thailand: the relative role of poultry production types in sustaining transmission and the impact of active surveillance in control. Journal of the Royal Society, Interface / the Royal Society 9, 1836–45.

Walsh, D.P., Miller, M.W., 2010. A weighted surveillance approach for detecting chronic wasting disease foci. Journal of wildlife diseases 46, 118–35.

Warnick, L.D., Nielsen, L.R., Nielsen, J., Greiner, M., 2006. Simulation model estimates of test accuracy and predictive values for the Danish Salmonella surveillance program in dairy herds. Preventive veterinary medicine 77, 284–303.

Wells, S.J., Ebel, E.D., Williams, M.S., Scott, A.E., Wagner, B. a, Marshall, K.L., 2009. Use of epidemiologic information in targeted surveillance for population inference. Preventive veterinary medicine 89, 43–50.

Vergne, T., Calavas, D., Cazeau, G., Durand, B., Dufour, B., Grosbois, V., 2012a. A Bayesian zero-truncated approach for analysing capture-recapture count data from classical scrapie surveillance in France. Preventive veterinary medicine 105, 127–35.

Vergne, T., Grosbois, V., Durand, B., Goutard, F., Bellet, C., Holl, D., Roger, F., Dufour, B., 2012b. A capture-recapture analysis in a challenging environment: assessing the epidemiological situation of foot-and-mouth disease in Cambodia. Preventive veterinary medicine 105, 235–43.

Willeberg, P., Nielsen, L.R., Salman, M., 2012. Designing and evaluating risk-based surveillance systems: potential unwarranted effects of applying adjusted risk estimates. Preventive veterinary medicine 105, 185–94.

Willeberg, P., Paisley, L.G., Lind, P., 2011. Epidemiological models to support animal disease surveillance activities. Revue scientifique et technique (International Office of Epizootics) 30, 603–614.

Williams, M.S., Ebel, E.D., Wells, S.J., 2009a. Population inferences from targeted sampling with uncertain epidemiologic information. Preventive veterinary medicine 89, 25–33.

Williams, M.S., Ebel, E.D., Wells, S.J., 2009b. Poisson sampling: a sampling strategy for concurrently establishing freedom from disease and estimating population characteristics. Preventive veterinary medicine 89, 34–42.

7 ANNEX

7.1 ANNEX I

List of the 69 scientific articles included in the review of the surveillance systems for endemic disease, including information on the extent of multi-objective surveillance activities.

Alban, L., Pozio, E., Boes, J., Boireau, P., Boué, F., Claes, M., Cook, a J.C., Dorny, P., Enemark, H.L., van der Giessen, J., Hunt, K.R., Howell, M., Kirjusina, M., Nöckler, K., Rossi, P., Smith, G.C., Snow, L., Taylor, M. a, Theodoropoulos, G., Vallée, I., Viera-Pinto, M.M., Zimmer, I. a, 2011. Towards a standardised surveillance for Trichinella in the European Union. Preventive veterinary medicine 99, 148–60.

Alexandrovl, T., Kamenovi, P., Depner, K., 2011. Surveillance and control of classical swine fever in Bulgaria , a country with a high proportion of non-professional pig holdings 140–142.

Ali, S.N., Asif, M., Rehman, A., Jat, L.A., Ali, Q., Hussain, M., 2006. Participatory Surveillance of Livestock Diseases in District Karachi – Pakistan. Internation Journal of Agriculture and Biology 8, 652–656.

Allworth, M.B., Kennedy, D.J., 2000. Progress in national control and assurance programs for ovine Johne' s disease in Australia 77, 415–422.

Azhar, M., Lubis, A.S., Siregar, E.S., Alders, R.G., Brum, E., McGrane, J., Morgan, I., Roeder, P., 2010. Participatory disease surveillance and response in Indonesia: strengthening veterinary services and empowering communities to prevent and control highly pathogenic avian influenza. Avian diseases 54, 749–53.

Bartlett, P.C., van Buren, J.W., Neterer, M., Zhou, C., 2010. Disease surveillance and referral bias in the veterinary medical database. Preventive veterinary medicine 94, 264–71.

Bustamante, D.M., Lord, C.C., 2010. Sources of error in the estimation of mosquito infection rates used to assess risk of arbovirus transmission. The American journal of tropical medicine and hygiene 82, 1172–84.

Carver, S., Mills, J.N., Kuenzi, A., Flietstra, T., Douglass, R., 2010. Sampling frequency differentially influences interpretation of zoonotic pathogen and host dynamics: Sin Nombre virus and deer mice. Vector borne and zoonotic diseases (Larchmont, N.Y.) 10, 575–83.

Chazel, M., Tardy, F., Le Grand, D., Calavas, D., Poumarat, F., 2010. Mycoplasmoses of ruminants in France: recent data from the national surveillance network. BMC veterinary research 6, 32.

Christensen, J., 1996. Multiple change-point analysis of disease incidence rates 99, 53–76.

Christensen, J., Ellegaarda, B., Petersen, B.K., Willeberg, P., 1994. Pig health and production surveillance in Denmark : sampling design , data recording , and measures of disease frequency 5877.

Cotilla, I., Delibes-Mateos, M., Ramírez, E., Castro, F., Cooke, B.D., Villafuerte, R., 2010. Establishing a serological surveillance protocol for rabbit hemorrhagic disease by combining mathematical models and field data: implication for rabbit conservation. European Journal of Wildlife Research 56, 725–733.

De Koeijer, A., Schreuder, B., Bouma, A., 2002. Factors that influence the age distribution of BSE cases : potentials for age targeting in surveillance 76, 223–233.

Del Rio Vilas, V.J., Hopp, P., Nunes, T., Ru, G., Sivam, K., Ortiz-Pelaez, A., 2007. Explaining the heterogeneous scrapie surveillance figures across Europe: a meta-regression approach. BMC veterinary research 3, 13.

Diefenbach, D.R., Rosenberry, C.S., Boyd, R.C., 2004. From the Field : Efficacy of detecting Chronic Wasting Disease via sampling hunter-killed white-tailed deer 32, 267–272.

Driotl, C., Pradel, J., Teissier, R., Redon, J.M., Vachiery, N., Gerbieri, G., Lefrancois, T., 2011. Establishment of Heartwater surveillance in an enzootic situation : Example in Guadeloupe , French West Indies . Guadeloupe Franoe 431–433.

Ebel, E.D., Williams, M.S., Tomlinson, S.M., 2008. Estimating herd prevalence of bovine brucellosis in 46 USA states using slaughter surveillance. Preventive veterinary medicine 85, 295–316.

EFSA, 2011. Scientific Opinion on bluetongue monitoring and surveillance 1 9.

Elbers, A.R.W., Dekkers, L.J.M., van der Giessen, J.W.B., 2000. Sero-surveillance of wild boar in the Netherlands, 1996-1999. Rev.sci.tech.Off.int.Epiz. 19, 848–854.

Enøe, C., Christensen, G., Andersen, S., Willeberg, P., 2003. The need for built-in validation of surveillance data so that changes in diagnostic performance of post-mortem meat inspection can be detected. Preventive Veterinary Medicine 57, 117–125.

Ersbøll, A.K., Nielsen, L.R., 2011. Spatial patterns in surveillance data during control of Salmonella Dublin in bovine dairy herds in Jutland, Denmark 2003-2009. Spatial and spatio-temporal epidemiology 2, 195–204.

Food, E., Authority, S., 2009a. Technical specifications for harmonised national surveys on Yersinia enterocolitica in slaughter pigs 1 7.

Food, E., Authority, S., 2009b. SCIENTIFIC REPORT OF EFSA Technical specifications for the monitoring and reporting of verotoxigenic Escherichia coli (VTEC) on animals and food (VTEC surveys on animals and food) 1 7, 1–43.

Frössling, J., Ohlson, A., Björkman, C., Håkansson, N., Nöremark, M., 2012. Application of network analysis parameters in risk-based surveillance - examples based on cattle trade data and bovine infections in Sweden. Preventive veterinary medicine 105, 202–8.

Giovannini, A., Savini, L., Conte, A., Fiore, G.L., 2005. Comparison of BSE prevalence estimates from EU countries for the period July to December 2001 to the OIE and EU GBR classifications. Journal of veterinary medicine. B, Infectious diseases and veterinary public health 52, 262–71.

Gonzales, J.L., Elbers, A.R.W., Bouma, A., Koch, G., de Wit, J.J., Stegeman, J.A., 2010. Low-pathogenic notifiable avian influenza serosurveillance and the risk of infection in poultry - a critical review of the European Union active surveillance programme (2005-2007). Influenza and other respiratory viruses 4, 91–9.

Gonzales-Barron, U., Soumpasis, I., Butler, F., Prendergast, D., Duffy, G., 2008. Prevalence of Salmonella in caecal contents of slaughter pigs in Ireland as estimated from meat juice serology data, in: CIGR - International Conference of Agricultural Engineering.

Greineri, M., Selhorst, T., Johnson, W.O., Doherr, M., 2011. Sensitivity-adjusted BSE Prevalence can be Estimated Using Surveillance Data Without External Information on Incubation Time and Age at Infection 314–315.

Gubbins, S., 2008. Prevalence of sheep infected with classical scrapie in Great Britain: integrating multiple sources of surveillance data for 2002. Journal of the Royal Society, Interface / the Royal Society 5, 1343–51.

Gulliksen, S.M., Lie, K.I., Østerås, O., 2009. Calf health monitoring in Norwegian dairy herds. Journal of dairy science 92, 1660–9.

Holt, H.R., Alarcon, P., Velasova, M., Pfeiffer, D.U., Wieland, B., 2011. BPEX Pig Health Scheme: a useful monitoring system for respiratory disease control in pig farms? BMC veterinary research 7, 82.

Häusermann, C., Schwermer, H., Oevermann, A., Nentwig, A., Zurbriggen, A., Heim, D., Seuberlich, T., 2010. Surveillance and simulation of bovine spongiform encephalopathy and scrapie in small ruminants in Switzerland. BMC veterinary research 6, 20.

Kaneene, J.B., Miller, R., Meyer, R.M., 2006. Abattoir surveillance: The U.S. experience 112, 273–282.

Kluiters, G., Chaignat, V., Schwermer, H., 2008. Spatial distribution of bluetongue surveillance and cases in Switzerland. Schweizer Archiv für Tierheilkunde 150, 543–52.

Lee, B.Y., Higgins, I.M., Moon, O.K., Clegg, T.A., McGrath, G., Collins, D.M., Park, J.Y., Yoon, H.C., Lee, S.J., More, S.J., 2009. Surveillance and control of bovine brucellosis in the Republic of Korea during 2000-2006. Preventive veterinary medicine 90, 66–79.

Lombard, J.E., Gardner, I.A., Jafarzadeh, S.R., Fossler, C.P., Harris, B., Capsel, R.T., Wagner, B.A., Johnson, W.O., 2013. Herd-level prevalence of Mycobacterium avium subsp. paratuberculosis infection in United States dairy herds in 2007. Preventive veterinary medicine 108, 234–8.

Lynn, T., Grannis, J., Williams, M., Marshall, K., Miller, R., Bush, E., Bruntz, S., 2007. An evaluation of scrapie surveillance in the United States. Preventive veterinary medicine 81, 70–9.

Martinez, M., Perez, A.M., de la Torre, A., Iglesias, I., Muñoz, M.J., 2008. Association between number of wild birds sampled for identification of H5N1 avian influenza virus and incidence of the disease in the European Union. Transboundary and emerging diseases 55, 393–403.

Miró, G., Montoya, A., Mateo, M., Alonso, A., García, S., García, A., Caballero, M.J., Molina, R., 2007. A leishmaniosis surveillance system among stray dogs in the region of Madrid: ten years of serodiagnosis (1996-2006). Parasitology research 101, 253–7.

Mulatti, P., Bonfanti, L., Capelli, G., Capello, K., Lorenzetto, M., Terregino, C., Monaco, F., Ferri, G., Marangon, S., 2012. West Nile Virus in North-Eastern Italy, 2011: Entomological and Equine IgM-Based Surveillance to Detect Active Virus Circulation. Zoonoses and public health 1–8.

Mweu, M.M., Nielsen, S.S., Halasa, T., Toft, N., 2012. Annual incidence, prevalence and transmission characteristics of Streptococcus agalactiae in Danish dairy herds. Preventive veterinary medicine 106, 244–50.

Nielsen, L.R., Rattenborg, E., 2011. Active Surveillance and Control Programme for Salmonella Dublin in Cattle: Alternatives to Acceptance of Endemic Infection with Poor Control Options 210–212.

Nielsen, T.D., Nielsen, L.R., Toft, N., 2011. Bayesian estimation of true between-herd and within-herd prevalence of Salmonella in Danish veal calves. Preventive veterinary medicine 100, 155–62.

Nusser, S.M., Clark, W.R., Otis, D.L., Huang, L., 2008. Sampling Considerations for Disease Surveillance in Wildlife Populations. Journal of Wildlife Management 72, 52–60.

O'Brien, D., Schmitt, S.M., Fierke, J.S., Hogle, S.A., Winterstein, S.R., Cooley, T.M., Moritz, W.E., Diegel, K.L., Fitzgerald, S.D., Berry, D.E., Kaneene, J.B., 2002. Epidemiology of Mycobacterium bovis 54, 47–63.

O'Brien, D.J., Schmitt, S.M., Berry, D.E., Fitzgerald, S.D., Lyon, T.J., Vanneste, J.R., Cooley, T.M., Hogle, S. a, Fierke, J.S., 2008. Estimating the true prevalence of Mycobacterium bovis in free-ranging elk in Michigan. Journal of wildlife diseases 44, 802–10.

O'Brien, D.J., Schmitt, S.M., Berry, D.E., Fitzgerald, S.D., Vanneste, J.R., Lyon, T.J., Magsig, D., Fierke, J.S., Cooley, T.M., Zwick, L.S., Thomsen, B. V, 2004. Estimating the true prevalence of Mycobacterium bovis in hunter-harvested white-tailed deer in Michigan. Journal of wildlife diseases 40, 42–52.

Pearce, B.H., Fosgate, G.T., Ward, M.P., Roussel, A.J., Norby, B., Tavornpanich, S., Ellis, D., 2008. Comparison of three methods of surveillance with application to the detection of Johne's disease seropositivity in Texas cattle. Preventive veterinary medicine 86, 1–7.

Prattley, D.J., Cannon, R.M., Wilesmith, J.W., Morris, R.S., Stevenson, M.A., 2007. A model (BSurvE) for estimating the prevalence of bovine spongiform encephalopathy in a national herd. Preventive veterinary medicine 80, 330–43.

Presi, P., Heim, D., 2010. BVD eradication in Switzerland--a new approach. Veterinary microbiology 142, 137–42.

Radunz, B., 2006. Surveillance and risk management during the latter stages of eradication: experiences from Australia. Veterinary microbiology 112, 283–90.

Sala, C., Morignat, E., Ducrot, C., Calavas, D., 2009. Modelling the trend of bovine spongiform encephalopathy prevalence in France: Use of restricted cubic spline regression in age-period-cohort models to estimate the efficiency of control measures. Preventive veterinary medicine 90, 90–101.

Sala, C., Ru, G., 2009. Time trends in exposure of cattle to bovine spongiform encephalopathy and cohort effect in France and Italy: value of the classical Age-Period-Cohort approach. BMC veterinary research 5, 34.

Santman-Berends, I.M.G. a, Bartels, C.J.M., van Schaik, G., Stegeman, J. a, Vellema, P., 2010. The increase in seroprevalence of bluetongue virus (BTV) serotype 8 infections and associated risk factors in Dutch dairy herds, in 2007. Veterinary microbiology 142, 268–75.

Sergeant, E.S.G., Baldock, F.C., 2002. The estimated prevalence of Johne's disease infected sheep flocks in Australia. Australian Veterinary Journal 80, 762–768.

Smith, R.P., Sanchez-Vazquez, M.J., Cook, A.J.C., Edwards, S.A., 2011. Abattoir-based study investigating the association between gross pathological lesions and serological tests for Salmonella infection in pigs. The Veterinary record 168, 240.

Sugiura, K., 2006. Adjusted incidence risks of BSE in risk subpopulations of cattle in Japan. Preventive veterinary medicine 75, 163–76.

Supervie, V., Costagliola, D., 2007. Estimating incidence of the French BSE infection using a joint analysis of both asymptomatic and clinical BSE surveillance data. Mathematical biosciences 209, 90–107.

Supervie, V., Ostagliola, D.C., 2004. The unrecognised French BSE epidemic 35, 349–362.

Walker, P., Cauchemez, S., Hartemink, N., Tiensin, T., Ghani, A.C., 2012. Outbreaks of H5N1 in poultry in Thailand: the relative role of poultry production types in sustaining transmission and the impact of active surveillance in control. Journal of the Royal Society, Interface / the Royal Society 9, 1836–45.

Walsh, D.P., Miller, M.W., 2010. A weighted surveillance approach for detecting chronic wasting disease foci. Journal of wildlife diseases 46, 118–35.

Warnick, L.D., Nielsen, L.R., Nielsen, J., Greiner, M., 2006. Simulation model estimates of test accuracy and predictive values for the Danish Salmonella surveillance program in dairy herds. Preventive veterinary medicine 77, 284–303.

Wells, S.J., Ebel, E.D., Williams, M.S., Scott, A.E., Wagner, B. a, Marshall, K.L., 2009. Use of epidemiologic information in targeted surveillance for population inference. Preventive veterinary medicine 89, 43–50.

Vergne, T., Calavas, D., Cazeau, G., Durand, B., Dufour, B., Grosbois, V., 2012a. A Bayesian zero-truncated approach for analysing capture-recapture count data from classical scrapie surveillance in France. Preventive veterinary medicine 105, 127–35.

Vergne, T., Grosbois, V., Durand, B., Goutard, F., Bellet, C., Holl, D., Roger, F., Dufour, B., 2012b. A capture-recapture analysis in a challenging environment: assessing the epidemiological situation of foot-and-mouth disease in Cambodia. Preventive veterinary medicine 105, 235–43.

Willeberg, P., Nielsen, L.R., Salman, M., 2012. Designing and evaluating risk-based surveillance systems: potential unwarranted effects of applying adjusted risk estimates. Preventive veterinary medicine 105, 185–94.

Willeberg, P., Paisley, L.G., Lind, P., 2011. Epidemiological models to support animal disease surveillance activities. Revue scientifique et technique (International Office of Epizootics) 30, 603–614.

Williams, M.S., Ebel, E.D., Wells, S.J., 2009a. Poisson sampling: a sampling strategy for concurrently establishing freedom from disease and estimating population characteristics. Preventive veterinary medicine 89, 34–42.

Williams, M.S., Ebel, E.D., Wells, S.J., 2009b. Population inferences from targeted sampling with uncertain epidemiologic information. Preventive veterinary medicine 89, 25–33.

7.2 ANNEX II

List of variables collected from the papers selected for the literature review of surveillance approaches for endemic disease, including information on the extent of multi-objective surveillance activities.

Variable	Further descriprion
Author	
Year of publication	
Aim of the paper	Describe the aim(s) of the article
Threat	Disease or condition under surveillance
Zoonosis	Binary, indicating whether the threat investigated is zoonotic.
Disease status	Endemic, low prevalence or absent in the area under investigation
Surveilled species	Divided into: a. Dairy cattle b. Beef cattle c. Pigs d. Sheep e. Goats f. Horses g. Poultry h. Pets (Dogs + Cats) i. Wild boars j. Wild cervids k. Wild carnivores l. Wild birds m. Wild rodents n. Arthropods
Multi-objective surveillance	Whether surveillance was targeted to one threat only or possibly to more than one. For example, monitoring schemes aiming at identifying “pig diseases” have been referred to multi-objective, because they can detect several different diseases.
Risk-based surveillance	Whether surveillance is risk-based
Risk definition	In case of risk-based surveillance, what defines the risk groups
Country	Where the described surveillance is implemented
Underlying surveillance programme	Whether the data/methods refers to a surveillance system currently in place. This because methodological studies often make use of simulations and they refer to hypothetical surveillance strategies.
Aim of surveillance programme	e.g., case finding, demonstrating freedom...
Starting year of surveillance programme	if provided
Legal requirement for surveillance	e.g., mandatory in EU, national program, voluntary joining, etc
Surveillance components	active, passive, both
Epidemiological unit	animal or herd
Sampling scheme	Brief description: e.g., inspect all pig holdings,

	serological test on a sample of pigs per farm.
Sample size - FARMS	How many farms are sampled or what is the criterion to estimate sample size.
Sample size – ANIMALS	How many animals are sampled or what is the criterion to estimate sample size.
Pooled samples	Are sampled pooled?
Sampled material	e.g., blood, brain, milk...
Lab test	e.g., ELISA, PCR....
Test Se	If provided
Test Sp	If provided
Adjustment for test accuracy	Whether methods to estimate disease frequency/presence account or not for diagnostic test accuracy
Results of surveillance activities	Does the paper report results of surveillance activities?
Real data/ simulations	Is the paper based on real data or on simulations?
# Years data available	Number of years of surveillance data used in the study
Measure of disease	e.g., prevalence, annual incidence, cumulative number of cases...
Statistical model/methods for case detection or prevalence estimate	e.g., Cox proportional hazard model including frailty effect
Methods to evaluate surveillance	e.g. evaluation of spatial clustering of surveillance data for each surveillance component
Cost evaluation	Does the study include any cost evaluation?
Improvements proposed	Methods introduced to improve surveillance activities.