PART 1

SURVEILLANCE DESIGN
and
EVALUATION

DATA AND TOOLS

Applications of the web-based BioPortal system in animal disease surveillance: HPAI H5N1 among wild birds in Sweden and Denmark, 2006

P. Willeberg[1*], M. AlKhamis[1], U. Carlsson[2], R. Carrasco-Medanic[1], Z. Whedbee[1] and A. Perez[1, 3]

Abstract

Infection with highly pathogenic avian influenza (HPAI) H5N1 occurred for the first time in Sweden and Denmark in 2006 during the last part of the European epidemic that mainly affected migrating wild birds. This study describes the spatial and temporal distribution of test-positive birds from the two countries, initially dominated by cases among Tufted Ducks with subsequent spread to other wild bird species in the vicinity. Analysis of the surveillance data also suggests an apparent die-out of the regional epidemic. Data handling, visualization and analysis were supported using the Disease BioPortal which is an IT system for disease surveillance that utilizes a web-based platform. Other similar surveillance projects and pilot applications of the Disease BioPortal are encouraged.

Keywords: Sweden, Denmark, avian influenza, Disease BioPortal, web-based surveillance.

Introduction

The Disease BioPortal is a web-based system that provides real-time or near-real time access to local, regional, and global disease information and data [1]. The system provides access to publicly available databases, as well as to private data through secure routing and sharing mechanisms. Tools are available for spatio-temporal display, graphics, and phylogenetic analysis of the data, as well as for downloading or uploading data. The Disease BioPortal is operated and maintained by the FMD Laboratory, Center for Animal Disease Modeling and Surveillance at the University of California, Davis, and is supported through a consortium of national and international institutions, agencies, and organizations. We have agreements with both scientific and executive users to accommodate their over-arching need for access to tools that facilitate the application of a combination of modern technology, versatility, science-based methodology, graphical visualization, processing power, data-entry and storage capacity, central as well as local applications, among other attributes.

As an example to illustrate the potentials of the Disease BioPortal in sustaining disease surveillance activities we use outbreak data from the avian influenza epidemic that recently affected Asia and Europe [2]. This was one of the most challenging and recent international examples of the introduction and spread of an exotic and emerging infection, which exhibits transboundary and zoonotic importance, and still threatens the international society due to continued spread and potentially increasing risk caused by molecular changes in the virus genome. Animal and public health authorities worldwide therefore need to consider planning and organizing surveillance systems to cater not just for human and domestic animal surveillance, but also to engage in wildlife surveillance for HPAI.

Materials and methods

The Danish epidemic has previously been documented in official reports from the Danish Veterinary and Food Administration [3] and from the European Commission [4]. The particular spatial distribution of the infection within the country has been presented [2, 5], phylogenetic data from 8 of the Danish wild bird virus isolates have been published [6], and the potential public health aspects have been described [7]. In other reports the Danish data were combined with similar information from other European countries [8, 9]. The official Danish wild bird surveillance database for 2006 includes more than 6,700 records of tested samples, of which over 5,500 were fecal samples obtained from migrating wild birds during resting (active surveillance data). Approximately 1,200 samples were from collected dead wild birds (passive surveillance). Within the risk period of February 15 to the end of May, approximately 1,000 dead birds were tested, of which 951, including all the positive samples, had geo-coordinates for their finding location recorded.

The Swedish 2006 surveillance dataset contains more than 4,800 sample records of which approximately 1,000 samples were tested during the risk period of February 15 to the end of May. Within this period, 518 birds were tested in the passive surveillance program comprising diseased or dead wild birds. Parts of the Swedish data have been reported [4, 8 and 9], and in addition the pathological findings in the Swedish Tufted Duck cases have been described [10]. Characterization of the isolated Swedish virus strains has been presented [11, 12].

Excel-spreadsheet format was used to enter both national datasets into the Disease BioPortal. Spatial-temporal cluster detection in the Danish data using SaTScan procedures [13] was performed with uni- and multivariate methodology [14]. These analyses were carried out off-line, the members of the detected clusters were identified in the Excel database and cluster perimeters estimated by SaTScan were visualized in the Disease BioPortal as overlays in STV. All other presentation and analysis tools were applied on-line during BioPortal web-sessions.

Results

The first positive Swedish bird was submitted on February 24, 2010. Among the passive surveillance

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[1] Center for Animal Disease Modeling and Surveillance, School of Veterinary Medicine, University of California, Davis, USA
[2] National Veterinary Institute, Uppsala, Sweden
[3] CONICET-Fac. Cs. Veterinarias UNR, Argentina
* pwilleberg@ucdavis.edu

samples 65 birds were found positive to HPAI H5N1 using RT-PCR.

No cases were detected in the active surveillance program (birds trapped or hunted).

Published sequence data from isolated virus revealed two distinct sub-lineages [11, 12]. One bird was found positive on March 20 in a game holding primarily with mallards, located within the active surveillance zone around the index case,

In Denmark, the first positive bird was found on March 13, 2006. The total number of H5N1-positive wild bird samples was 45, of which only one positive sample was found through active surveillance, whereas passive surveillance of dead wild birds provided 44 cases [2]. A total of 22 HPAI H5N1 viruses were isolated, of which 8 have been sequenced and were found to be closely related [6]. The other 22 positive birds were positive in RRT-PCR testing, as described in [6]. In addition, several birds in a mixed backyard poultry flock located close to a previously found wild bird case were test-positive in May at the end of the epidemic [3].

Comparing data on the epidemics in the two countries reveals several common characteristics: Most positive birds were found close to the shore along the shallow waters of the Baltic Sea and its associated sounds and belts (Figure 1); the duration of the epidemics (the period between the first and the last detection of a positive case) was 56 days for Sweden (February 24 to April 21) and 70 days for Denmark (March 13 to May 22); and each country experienced one positive poultry farm, both with a mix of species, including ducks.

Figure 1: Cases of HPAI H5N1 in Sweden (SE) and Denmark (DK) by sampling location along the shorelines; from the AI BioPortal's STV-tool

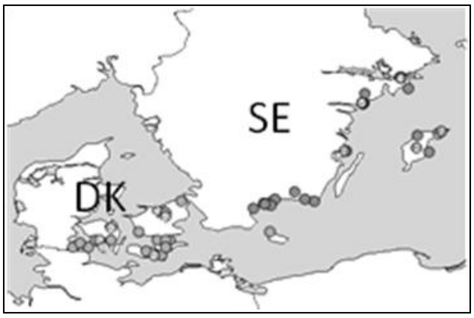


Table 1 summarizes the numerical composition of the joint database by country and species (Tufted Ducks and other species, respectively), as well as the resulting Relative Risk estimates for species (Tufted Ducks vs. other species) by country, and for country (Denmark vs. Sweden) by species.

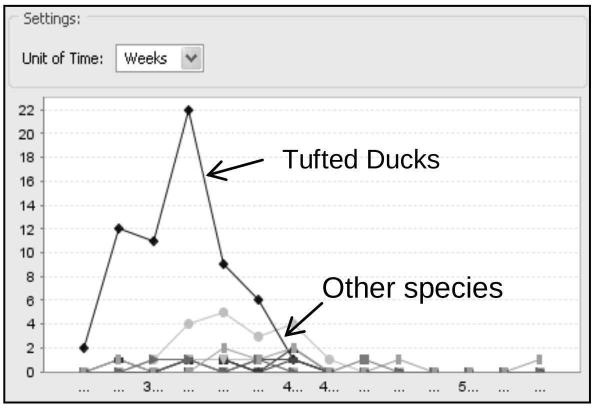
Overall, the prevalence was greater in Sweden than in Denmark, except among Tufted Ducks where the reverse was true (Table 1). The proportion of Tufted Ducks that tested positive was high in both countries (Table 1) [4], and positive Tufted Ducks were especially prevalent during the first period of the epidemic (Figure 2).

The multivariate SaTScan analysis detected clustering among Tufted Ducks related in time and space to clustering among other species, as shown in Figures. 3 and 4. The univariate Bernoulli-SaTScan model (B-STM) detected the cluster for the same time interval, but among all species combined (Figure 4). The clustering detected in both models was statistically significant at $p< 0.001$ [2]).

Table 1: Number of positive and tested birds by country and species, and Relative Risk by species and by country

	Species		Tested		Relative Risk	
Country		Positive		% positive	Species	Country
Sweden	All	65	518	12.5	-	1
	Tufted d.	36	83	43.4	6.5	1
	Other	29	435	6.7	1	1
Denmark	All	44	951	4.6	-	0.4
	Tufted d.	26	36	72.2	36.7	1.7
	Other	18	915	2	1	0.3
Total	All	109	1,469	7.4	-	-

Figure 2: Cases of HPAI H5N1 in Sweden and Denmark combined, by species and week: Tufted Ducks dominate early in the epidemic; from the AI BioPortal's STV-tool


Settings:

Unit of Time: Weeks

Figure 3: Map showing the location of the Tufted Duck multivariate cluster members in Denmark (see also Figure 4). The temporal window for the cluster is March 15 - 23, 2006; screen-shot of the AI BioPortal Google Earth tool.

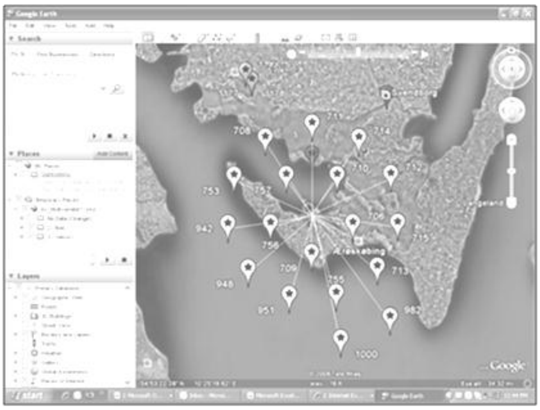
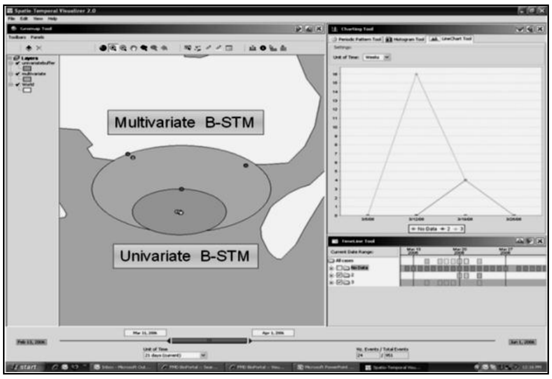


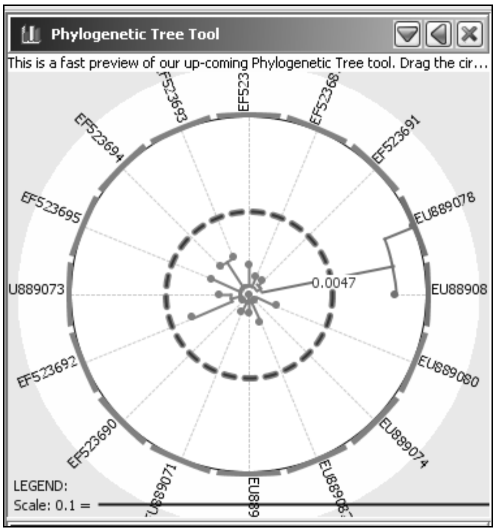
Figure 5 illustrates the phylogenetic tool (STGV) imbedded in the Disease BioPortal as applied to sequence data available from 8 Swedish and 8 Danish virus isolates. The tree clearly identifies the distance between the clusters of the two sub-lineages found in Sweden, of which one also comprises all of the Danish isolates [6, 11, 12].

Figure 4: Univariate and multivariate SaTScan cluster perimeters around respective HPAIV H5N1 cases in Denmark, March 15 – 23, 2006 shown in a screen-shot of the AI BioPortal STV-tool



When working with the STGV tool in the Disease BioPortal, the spatial (Figure 1) and the phylogenetic relationships (Figure 5) are simultaneously displayed on the monitor during the on-line session (in color coding) similar to the screen-shot shown in Figure 4.

Figure 5: Phylogenetic tree tool (STGV) from the AI BioPortal: The combined pool of 8 Danish and 8 Swedish sequenced HPAI H5N1 Virus.



This is a fast preview of our up-coming Phylogenetic Tree tool. Drag the cir...

Discussion

Prerequisite to understanding and managing the changing local, regional, or global distributions of disease or disease risks is the rapid access to current information that can provide the necessary situational awareness of disease and of factors potentially associated with disease risk. Most existing animal disease surveillance systems, however, are limited in their scope and do not contribute to global, real-time surveillance of emerging animal and zoonotic infections [15]. The Disease BioPortal was developed to fill this gap as a generic, globally accessible system providing flexible input and output solutions [1].

Here we present the features of the Disease BioPortal using a joint dataset of Swedish and Danish records from the HPAI H5N1 regional epidemic affecting mainly wild birds around the Baltic Sea during the winter-spring of 2006, as described earlier for the Danish dataset [2]. The Swedish dataset was recently uploaded to the newest version of the Disease BioPortal system. Preliminary contacts have been made with authorities of other affected countries in the Baltic Sea region to extend these analyses with a view to serve as a prototype for an international AI BioPortal.

Focusing on a restricted geographical region, the present comparative and joint study used and documented some of the Disease BioPortal's visualization tools: STV (Figures 1, 2 and 4), Google Earth (Figure 3) and STGV (Figure 5). The most recent Disease BioPortal version also accommodates SaTScan analysis as an integral part of the on-line functionality.

It should be emphasized, that not all the detailed findings reported above may be biologically significant, since passive surveillance data are likely to be influenced by various sampling biases [2].

Interested parties may test the functionality of the Disease Bioportal by login to the Swedish and Danish datasets at:

http://fmdbioportal.ucdavis.edu/ ,
Username: "Sweden" and Password: "avianflu"

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Piloting mobile phone-based syndromic surveillance of livestock diseases in Kenya

J.G. Walker*[1,2], E. Ogola[3] and D. Knobel[2,4]

Abstract

Livestock production is an important industry in Kenya, contributing over 12% to GDP, with the majority of the sector made up of small scale producers. As a result, diseases of livestock can have a devastating effect on the livelihoods of individuals that rely on livestock for subsistence; in addition livestock handlers are at risk for transmission of zoonotic diseases. However, current disease surveillance by the Department of Veterinary Services is limited and paper-based reports are slow to reach a central database. More extensive and timely disease surveillance should be a priority in order to detect outbreaks of diseases, including emerging and zoonotic diseases, before they are widespread. Mobile technology has been used in various sectors to transmit data from resource poor areas. Building on the existing software FrontlineSMS, we implemented a community-based livestock disease surveillance system using mobile phone reporting in Asembo, Kenya from September to November 2010. Challenges to successful implementation included problems of network coverage as well as underreporting of incidents. The results of the pilot study as well as lessons learned and plans for the execution of a more robust and scalable system are presented.

Keywords: multiple disease/species surveillance, syndromic surveillance, event-based surveillance, new technologies for data collection and transmission

Introduction

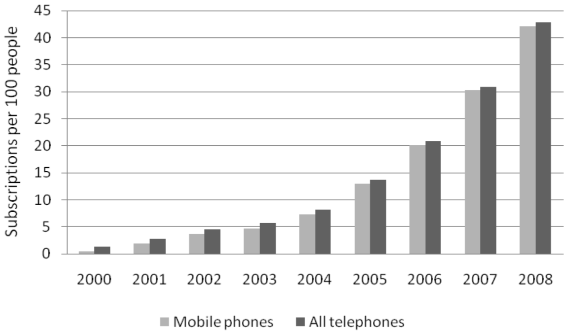
Almost 75% of the population in Kenya is engaged in agriculture, with half of agricultural revenue coming from livestock production, resulting in a total contribution to GDP from livestock of 12% [1]. The livestock sector is predominantly made up of small scale subsistence farmers in rural areas. In the rural division of Asembo in Nyanza province in Kenya, 89% of the population own domestic animals. The livestock density in Nyanza province is the second highest in the country, with 137.96 cattle per square kilometer [2]. However, access to animal health care in the area is limited, and Kenya overall is ranked 61st out of 89 countries by the ratio of veterinary personnel to livestock [2].

Current animal disease surveillance efforts in Kenya conducted by the Department of Veterinary Services are limited, with paper reports of notifiable diseases taking a long time to reach a central database. This time delay can have devastating effects. In 1997 an outbreak of Rift Valley Fever in Kenya led to 400 human deaths before reports were received at the national level; later studies showed that the human epidemic was preceded by high rates of abortion and death in the livestock owned by the affected community [3]. Challenges to implementation of a livestock disease surveillance system include inadequate road network and electricity infrastructure. Electronic transmission over mobile networks could allow for more timely transmission of animal disease surveillance data and trigger alerts of outbreaks of zoonotic diseases and economically important diseases of livestock early enough in the outbreak for preventive measures to be taken. By conducting syndromic surveillance, it is possible to detect a wide range of diseases other than those that are currently notifiable, such as new or emerging diseases.

Although more than half of the rural population in Kenya lives below the poverty line [1], many people have access to a mobile phone. Mobile phone coverage is growing rapidly in Kenya, with 42 mobile subscribers per 100 people in 2008; on the other hand landline telephone infrastructure is extremely limited, with only 0.65 telephone mainlines per 100 people in the same year [4] (Figure 1).

In order to investigate the success of mobile phone based syndromic disease surveillance and the potential for ease of uptake by the Department of Veterinary Services, we piloted mobile phone-based syndromic disease surveillance in 10 villages in western Kenya in 2010.

Figure 1: Telephone subscriptions in Kenya, 2000-2008 (per 100 people) [4]



Materials and methods

A mobile phone-based syndromic surveillance system for ruminant diseases was implemented in September 2010 in 10 villages in Asembo division, Nyanza Province, Kenya.

The system, known as ADSARS (Animal Disease Surveillance and Response System), is triggered by SMS reports from animal health reporters in the

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[1] Compton Mentor Fellowship - * jogwalker@gmail.com

[2] Visiting scientist, KEMRI/CDC Research and Public Health Collaboration

[3] KEMRI/CDC Research and Public Health Collaboration

[4] Faculty of Veterinary Science, University of Pretoria

community. A response team of animal health technicians based at the center of the study area responds to each report and examines the animal, recording data on clinical signs and collecting diagnostic samples to submit to the lab at the KEMRI/CDC base in Kisumu.

One to two community-based animal health reporters (AHRs) were identified in each village. Those selected were well established in the village and have knowledge of livestock management and as a result tend to be older individuals. The AHRs were employed as casuals by KEMRI/CDC and reimbursed 350 KES for each day's work associated with a valid report in order to cover the cost of the SMS and the work associated with each report. This work includes assessing whether a report fits within the syndrome definitions of the study and acting as a liaison between the response team and the animal's owner.

Each AHR was provided with a Nokia 2730 with the FrontlineSMS add-in java application FrontlineForms [5] installed and loaded with a report form in the local language, Dholuo. The form includes alphanumeric entry fields for identifying the name of the animal owner and his or her location as well as checkboxes for the species of animal and the syndromes exhibited. Two training sessions were held to ensure that the AHRs were comfortable entering data into the form. When the form is submitted, an encoded SMS is sent to a hub computer with a GSM modem linked to FrontlineSMS software in the response team's office.

When a form is received, the response team contacts the AHR to arrange to visit the animal as soon as possible. At the visit, informed consent is obtained from the head of the household before the animal is examined and data on clinical signs are entered in a personal digital assistant (PDA) and diagnostic samples are collected. One treatment dose is provided at no cost.

In the pilot phase of the program, reports were considered valid and data collected if the animal was a domestic ruminant (cow, sheep, or goat) and had displayed clinical signs that fit within the syndromes of abortion/ stillbirth, nervous signs, or red urine within the preceding 24 hours. These syndromes were selected based on the clinical presentation of zoonotic or emerging diseases that are known or suspected to be present in the study area, for example Q fever, brucellosis, and babesiosis. Reports of live birth were also investigated.

Baseline data on the livestock population in the villages were collected through a cross-sectional survey.

Results

SMS reports were successfully received into the FrontlineSMS program only intermittently, although troubleshooting tests suggest that messages were sent successfully by AHRs. As a result, AHRs called to follow up on reports that were sent and resubmitted reports orally if they had not been received.

A total of 95 reports were submitted between 17 September and 18 November 2010. Of the 95 reports submitted, only 35 (37%) were successfully received via SMS in FrontlineSMS.

Reports were received from each of the fourteen AHRs in the ten villages, with a mean of 6.8 reports per AHR (range = 1 to 20; median = 5.5) or 9.5 reports per village (range = 1 to 23; median = 5.5). Of these, 91 (96%) were valid reports that were investigated further (Table 1).

The four invalid reports were all received within the first nine days of the pilot study. Three were reports of live birth while one was abortion/stillbirth. They were considered invalid because more than 24 hours had elapsed between the event and the submission of the report.

Table 1: Valid reports by syndrome and species

	Cattle	*Sheep*	*Goats*	**Total**
Live birth	35	21	25	81
Abortion/stillbirth	2	1	5	8
Nervous signs	2	-	-	2
Blood in urine	-	-	-	-
Total	39	22	30	91

By comparing the reports received to the live birth and abortion rates predicted for the total livestock population in the 10 villages, the percent of underreporting was estimated (Table 2).

Table 2: Estimated underreporting of live births and abortions by species

	Cattle	*Sheep*	*Goats*
No. adult females	2194	753	2486
Births/adult female/year	0.57	0.72	0.85
Predicted births in 2 months	208	90	352
Reported births in 2 months	35	21	25
Estimated % underreporting	83.21	76.77	92.90
Abortions*/adult female/year	0.02	0.05	0.04
Abortions*/year	44	38	99
Predicted abortions* in 2 mo.	7	6	17
Reported abortions* in 2 mo.	2	1	5
Estimated % underreporting	72.66	84.07	69.84

*Includes stillbirths

Discussion

The results of this pilot study highlight several challenges of livestock disease surveillance, and particularly mobile-phone based surveillance in Kenya. These results should be taken into account in the creation of surveillance systems based on mobile technology in the developing world. Critical challenges include the reliability of mobile phone networks and electricity in the study site. Mobile phone literacy especially among older community members may be limited, and as a result extensive training was necessary to ensure the AHRs were comfortable with SMS reporting.

The failure of the FrontlineSMS software to receive the majority of SMS reports can be explained either by the very poor network coverage in the office where the hub computer was located or by a failure of the software to properly communicate with the GSM modem. In order to resolve this problem, the server computer could be relocated to a remote location with better network coverage and SMS alerts could be automatically forwarded to the response team in the field when a report is received.

The abortion and live birth reports indicate that in the pilot phase of the study there was significant under-reporting of events. Limited conclusions can be drawn from only two months of data, especially for abortion rates which are likely to be highly seasonal and dependent on outbreaks. However, given a longer time period and data on seasonality, live birth reports will be a valuable source of information for indicating under-reporting in the system because the predicted birth rate can be estimated from existing data on livestock numbers.

Under-reporting in surveillance systems can occur for a variety of reasons and common factors have been outlined in a recent report by the World Bank [6]. The primary reasons are divided into unwillingness or inability to report. In this case, underreporting due to unwillingness is likely to come from the farmers rather than the AHRs since the AHRs are compensated for their efforts. Unwillingness could be due to lack of compensation or incentives for farmers. In this study we attempted to incentivize reporting by providing a free dose of treatment for the animal. However, farmers may not feel a need to report successful live births because the animal is not ill. Inability is further divided into inability to detect and inability to report. In order to avoid inability to detect, the syndromes were chosen to be easily identifiable without any equipment or special knowledge. Although AHRs are based in each community, if a farmer does not own a mobile phone he or she might have to walk to find the AHR, and this could contribute to inability to report.

An additional cause of underreporting could be a lack of awareness of the threat of a disease. For endemic diseases, people may become accustomed to animals falling ill and not consider a disease event to be worth reporting [6]. In addition, interviews we conducted in the study area indicate that there is limited knowledge of zoonotic diseases. The advantage of an animal disease surveillance system that involves a response by a trained animal health professional, even if animal health technicians rather than veterinarians, is that it provides an opportunity for education each time the community members interact with the animal health providers. When responding to a report, the response team should make sure to discuss methods for preventing transmission of zoonoses and other livestock diseases. In addition, community based animal health reporters can learn each time they are involved with a report and bring that knowledge back to the community.

Future Work: Based on the results of this pilot study a similar mobile phone based syndromic surveillance system will be implemented in 33 villages in the same area. The SMS server will be moved to a central location with reliable cell phone coverage, internet, and electricity. When a report is received, an SMS will be automatically sent to the field team. Simple diagnostic tests will be conducted in the field lab and further samples tested in the lab in Kisumu and lab results shared with the farmers.

The reliance of the system on mobile technology will be expanded, with data on clinical signs collected on smart phones instead of PDAs. A diagnostic support tool will be integrated into the clinical signs collection interface on the smartphone to provide assistance to the response team of animal health technicians. The system will be based on Bayesian belief networks and particularly on the existing BOSSS [7] and the CaDDiS [8] systems. The use of such a system will promote uptake and sustainability of the system by providing an incentive to animal health technicians and livestock keepers in the form of differential diagnoses and advice on further action.

The use of smartphones for clinical signs data collection will allow the data to be transmitted to a central server in real time. Pattern recognition software will be run on the central clinical signs database for early detection of outbreaks of diseases with known syndrome definitions or of unknown emerging diseases with anomalous clinical sign combinations.

The system will be evaluated for its ability to detect outbreaks of zoonotic diseases by comparison to a hospital-based human disease surveillance system currently conducted by KEMRI/CDC in the same region.

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Surveillance of cattle population through real-time mortality monitoring

J.-B. Perrin[1,3]*, P. Hendrikx[2], J.-L. Vinard[1], C. Ducrot[3] and D. Calavas[1]

Abstract

The OMAR project has been launched in 2009 to model livestock mortality in space and time, and design a monitoring system able to detect anomalies possibly associated with health events. Since our first results seemed to confirm the interest of mortality as unspecific surveillance indicator, we are currently implementing a near real-time cattle mortality monitoring system, based on data collected daily by rendering plants.

Keywords: mortality monitoring, syndromic surveillance, early warning systems, use of existing data

The full text of this paper will be published in a special edition of Preventive Veterinary Medicine.

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[1] Epidemiology Unit, French Agency for Food, Environmental and Occupational Health & Safety (Anses), Lyon, France - *jean-baptiste.perrin@anses.fr

[2] Scientific Directorate for Laboratories, French Agency for Food, Environmental and Occupational Health & Safety (Anses), Lyon, France

[3] Animal Epidemiology Unit, UR346, INRA, St Genès Champanelle, France

Echinococcosis surveillance: Bayesian time-space analysis of *Echinococcus multilocularis*-infections in foxes in Thuringia, Germany

C. Staubach[1], L. Hoffmann[2], V. Schmid[3], M. Ziller[1], K. Tackmann[1] and **F.J. Conraths**[1*]

Abstract

The prevalence of *Echinococcus multilocularis* in foxes in Thuringa, Germany, was monitored from 1990 through 2009, by sampling 26,220 foxes. Data were analysed in space and time using a hierarchical Bayesian model. The prevalence increased from 11.9% (9.9-14.0%) in 1990 to 42.0 (39.1-44.1%) in 2005. The infection had spread from North-western parts over the entire state by 2004. The model helped to overcome problems of missing data and varying sample sizes in different spatial and temporal units and to evaluate the monitoring strategy.

Keywords: *Echinococcus multilocularis*, alveolar echinococcosis, fox, monitoring, Bayesian statistics.

Introduction

Alveolar echinococcosis is a rare human disease that ends often lethal if left untreated. It is caused by the larval stage of the cestode parasite, *Echinococcus multilocularis*. In central Europe, the main definitive host of *E. multilocularis* is the red fox (*Vulpes vulpes*), but occasionally the parasite is also found in dogs and cats [1, 2]. Raccoon dogs (*Nyctereutes procyonoides*), which invaded large territories in Europe in recent decades, represent a new definitive host whose epidemiological role is not yet clear. To assess the risk for human infection, it is important to monitor the epidemiological situation of *E. multilocularis* in its definitive hosts in time and space.

The spatial and temporal analysis of wildlife diseases is particularly challenging, because the population size of the target species is usually unknown, random sampling of animals is often not possible, and the spatial boundaries of epidemiologic units may be artificially chosen and not relevant to disease spread [3]. Hunting foxes, the most important definitive hosts of *E. multilocularis* in Europe, is not a random selection. With respect to their spatial origin, samples of foxes obtained by hunting are usually heterogeneous and not randomly distributed.

Moreover, random variation in the estimated prevalence per geographic unit is possible, so that the significance of spatial and temporal changes is difficult to assess. Data may be missing for several spatial or temporal units leading to increased uncertainty and different sample sizes may be available from the spatial units. The sample size in some spatial units or strata may even be too low to obtain reliable prevalence estimates [3].

To overcome these constraints, a hierarchical Bayesian space-time model [3] was used and the distribution of the model parameters and their variability estimated by using a Markov chain Monte Carlo (MCMC) simulation technique, on the basis of the sample size, number of cases per spatial unit and time interval, and the adjacency matrix of the municipalities respectively.

Materials and methods

A total of 26,220 foxes that were hunted or found dead in the state of Thuringia, Germany, between 1990 and 2009 were examined using an OIE/WHO standard protocol, the intestinal scraping technique [4]. Data on the foxes including the date of hunting/death, location (local community; district) and the result of the examination for *E. multilocularis* were recorded [5] and exported into a data base (Microsoft Access) that could be linked to a geographical information system. Further data management and mapping was done in ArcGIS Arcview 9.3 (ESRI, Redlands, CA, USA).

A hierarchical Bayesian space-time model was set up to analyse the data from the state of Thuringia from 1990-2009, and to test for significance of temporal and spatial effects in the study area. The model is based on a Bernoulli observation model and is an extension of an existing hierarchical model proposed for disease mapping [Staubach *et al.*, 2002], with the addition of time effects. In this model, the number of cases x is binomial distributed in each spatial unit i at each time t

$$x_{it} \sim \text{Bin}\,(n_{it}\,,\,\pi_{it})$$

where n is the sample size and π the prevalence. The parameter π it is modelled with a logistic link

$$\eta_{it} = \log\,(\pi_{it} / 1 - \pi_{it}) = \mu + \upsilon_i + \nu_i + \phi_t$$

where

μ is the intercept (average logit prevalence),

υ_i is a structured spatial effect in the area *i*,

ν_i is an unstructured random effect, taking into account the heterogeneity mainly based on the sample size per spatial unit

ϕ_t is a time effect, as deviation from the average logit prevalence at the time *t*.

The effect υ_i covers spatial dependencies, which can be described by a Gaussian Markov Random field (GMRF):

$$\upsilon_i \sim N\,(\upsilon_{\text{neigh}} / k\,,\,\sigma_\upsilon / k\,)$$

with $\upsilon_{\text{neigh}} = \upsilon_i$

and k = number of neighbouring units *j* of unit *i*.

Only the first neighbours of each spatial unit were taken into account. The unstructured random effect ν_i has a priori a Gaussian distribution:

$$\nu_i \sim N\,(0\,,\,\sigma_\nu).$$

In units with no observation, ν_i is set to 0.

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[1] Friedrich-Loeffler-Institut, Federal Research Institute for Animal Health, Wusterhausen, Germany - * franz.conraths@fli.bund.de

[2] Thuringian State Authority for Food Safety and Consumer Protection, Bad Langensalza, Germany.

[3] Ludwig-Maximilians-University, Department of Statistics, Munich, Germany

The time effect ϕ_t is a special case of the random walk (RW), that is, the time effect has a priori a Gaussian distribution. We assume a linear trend, which can be described as random walk of second order:

$\phi_t \sim N(2\,\phi_{t-1} - \phi_{t-2}, \sigma_\phi)$.

For the unknown variance parameters, Inverse Gamma priors with the following hyper parameters were used:

$\sigma_\upsilon \sim$ Inv-gamma (1 , 0.001)
$\sigma_v \sim$ Inv-gamma (1 , 0.05), and
$\sigma_\phi \sim$ Inv-gamma (1 , 0.05).

The joint distribution of the full Bayesian model is analytically intractable. Therefore, a MCMC algorithm was used in form of a combination of Metropolis-Hastings and Gibbs steps in order to estimate the distribution of the model parameters and their variability on the basis of the sample size, the number of cases per spatial unit and time interval, and the adjacency matrix of the municipalities in a C++ program with Fortran code [3, 6, 7]. After 1,000 iterations, which were considered as burn-in phase, every 50th iteration of the next 50,000 iterations was saved as a sample from the posterior distribution.

Statistical analysis and evaluation of the model output was done in the R software package (R Development Core Team, 2010). Convergence of the MCMC chain was assessed using standard diagnostic plots and tests in the CODA library of R.

Result

In a total of 26,220 foxes sampled in Thuringia between 1990 and 2009, 6853 animals were found infected with *E. multilocularis.* An explorative analysis of sample sizes at district level for 1990-2009 showed that the sampling sizes per spatial and time unit were often too low to obtain reliable prevalence estimates (Figure 1), although efforts had been made to make the sample size as large as possible. Moreover, the sample sizes obtained from different spatial units varied considerably over time.

Spatial analysis of the data using the Bayesian model clearly showed a substantial expansion of the area where *E. multilocularis* infections occurred in foxes. In 1990, the highest prevalence was estimated in the Northwest of Thuringia, whereas most of the eastern districts were still free from the parasite or the estimated prevalence of infected foxes was lower than 10%. Until 1993, the prevalence had increased in the western districts. In 1998, the estimated prevalence in two south-eastern districts, where only 11 or 1 infected foxes had been detected in the years before, had risen to more than 30%. By 2004, the infection had spread over the entire state. This situation remained unchanged until 2009, although the estimated prevalence varied in some districts over time. The results show that the prevalence increased in particular in the western part of the state and that the infection spread in eastern direction.

Temporal analysis indicates a clear increase of the estimated prevalence from 11.9% (95% confidence interval 9.9-14.0%) to values between 30 and approximately 40 percent in recent years with a peak of 42.0 (95% confidence interval 39.1-44.1%) in 2005. The time effect as analysed by the Bayesian model shows a significant increasing trend during the whole observation period, even if years with lower sample sizes are taken into account (Figure 2).

Figure 1: Distribution of test results on foxes for *E. multilocularis* per spatial unit and year.

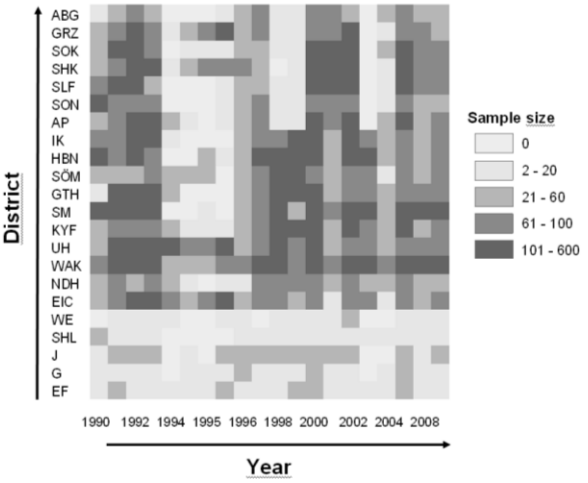
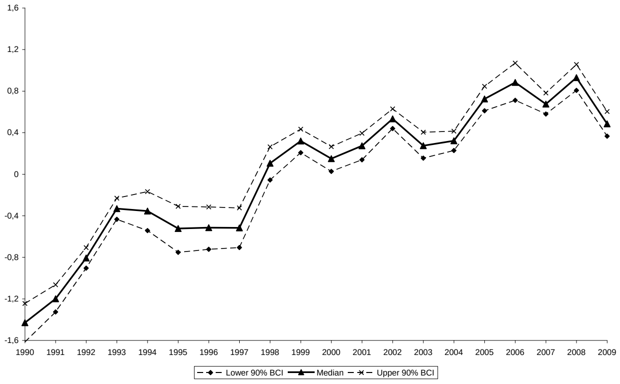


Figure 2: Median time effect ϕ_t and 90 Bayesian confidence intervals (BCI) of the Bayesian model for the period 1990-2009

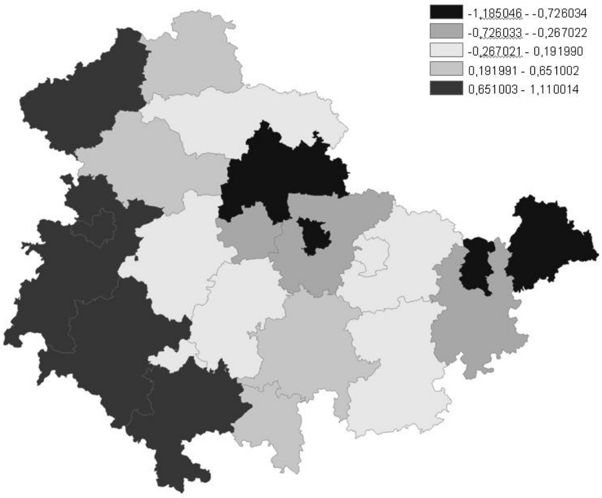


An increased risk of infection adjusted for the temporal trend in the Bayesian model can be observed particularly in the western districts of Thuringia, while a negative spatial effect is evident in the eastern part of the study region (Figure 3).

Discussion

Human alveolar echinococcosis is an emerging disease in Europe [8]. Surveys conducted in central Europe in the past 20 years revealed that *E. multilocularis* is more widely distributed than previously anticipated [2, 8]. The prevalence of *E. multilocularis* in its definitive hosts can vary widely between countries and regions from about 1 to over 60% [9]. Small endemic foci with a diameter of approximately 25 km can exist [5].

Figure 3: Median structured spatial effect υ_i per district of the Bayesian model for the period 1990-2009



The spatial and temporal dynamics of the infection in a number of affected countries have been controversially discussed but the quality of the availably monitoring data was often not sufficient to assess whether the prevalence was increasing in particular regions or if endemic areas were extending. We addressed this issue by analysing monitoring data from Thuringia, Germany, as an example, since a comprehensive set of monitoring data for the period from 1990 through to 2009 was available and because circumstantial evidence suggested an increase of the prevalence, at least in some areas, and a widening of the endemic area.

The analysis of variation of the risk for a given disease in space and time is a key issue in descriptive epidemiology. An infectious disease typically spreads via contact between infected and susceptible animals. Often administrative structures are the only feasible way to map samples in wildlife population surveys. Therefore, available data are frequently aggregated on the level administrative units and regular time intervals. However, when data are stratified to reflect a potential space-time variation, maximum likelihood estimates of the area-specific prevalence and of its time-trend can be seriously affected by random variation due to the low number of cases and the corresponding sample size in a given unit of space and time [3]. Furthermore, the detection of spatial patterns is complicated by missing data as it is nearly impossible to cover of all areas and time intervals with samples in wildlife surveys. Therefore, the mapping of raw surveillance data may lead to false interpretations of disease clusters, disease-free areas and time-trends [3]. We therefore applied a model which is an extension of an existing hierarchical spatial model proposed for disease mapping that also accounts for time effects and potentially allows the inclusion of covariates (*e.g.* age, landscape proportions) and space-time interaction terms. The model uses spatial and temporal dependencies to make estimates in space-time units with low sample size more robust, and even allows estimating the prevalence in units with no samples at all if samples from neighbouring units exist.

By using an auxiliary variable approach [7], the MCMC simulation becomes more efficient [6] than in the original approach [3]. As most full conditional distributions in this model are multivariate Gaussian, we used a block update algorithm [10] to decrease simulation error and to save time. It has been shown, however, that approximate Bayesian inference using integrated nested laplace approximation (INLA) might reduce the computing time dramatically without increasing the error of the estimates significantly [11]. We are currently investigating if such algorithms can be used to estimate the parameters of our model.

We believe that the model we used to evaluate the data is widely applicable and can be applied to analyse data sets with gaps and variable sample sizes per spatial and temporal unit.

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Dioxins and dioxin-like polychlorinated biphenyls in the dairy products from a small area in Northern Italy: surveillance data supported the hypothesis of a common source contamination

R. Desiato[1]*, S. Bertolini, E. Baioni, I. Francesco and G. Ru

Abstract

PCDD/Fs and DL-PCBs levels exceeding the legislation limits were detected in bovine milk and meat samples collected in Piedmont region (Valsusa valley) between 2004 and 2007. Data coming from risk-based surveillance carried out between 2004 and 2007 and data from the national residue plan were used to design two different studies: a fingerprint study and a spatial study. The aim of this work was to assess whether the contamination in milk and meat was consistent with a common source or different sources.

1. Fingerprints study. Seventy samples of milk and 68 samples of muscle were considered, of which respectively 45 and 23 coming from Valsusa whereas the remaining samples obtained through the national residue plan in other Italian regions. Cluster and principal component analyses was performed to identify chemical profiles based on congeners' distribution.

2. Spatial study. Data of concentration values of PCDD/Fs and DL-PCBs in the bulk milk from 27 herds, sampled in a 4-year period (2004-2007) were matched to each georeferenced land parcel used for fodder production.

The cluster analysis applied to values in milk showed two main clusters by geographical location; a similar pattern was obtained for meat samples and also when carrying out the analysis on DL-PCBs data. Choropleth maps obtained through the spatial interpolation technique applied to either PCDD/Fs or DL-PCBs indicated the highest level of pollution geographically juxtaposed to the steel plant location

The results of both the studies support the hypothesis of a common source contamination.

Keywords: dioxin, surveillance, kriging, choropleth maps, congeners profile.

Introduction

Persistent organochlorine compounds such as polychlorinated dibenzo-p-dioxins, polychlorinated dibenzofurans (PCDD/Fs), and dioxin-like polychlorinated biphenyls (DL-PCBs), for a total of 29 congeners, are potent endocrine-disrupting chemicals, unintentional byproducts of a variety of industrial and combustion processes involving chlorine-containing materials.

In case of micropollutants in foods of animal origin the European legislation requires investigations to trace-back the pollution source in order to implement the needed risk management measures.

In our case, PCDD/Fs and DL-PCBs levels exceeding the legislation limits were detected in bovine milk and samples collected in a mountainous valley (Valsusa) of the Piedmont region between 2004 and 2007 and leading to the temporary suspension of activity for a number of farms.

The exposure to PCDD/Fs and DL-PCBs in cattle is mainly related to feed and often caused by ingestion of contaminated fodder. Although a few samples of soil, vegetables and atmospheric emissions were available from the area suggesting a local steel plant as potential source of contamination, relevant data on the geographical distribution of the environmental contamination were missing.

The aims of this study, which is an exposure assessment exercise part of a more extended risk assessment, were:

1. to assess whether the contamination in milk and meat was consistent with a common source or different sources, by identifying pollutants fingerprints in contaminated food products [1]. In particular, a characterization of congeners was carried out in order to assess whether the local samples belong to a single group whose characteristics (the so called congener profile) differ from those of contaminated samples from other Italian areas;
2. to identify and characterize the area of contamination using available data on PCDD/Fs and DL-PCBs concentration in milk and on the location of origin of the fodder used to feed the dairy cows.

Materials and methods

Data coming from risk-based surveillance carried out between 2004 and 2007 were used to design two different studies:

1. Fingerprints study. Analytical data in bulk milk and meat collected during veterinary official controls in two different campaigns (between 2004 and 2006 and in 2007) were obtained with the detail of the congeners. To perform comparisons with samples of other geographical origin, parallel data from the national residue plan were obtained too. Overall 70 samples of milk and 68 samples of muscle were considered, of which 45 and 23 coming from Valsusa respectively. A hierarchical agglomerative cluster analysis based on the concentration of individual congeners determined in each sample has been used to group the samples by their more or less similar relative congener concentration [2].

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[1] BEAR, Biostatistica Epidemiologia & Analisi del Rischio, Istituto Zooprofilattico Sperimentale di Piemonte, Liguria e Valle d'Aosta, Torino, Italy - * rosanna.desiato@izsto.it

PCDD/Fs and DL-PCBs were treated separately. Moreover a principal component analysis was performed to identify chemical congener profiles. All statistical analysis were carried out using Stata 9.

2. Spatial study. Assuming that the exposure was related to a general environmental contamination and not to dangerous practices in each of the farms involved by the contamination, a geographical study was carried out. Three sets of data were available and used:
   a. data of concentration values of PCDD/Fs and DL-PCBs in the bulk milk from 27 herds, sampled in a 4-year period (2004-2007). When more than one value of concentration was available, the highest one was used for the statistical analysis;
   b. the list of any singular land parcel as identified by the regional rural register that each of the 27 farmers uses for fodder production;
   c. the complete georeferenced data of all land parcels (as identified by the regional land register) of the 23 municipalities of the Valsusa, our study area severely polluted by PCDD/F and PCBs.

Concentration values of PCDD/Fs and DL-PCBs detected in bulk milk were matched to each georeferenced land parcel used for fodder production and assigned as an attribute to the parcel's centroids. After that, the empirical semivariogram was used to verify the spatial dependency of data and to quantify the local spatial variability as a function of distance [3]. As the farmer land parcels represent sample point locations of the overall area, spatial ordinary and lognormal kriging techniques, *i.e.* an interpolation method, have been applied to generate a spatially continuous representation. Finally choropleth maps were used to display results. All spatial analysis were carried out using the Spatial Analyst extension of the ArcView 9.2 software.

Result

Fingerprints study. The cluster analysis allowed to build dendrograms by group of samples. With regards to PCDD/Fs, values in milk showed two main clusters by geographical location: most of the local samples has been grouped in a distinct cluster from those with different Italian geographical origin (Figure 1). A similar pattern was obtained for meat samples and also when carrying out the analysis on DL-PCBs data. Moreover two further subgroups by control campaign were identified with regards to DL-PCBs. Principal component analysis on milk samples gave similar results to cluster analysis in discriminating on a geographical basis the two main groups (Figure 2); moreover it allowed the identification of a different DL-PCBs congener profile for the samples collected in 2007 compared with those from the previous monitoring campaign. When applying principal component analysis technique to the meat samples, only PCDD/Fs data allowed a geographical discrimination.

Spatial study. The choropleth maps obtained through the kriging interpolation applied to either PCDD/Fs (Figure 3) or DL-PCBs were consistent in indicating the highest level of pollution geographically juxtaposed to the steel plant location. Moreover, a progressively decrease in the contamination was evident at increasing distance from the source.

Figure 1: Dendrogram of PCDD/Fs in milk samples from Valsusa (Piedmont) compared with milk samples from other Italian regions; almost all samples coming from Valsusa have been clustered in a single group

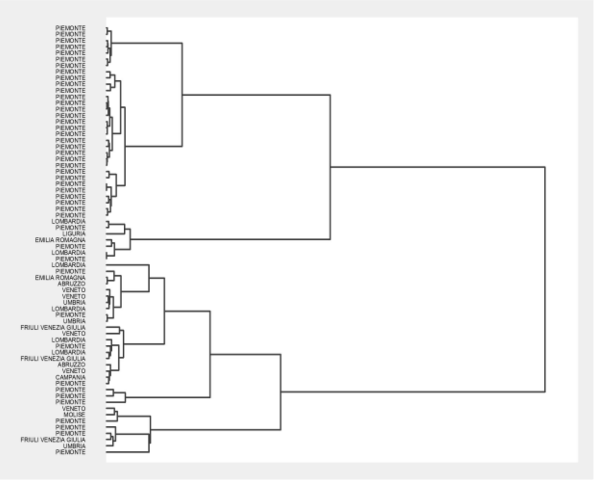


Figure 2: Score plot of component 1 and component 2 for dioxins values in milk by region; Valsusa samples are clustered in the right part for component 1 value > -1.

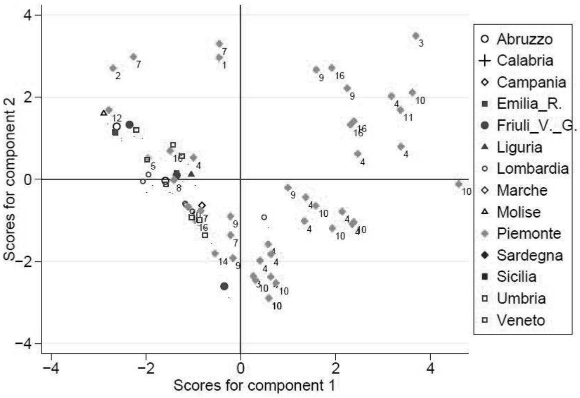
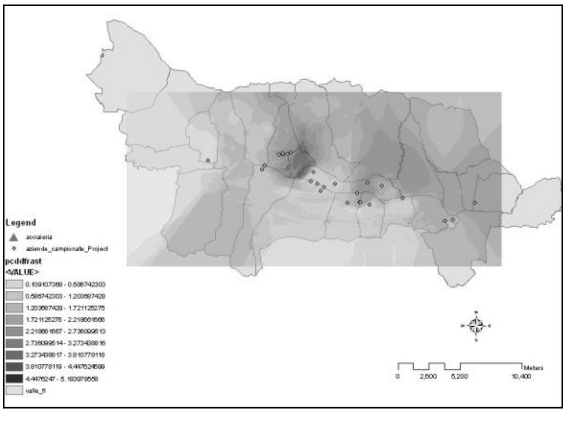


Figure 3: Ordinary kriging on concentration values of PCDD/Fs detected in bulk milk matched to each georeferenced land parcel used for fodder production



Discussion

The results of both the studies support the hypothesis of a common source contamination. In particular the statistical techniques applied to characterize the contamination fingerprints are consistent and point out a relative homogeneity among the local samples and heterogeneity with respect to those obtained from other Italian regions. Moreover the possibility of matching the information of pollutants concentration values in milk with the locations of fodder production allowed the identification of the likely main source of contamination and the description of the its geographical distribution in the surrounding farmland. The maps obtained were helpful for health authorities in identifying priorities for pollution mitigation and in improving the targeting of the monitoring activities of the local dairy products. After the conclusion of the study our results have been used by the local authorities to inform the risk management measures applied to reduce the exposure.

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Capture-recapture as a tool to assess animal disease surveillance: the example of foot-and-mouth disease in Cambodia

T. Vergne[1,2*], F. Goutard[1], D. Holl[3], C. Bellet[1], F. Roger[1], V. Grosbois[1] and B. Dufour[2]

Abstract

We performed a two-source capture-recapture analysis on foot-and-mouth disease in Svay Rieng province (Cambodia) to estimate the number of outbreaks that occurred in this province in 2009. As the first source, we used the list of infected villages that were reported to the national level, and as the second source, we used a protocol designed specifically for this analysis that was based on a participatory approach in villages selected by a targeted strategy. We developed a case matching protocol to be consistent with the outbreak definition of the OIE, and in so doing, we estimated that the number of FMD outbreaks in Svay Rieng province in 2009 was 11.3 ($CI_{95\%}$ 7.0-29.4), and that the sensitivity of the report to the national level was 0.66 ($CI_{95\%}$ 0.27-1.00).

Keywords: capture-recapture, surveillance, foot-and-mouth disease, participatory epidemiology, Cambodia

The full text of this paper will be published in a special edition of Preventive Veterinary Medicine.

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[1] CIRAD, AGIRs unit, Montpellier, France - * timothee.vergne@cirad.fr

[2] ENVA-Anses, USC EpiMAI, Ecole Nationale Vétérinaire d'Alfort, Maisons-Alfort, France

[3] National Veterinary Research Institute, Phnom Penh, Cambodia

Dog population size and dynamics: a method for control

E. Baioni[1*], K. Capello[2], A. Biggeri[3], F. Mutinelli[2] and M. Vascellari[2]

Abstract

Estimation of the dog population size at the national level is essential for planning animal welfare and control strategies. We devised a reliable method to estimate a regional dog population and to improve the local canine register office database.

Keywords: size, population, pet, control.

Introduction

There are several reasons why during the last thirty years some public and private enterprises were urged to attempt an estimate of a country's dog and cat census. Prominent among those motivations are goals relevant to public health:

- The study of shared human pathologies so as to acquire a better understanding of their pathogenesis and aetiology [1, 2].
- The determination of the abundance and distribution of the dog and cat population for the study of the incidence of some zoonoses (*e.g.*, leishmaniasis, rabies, toxoplasmosis).
- The investigation of the variations in dog and cat population and the need to plan for their control.

In addition economic reasons are relevant to the veterinary field: market research in the use of products for common pets and of the veterinary services of a given area [3, 4].

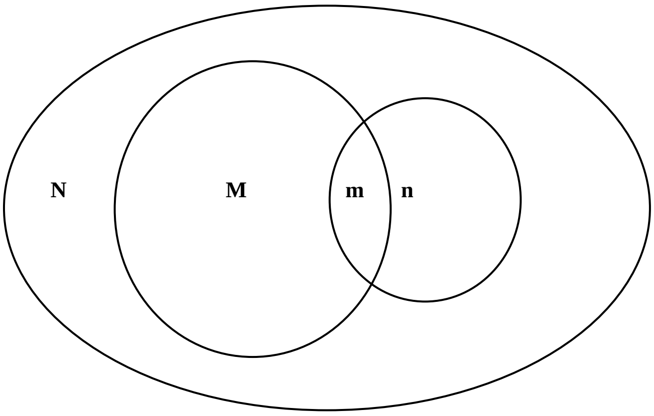
Our research group has recently performed an evaluation of the canine and feline population of the Venezia and Vicenza provinces in order to create a canine and feline cancer registry. At the moment we are working for the estimation of the canine population of the entire Veneto region. A small number of studies concerning this field are published [5, 6]. Some countries obtain estimates through the work of national institutes of statistic research. For instance, in the US the American Veterinary Medical Association calculated different coefficients that, mapped with the number of families or inhabitants in a certain area, makes it possible to guess the pertinent canine and feline population.

Unlike other countries, Italy set up centralized dog registry offices; in spite of this, the lack of an active and continuous update of data produces unreliable figures. This may result in an overestimation of the population, caused by the failure to eliminate the deceased subjects from the database. The only available national estimates attribute to our country a population of 6.5 million dogs [7]. For this reason in the past we used a different method to estimate the canine population especially. A regression model was developed and, starting from data of the canine population of the same area, it was possible to estimate the number of dogs in the two provinces municipalities; two variables were considered as more influent on the estimate: the inhabitant density per square kilometre and the number of families per municipality. The model fitted accurately the data resulted from small-medium municipalities, but it was found more inaccurate in the urban population estimate. The principal reason was the lack of data from the biggest municipalities of the Piedmont area. In order to obtain a more reliable method to use for the whole Veneto region and then for the whole Italian territory, we are testing a capture-recapture method crossing the census data of the municipalities with the data obtained by interviewing a sample of families from a bigger number of larger sized municipalities.

Materials and methods

The capture-recapture (CR) method (Lincoln Petersen) - normally used in ecology - is being adopted and applied to the canine population of the Veneto region. The first stage of CR is the capture of a number of individuals (M) that were marked and subsequently released within the general population. At a second stage a new random sample (n) is captured out of which (m) results to be already marked. If the marked subjects perfectly merge with the unmarked animals, the proportion of the marked individuals within the unknown overall population N and within the second sample n remain constant: m / n = M / N (Figure 1).

Figure 1: Capture-recapture method model



N= Veneto region dog population
M= canine register office data (capture)
n = household survey data (recapture)
m = individuals captured twice

Using the Chapman variation, N is equal to
$(M + 1)(n + 1)/(m + 1) - 1$

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[1] Istituto Zooprofilattico Sperimentale of Piemonte Liguria and Valle D'Aosta, Torino, Italy
[2] Istituto Zooprofilattico Sperimentale delle Venezie, Legnaro (Padova), Italy
[3] Firenze University - Statistic Department, Firenze, Italy
[*] elisa.baioni@izsto.it

In this study, the first 'capture' is represented by the data from the regional canine general office, properly corrected by excluding the deceased subjects (correction carried out on the basis of a pilot telephone survey). The second sample (recapture) is obtained by a sample survey that allows to estimate the proportion of unregistered dogs and therefore the overall population.

The recapture sample was drawn from the register office database. A database was created and a computerised interviewing system was set up to ensure the correct editing of survey responses. The database collects data about possession of dogs in the contacted families, the presence or not of the microchip for dog identification and detailed information about breed, sex and age of the animal.

Result

A sample of one hundred and fifty househols has been extracted for the pilot survey conducted on the registry office database. Ninety-six households have been successfully contacted (response rate of 96). The study has highlighted a 16% of deceased subjects.

The capture sample is composed by 693,554 dogs currently registered in the canine registry office of the Veneto region. The recapture sample size is correlated with the expected prevalence of dogs in the Veneto region. A survey conducted in 2006 by the Istituto Zooprofilattico delle Venezie attested an average number of dog per household of 0.45 [8]. Using the formula of sample size determination for a confidence interval of prespecified width [9], we obtained the result showed in Table 1.

Table 1: Recapture sample size

Width CI 95%	DOGS	HOUSEHOLDS
4	2450	**5440**

The sample of 5,440 households was extracted by the register office database of the Veneto region stratified by number of families per municipality.

Discussion

The method described here is the first published for the estimation of a dog population in Italy. The next outcome expected from the research project is the implementation of the Chapman model with the results of the telephone survey. Secondly, we would extend the application of the method to different areas of the Italian territory, obtaining trustworthy estimates of the domestic animal populations in a practical and affordable manner.

The methodology could also be available for some public health organizations for dog population management and modeling purposes (Local Health Units, Italian National Health Institute and Istituti Zooprofilattici Sperimentali) as well as for private organizations who require the method as a valid aid in marketing investigations.

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The Alberta Veterinary Practice Surveillance Network: A Veterinary Practice Surveillance System for Cattle in Alberta, Canada

J. Berezowski[1]*, S. Checkley[2], R. Clarke[1], S. Clarke[1], C. Dary[1], G. Hauer[1], T. Herntier[1], J. Keenliside[1], C. Morley[1], S. Otto[1], J. Patel[1], D. Peters[1], S. Turner[1] and J. Vance[1]

Abstract

The Alberta Veterinary Surveillance Network has developed and implemented a stable web-based veterinary practice surveillance system for cattle. The system collects data and valued information about the disease status of Alberta cattle.

Keywords: Endemic disease surveillance, emerging disease surveillance; monitoring systems; multiple disease/species surveillance; syndromic surveillance; detection of emerging disease, event-based surveillance, sentinel surveillance

Introduction

Effective livestock disease surveillance is essential for managing disease risk in livestock industries and for maintaining access to markets for livestock and livestock products [1, 2]. To be effective livestock disease surveillance must target many diseases including trans-boundary, emerging and re-emerging diseases and zoonotic diseases [1, 2, 3]. Meeting these and future surveillance needs of livestock industries will require a surveillance paradigm shift. Surveillance that targets individual or at best a few diseases in one or a few production types will need to be supplemented with surveillance systems that target many or all diseases in all production types. In effect this will be surveillance that detects disease by detecting changes in the health status of livestock populations and changes in livestock-based food production chains.

Private veterinary practice is an essential component of the infrastructure needed to support economically viable livestock industries, stable rural economies and viable, sustainable rural communities [1, 2]. Veterinarians are valued contributors to early animal disease outbreak warning systems because they are often one of the first responders to significant disease outbreaks on their clients operations [4]. Veterinarians also collect and hold data that has been shown to be important for livestock health surveillance [5].

The Alberta Veterinary Surveillance Network (AVSN) is a surveillance system that was built upon strong collaborative relationships between AVSN surveillance veterinarians and private practitioners. The purpose of the AVSN is early detection of important animal health events allowing rapid effective response and the production and communication of valid information about the health and disease status of livestock. This presentation describes a web-based veterinary practice approach to surveillance of cattle in the Province of Alberta, Canada, and provides examples of some of the information it has produced.

Materials and methods

A restricted access website for the collection of data about cattle diseases was developed by the AVSN team in 2005. The website was designed to transmit data from veterinary practices to a secure AVSN database by the Internet. The data entry website was critically examined by an advisory group consisting of AVSN surveillance veterinarians, academics, practicing veterinarians and representatives of the Alberta Veterinary Medical Association (AbVMA). The data entry web site was then tested and modified over a 6 month period by a small number [5] of practices.

Veterinarians in Alberta are required by the *Veterinary Profession Act* [6] to maintain the confidentiality of their clients. In order to ensure client confidentiality a second database was developed and is maintained by the AbVMA. It stores client names, addresses and other identifying information in an encrypted format independant of the AVSN. The AVSN database holds no client identifying information. To ensure client anonymity, geographic locations of individual farms are located only to the county in which they reside.

During the spring and summer of 2005 veterinary practices that serviced the cattle industry in Alberta were contacted and asked to voluntarily participate in a the web based cattle surveillance system. Practices interested in participating were enrolled and provided with training. The system has been continuously operational since that time.

Participating practices report data from all of the work they do with cattle, including non-disease related data. Data is collected on a submission basis, and there are two types of submissions.

1. Disease submission is a clinical disease in one or more cattle of the same age that were examined by a veterinarian on one date.
2. Non-disease submissions are activities or procedures performed by a veterinarian on one or more cattle of the same age on one date.

Multiple submissions are allowed on the same visit. For example a veterinarian who visits a farm and examines one cow with lameness and a calf with diarrhea would report two submissions.

Data collected includes the following variables: practice identity, date of the examination, county location of farm, number of cattle on the farm, number

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[1] Alberta Agriculture and Rural Development, Edmonton, Alberta, Canada - *john.berezowski@gov.ab.ca

[2] Department of Ecosystem Health, Faculty of Veterinary Medicine, University of Calgary, Calgary, Alberta, Canada

affected (or treated) production type, age of cattle, clinical syndrome, clinical diagnosis, laboratory and laboratory diagnosis if samples are submitted to a laboratory for further testing, if dead cattle are present, if a post mortem examination was performed and a number of other syndrome specific questions.

The program is voluntary, but veterinarians are paid a token amount to enter their data into the website. To encourage timely data entry veterinarians are paid a premium for data entered within 72 hours of an examination.

Results

During the period from January 1, 2006 to December 31, 2009, 25 to 27 veterinary practices consistently participated in the program. There was only one practice that withdrew from the program and that was a result of the practice being sold. During this time data was collected from 9,127 cattle farms that were located in 68 counties (Table 1). The number of cattle on the farms that were visited by veterinarians ranged from 1.3 to 2.0 million per year.

Table 1: Number of farms visited per operation per year

Operation	2009	2008	2007	2006
Backgrnder	43	47	26	43
Cow-Calf	3095	3802	4628	4184
Dairy	280	317	296	252
Feedlot	75	134	150	146
Total	**3405**	**4178**	**4977**	**4535**

During this time period there were 100,346 submissions. The number of submissions reported varied considerably from year to year (Table 2), mirroring the number of farms that were visited (Table 1). The vast majority of the submissions came from cow-calf operations, followed by dairies. However the average number of submissions per farm per year was greatest for dairies and feedlots (Table 3).

Table 2: Submissions by operation type per year

Operation	2009	2008	2007	2006
Backgrnder	70	70	35	66
Cow-Calf	8376	11102	15106	12371
Dairy	7077	7389	5911	4360
Feedlot	2132	2315	3569	4453
Total	**17655**	**20876**	**24621**	**21250**

Table 3: Average number of submissions per farm per year by operation

Operation	2009	2008	2007	2006
Backgrnder	1.6	1.5	1.3	1.5
Cow-Calf	2.7	2.9	3.3	3.0
Dairy	25.3	23.3	20.0	17.3
Feedlot	28.4	17.3	23.8	30.5

Veterinarians classified cattle into one of 12 syndromes (Table 4) and there was some variation on the frequency of syndrome submissions by operation. For cow-calf and dairy operations, reproductive syndrome submissions were the most numerous followed by gastrointestinal and ambulatory lameness. The most numerous submissions from feedlots were respiratory syndrome submissions followed by gastrointestinal, ambulatory lameness and sudden death.

Veterinarians report data on 190 distinct clinical diagnoses. There was variation in the frequency of clinical diagnoses depending on the operation type (Tables 5, 6). Obstetrical and related conditions were the top 4 clinical diagnoses reported on cow-calf operations in 2009. Left displaced abomasum (LDA) was the most common clinical diagnoses reported on dairy farms in 2009, followed by cystic ovarian disease and endometritis. Trauma and undifferentiated were in the top 10 most common clinical diagnoses for both operation types.

Table 4: Percent of disease submissions by syndrome for cow-calf, dairy and feedlot operations for 2009

Syndrome	Cow Calf	Dairy	Feedlot
Abortion/Birth Defect	0	0	0
Ambulatory Lameness	13	11	14
Anorexia Weight Loss/Decreased Milk	2	9	3
Gastrointestinal	13	21	15
Neurological Recumbent	6	6	6
Peripheral Edema/Misc Swelling	8	4	5
Repro Obstetrics	38	37	10
Respiratory	4	3	30
Skin Ocular Mammary	7	6	3
Sudden or Unexplained Death	7	3	13
Urologic	1	0	2
Vesicular Ulcerative	0	0	0

Table 5: Number of submissions for the top 10 clinical diagnoses for cow-calf operations for 2009

Clinical Diagnosis	Number
Dystocia/Traction/Fetotomy	537
C-Section	391
Prolapsed Cervix/Vagina +/- Rectum	313
Prolapsed Uterus	214
Undifferentiated	186
Trauma/Fractures	164
Trauma	164
Cancer Eye	142
Bloat	140
Abscess	128

Table 6: Number of submission for the top 10 clinical diagnoses for dairy operations for 2009

Clinical Diagnosis	Number
LDA	465
Cystic Ovarian Disease	444
Endometritis	310
Mucometra/Pyometra	239
Trauma	194
Abortion	169
Undifferentiated	151
Retained Placenta/Septic Metritis	147
Arthritis-Septic/Osteoarthritis	120
Abscess	108

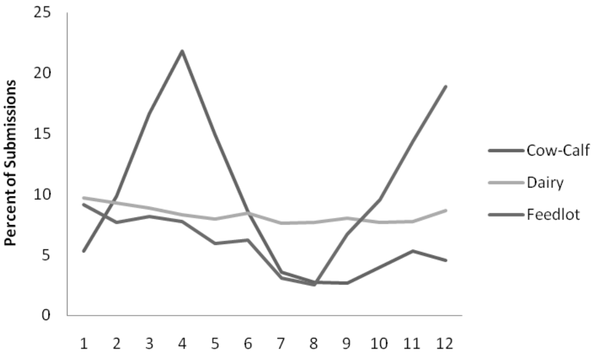
Clinical diagnoses also varied by age and operation type. The most common clinical diagnosis for both dairy and cow-calf operations was "undifferentiated" (no diagnoses defined at the time of the examination) followed by *E. coli*. However rotavirus was a more important clinical diagnosis for neonatal diarrhea in cow-calf operations than in dairy operations, and cryptosporidiosis was a more important clinical diagnosis of dairy operations than cow-calf operations.

Table 7: Number of clinical diagnoses for neonatal diarrhea for cow-calf and dairy operations for the period from Jan 1, 2006 to Dec 31, 2009

Clinical Diagnoses	Cow-Calf	Dairy
Undifferentiated	568	76
E. Coli	106	26
Rotavirus	72	8
Coccidiosis	66	9
Cryptosporidiosis	44	14
Corona Virus	36	8
Clostridial Enteritis	23	2
BVD	3	0

There was considerable seasonal variation in the rates of submission for some operation types. Peak submissions were received in the spring for cow-calf operations and in the fall for feedlots (Figure 1). Dairy operations had relatively stable submission rates throughout the year. There was seasonal variation in submission rates for some clinical syndromes and clinical diagnoses. Season variation for clinical syndromes and diagnoses also differed by operation type (data not shown).

Figure 1: Percent of submissions per month for the 2009 calendar year.



Discussion

Sustainable cattle health surveillance that creates useful information can be built upon veterinary practices. This paper has presented only a small amount of the information that is available from the AVSN veterinary practice surveillance system for cattle.

This veterinary practice surveillance system for cattle covers a relatively large portion of Alberta's cattle population as demonstrated by the large number of farms visited by veterinarians and the number of submissions received from those farms. Covering a large numbers of cattle is important for the validity of the program and also provides rapid access to a large number of cattle for targeted investigations or more detailed surveys.

The program has been well received by participating veterinarians as demonstrated by the strong, continued support by participating veterinarians.

Information from this system has been used to investigate changing disease patterns in Alberta's cattle population. It is valued by other stakeholders for estimating the importance of infectious diseases in cattle for vaccine development, and for providing veterinary students with current information about the diseases they will face when they enter practice.

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Rabies re-emergence in Northern Italy: development of a regional system for centralized data management of dog vaccinations

L. Bortolotti[1*], M. Lanari[1], M. Brichese[2], M. Cobianchi[1], L. Cazzola[3], A. Zampieri[1] and S. Marangon[1]

Abstract

Compulsory vaccination against rabies in part of the Veneto Region, due to its recent outbreak, led to the need to update the management software of the Regional Canine Registry Databank (BAC), in order to integrate specific functions for the management of the vaccination plan and to support the activity of the Veterinary Services of Local Health Units (LHUs) by gathering the data of dog vaccinations in a centralized database. The new functions which have a centralized collection of homogenous and updated vaccination data, enables a more efficient organization and better control of the trend of the vaccination plan.

Automated information processing makes it possible to verify the course of the vaccination operations, monitor the level of vaccinal protection of the population, and calculate the costs incurred.

Keywords: rabies emergency, vaccination, regional database

Introduction

In autumn 2009, following a rabies outbreak in wild animals in the province of Belluno, a series of emergency measures were implemented by health authorities to oppose the spread of the disease, one being the Regional Ordinance n. 251 of 24/11/2009. It requires that all dogs living in the provinces of Belluno, Treviso and in some municipalities in the province of Venice and Vicenza must be given a pre-infection rabies vaccination. Similarly, any dog that is brought into these areas, or passes through them, must be vaccinated 21 days before entering these areas.

The plan for mandatory vaccination of the dog population started at the end of November 2009 and had to be completed by March 31, 2010, involving:

- Veterinary Services (VS) of 8 LHUs, who had to make pet vaccinations available at public surgeries,
- Veterinary practitioners authorized by the VS to perform the immunizations at a fixed price at their own surgeries.

The provision of various logistic solutions and the application of fixed low-costs to encourage owners to get their dog vaccinated, have been clever choices for the success of the vaccination plan.

Carrying out the vaccination plan entailed great work on the part of the VS of the LHUs involved, both in terms of the administrative clerks and the veterinary staff. In this context, a consolidated Regional Canine Registry Databank (BAC), which stores the data and the movements of dogs in tandem with the personal data of the owner and the keeper of the animal, has demonstrated to be extremely useful. Moreover, the BAC has proven to be a fundamental tool not only to control strays, but also to guarantee quick access to data on the dog population, which is essential for the knowledge of the territory.

The purpose of this paper is to highlight specific information tools implemented for local and regional VS to update with new modules the BAC's management software that is already in use at the VS.

Materials and methods

ANACANI, BAC's management software, is a client-server program based on web services technology, designed according to the HTTP / SOAP / XML, resident on Web server Apache 2.2.8 and Windows 2003, developed in Delphi7.

The database is centralized on Oracle platform.

A preliminary analysis of software requirements highlighted a variety of operational needs in the LHUs, as each VS organized the immunization activities independently, calling for the optimization of available resources. Some of the VS, in fact, opted for the activation of special vaccination centers located in various parts of the territory, whereas others decided to use the clinics that were already operating at LHUs. In some cases owners were invited by appointment, in other cases they were not. In some cases the computer program was used in tandem with the vaccination, in other cases the vaccinations were recorded retrospectively.

Flexible modules were therefore designed to suit different needs and to fulfill the following tasks:

- organize appointments and print the invitation letter with the date, time and location of the appointment for the owners of dogs residing in a given municipality. All the data are automatically extracted from the BAC. The letters are organized into sections in order to schedule the appointments.
- massive data entry of vaccination information (brand and name of the product, batch number, date and place of vaccination, veterinary name and expiry date of immunization). Once the information is memorized, the editing mask does not require the same data to be re-entered. Data gathered automatically are pre-compiled (the expiry date of immunization from the date of vaccination and type of vaccine, the manufacturer from the product name).

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[1] Istituto Zooprofilattico Sperimentale delle Venezie. Legnaro (PD), Italy - * crev.lbortolotti@izsvenezie.it
[2] Regione Veneto. Venezia, Italy
[3] Azienda Ulss 2. Feltre (BL), Italy

- document print confirming the vaccination (Model 12) and receipt of the fees paid by the owner, pre-compiled from the data registered in the system.

  To assess the progress of the vaccination plan, starting from the vaccination data thus collected and from the dog population registered in BAC, indicators have been deduced and specific data extrapolation was stratified at the LHU level or municipality level. This information is available from the internet and provides:
- the number of dogs with a valid vaccination / number of dogs present in BAC;
- the number of unvaccinated dogs, by age groups (<12 years, between 12-18 years,> 18 years);
- the list of unvaccinated dogs associated with the owners' personal data.

The system finally enables the VS to calculate the amounts that each veterinary practitioner charged for the vaccination at a fixed rate.

Results

The management of emergencies calls for prompt action hence the development and adaptation of the ANACANI software had to be very rapid. In fact its operativity started the first week of December 2009.

An example of the application of the tools available comes from the LHU 2 which organized 46 mass vaccination events, inviting and vaccinating 6,833 dogs. The administrative office of the LHU used the software to automatise the activities and allow a cost-effective organization of the event. Invitation letters containing easy but exhaustive information were sent to the dog owners. Vaccination points, located throughout the territory, had a simple Internet connection via mobile device to assure network coverage and full use of the software features. The operators directly connected to BAC archives could, when recording a vaccination event, check the accuracy of the information on the dogs registered in BAC and if needed, make any appropriate update (*e.g.* change of residence, dog ownership, *etc.*).

Moreover the Vet practitioners after any vaccination have to send model 12 to VS. The latter have been recording the vaccination data until now, using the same software.

The VS then used the program to verify the amounts billed by them, while at the same time taking advantage of simpler administrative tasks.

At present the number of vaccinated dogs registered in the BAC is 192,787, and in some LHUs the registration procedures are still ongoing. The vaccinations performed compared to the vaccinations recorded are described in Table 1, Figure 1.

The vaccination status compared to the canine population is summarized in Table 2.

Table 1: Number of vaccinations registered in real time and afterwards

LHUs	No. vaccination		
	registered in real time	registered afterwards	Total
No.1	449	7,116	**7,565**
No.2	5,313	6,967	**12,280**
No.3	3,082	17,609	**20,691**
No.4	8,615	9,120	**17,735**
No.7	535	29,096	**29,631**
No.8	583	31,304	**31,887**
No.9	1,276	45,025	**46,301**
No.10	6,081	20,616	**26,697**

Figure 1: % of vaccinations data registered in real time/total vaccinations

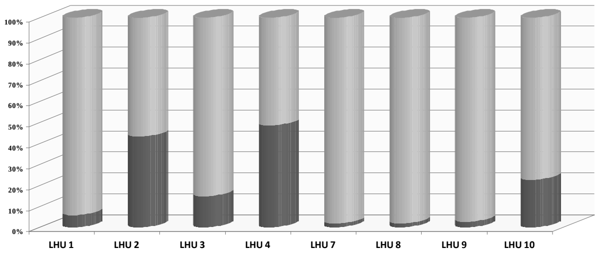


Table 2: Vaccinated and unvaccinated dogs divided into age groups

LHUs	No. vaccinated dogs	No. unvaccinated dogs		
		</= 12 years	>< 12-18 years	>/= 18 years
No.1	7,565	5,159	710	273
No.2	12,280	2,458	1,902	2,465
No.3	20,691	5,914	2,794	1,259
No.4	17,735	7,017	4,866	3,860
No.7	29,631	6,976	5,588	3,679
No.8	31,887	7,129	5,599	3,576
No.9	46,301	10,861	1,518	924
No.10	26,697	7,215	1,414	436
Total	**192,787**	**52,729**	**24,391**	**16,472**

Discussion

The computerization of data is the only way to effectively monitor and report the execution of the vaccination plan in the affected area [1], but it requires an investment in terms of administrative work. Therefore the software must be practical and must assure direct benefits to the operators of LHUs [2].

VS of LHUs n. 2, 4 and 10 have used the software during the vaccination operations. This choice has simplified the administrative work and has enabled the access to the vaccination data in real time.

The recording activity of the vaccinations given by the Vet practitioners required much more time. Health authorities are considering to have Vet practitioners directly register into the BAC any future vaccinations.

The procedure and the archives can now be used to manage the vaccinations booster and to conduct epidemiological analysis and health checks (*e.g.* assessment of antibody level in vaccinated animals).

The vaccination plan has also been a great opportunity to update the BAC. In fact, a data analysis shows a discrepancy between the number of dogs registered in BAC and the real presence of dogs in the area of interest.

Presumably, of the number of unvaccinated dogs in the higher age bracket sector (> 12 years), many dogs have already died though their position in the BAC has not been updated. Some VS, that have already finished vaccination recording, are calling the owners of unvaccinated dogs to verify and update their situation.

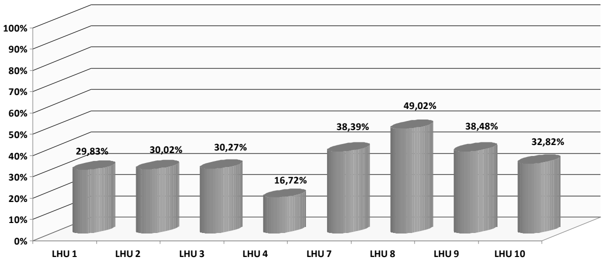
Furthermore, a number of cases saw owners who had become aware of the emergency health situation and naturally took their unidentified animals to VS to have them vaccinated. Many dogs have therefore been identified and registered in BAC, including adults, of whom there was no previous trace (see Table 3 and Figure 2).

Table 3: Number of dogs identified during the vaccination and number of already identified dogs

LHUs	dogs already identified	dogs identified during vaccination	Total vaccinated dogs
No.1	5,308	2,257	**7,565**
No.2	8,594	3,686	**12,280**
No.3	14,427	6,264	**20,691**
No.4	14,770	2,965	**17,735**
No.7	18,257	11,374	**29,631**
No.8	16,257	15,630	**31,887**
No.9	28,485	17,816	**46,301**
No.10	17,934	8,763	**26,697**

In some parts of the territory at least 50% of dogs that had been brought to be vaccinated were unidentified. It was therefore necessary to identify and record them in the BAC. For this reason the data recording is still in progress.

Figure 2: % of dogs identified during the vaccination/total vaccinated dogs in each LHU



In November 2009 the number of dogs in BAC was 593,508, while in November 2010 it increased to 693,554: at LHUs in which the rabies vaccination was compulsory, there was a six–fold increase in the registration of dogs in BAC in the first six months of 2010, compared to the same period in 2009.

The Veneto Region, seeing the notable number of dogs identifications, had to anticipate, by one year, the periodic contract for the supply of microchips to VS.

Currently, one of BAC's main setbacks is the gap found between the registered dogs and the realistic dog population on the territory. It highlights the problem related to the difficulty of implementing animal identification. The data obtained from vaccination areas are being studied and serve as an indicator to estimate the actual number of dogs in the other provinces of the Veneto Region.

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Companion Animal Practice Based Disease Surveillance in the UK

D. Brodbelt[1*], S. Middleton, D. O'Neill, J. Summers and D. Church

Abstract

Disease surveillance in companion animals in the UK has been limited by current data recording capabilities and data extraction methods. The aim of this study was to record standardised disease diagnosis during companion animal veterinary consultations in order to survey prevalence of disease seen in a group of veterinary practices.

Standardised veterinary diagnoses (the VeNom codes) were integrated into commercial practice management systems (PMS) and practices using these PMSs were recruited to participate in this study. Animal signalment, clinical examination notes and treatment were recorded during each consultation and in addition the veterinary surgeon was asked to assign the most appropriate diagnosis to the consultation from the standard list imbedded within their PMS. In the absence of a clinical diagnosis, a presenting sign was assigned. Data were exported to standard statistical software and the prevalence of major conditions was calculated.

Between 2007 and 2009, 3 pilot veterinary practices recorded 31,398 veterinary consultations in dogs and cats (11,305 feline and 20,093 canine). Twenty three veterinary surgeons contributed consultation data ranging from 6 to 3,915 consultations each (median: 1,102). Common conditions documented included diarrhoea, lameness, otitis externa, vomiting, Pyoderma and conjunctivitis. In cats, the most common reasons for consultations included cat bite abscesses, feline lower urinary tract disease (FLUTD), hyperthyroidism, dental disease, lameness, and anorexia.

The study highlights the potential to record disease data routinely within veterinary practice. Recruitment of further practices and practice groups is now ongoing to facilitate companion animal disease surveillance.

Keywords: Companion animal, VeNom codes, surveillance, disease, VEctAR.

Introduction

Recent work has highlighted the lack of surveillance and prevalence data for companion animal disease and has recommended greater routine recording of electronic data within veterinary practices [Anon, 2010; Asher *et al.*, 2009; Bateson, 2010; Summers *et al.*, 2010]. Disease surveillance in companion animals at the UK national level has been underdeveloped for some time, yet much of the required infrastructure has existed for over 10 years in veterinary practices. The vast majority of veterinary practices in the UK (>90%) [Gill, 2007], now record their clinical animal medical data within a practice management system (PMS). It has long been recognised that veterinary practices hold a wealth of disease data electronically within these PMSs, yet these systems have been configured to allow efficient billing and financial reporting rather than to allow identification of disease or facilitate clinical data extraction [Curruthers, 2009]. Limitations of non-standardised veterinary medical terminology and clinical data entry, poor clinical data storage and minimal clinical reporting facilities have restricted the potential for improved clinical disease surveillance using veterinary practice data.

The routine recording of clinical data in an easily extractable electronic format has been undertaken elsewhere in companion animal veterinary medicine. In the USA, the Banfield Veterinary Hospital Group has developed clinical recording capabilities [Moore *et al.*, 2007], though these data have limited relevance to disease monitoring in Europe. The referral institution collaboration, the Veterinary Medicine Database (VMDB), also in the USA, represents the major example of a multi-centre collaboration of electronic records [Guptill *et al.*, 2003], though these data relate to a referral population of animals and may not be relevant to disease prevalence in the UK. Data have previously been analysed from insurance databases [Dobson *et al.*, 2002; Edwards *et al.*, 2003] and have evaluated a number of conditions, though insurance databases have the potential bias towards chronic conditions and those difficult to manage, making their results difficult to interpret.

Veterinary disease data recording has also been limited by the lack of easily usable standardized disease terminology. Human medical terminology has been historically used (SNOMED etc), though these coding systems are not ideal for classification of animal disease, where terminology differs. In the UK, a multi-institution group, the VeNom Coding Group, has developed a set of standardised terminology for use for disease classification (www.venomcoding.org). These terms cover the spectrum of companion animal disease and have now been incorporated into a number of commercial PMS systems in the UK [Upjohn *et al.*, 2008; Summers *et al.*, 2010]. Hence, the aims of the current study were to improve clinical data recording processes within commercial PMS systems and collect clinical disease data from a set of UK companion animal veterinary practices.

Materials and methods

The study received institutional ethics committee approval. Standard diagnoses (the VeNom Codes) were incorporated into commercial practice management systems (RxWorks PMS) to allow recording of diagnoses during animal consultations. Veterinary practices using PMSs with the integrated standard codes were recruited to participate in the project (VEctAR, Veterinary Electronic Animal Record, www.rvc.ac.uk/VEctAR).

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[1] Royal Veterinary College, Hawkshead Lane, North Mymms, Hatfield, Herts, AL9 7TA

[*] dbrodbelt@rvc.ac.uk

Participating practices recorded their clinical consultations as per usual and in addition at the end of the consultation they assigned one or more standard diagnoses to the disease condition seen. If a diagnosis could not be made, due to insufficient diagnostic certainty, the veterinary surgeon was requested to record the most appropriate presenting complaint.

Data recorded included unique clinic, patient and consultation numbers, consultation date and veterinarian initials. Patient details included species, breed, neutering status, date of birth and weight. Consultation outcome details included clinical notes and diagnosis along with treatment received. The data were extracted from the practice PMS database using a clinical data query integrated within each participating practice's PMS system and data were entered into Microsoft Office Excel 2007 before checking and cleaning. The data were exported to Stata Version 11 (Stata Corporation). Analysis was undertaken separately for cats and dogs. Descriptive statistics were generated and the prevalence of major disease conditions was estimated.

Results

During this pilot study, 3 practices in England recorded standard diagnoses during their clinical veterinary consultations between 2007 and 2009. During this time, 31,398 veterinary consultations (20,093 canine and 11,305 feline) were recorded. Two practices were single-centre clinics contributing 15.5% (4,880) and 24.6% (7,733) of consultations respectively, while the third practice comprised of 5 clinics and contributed 59.8% (18,785) of consultations. Across these practices, 23 veterinary surgeons were involved and contributed between 6 to 3,915 consultations each (median 1,102). Pedigree status was accorded to 26.9% of cats and 84.6% of dogs. For cats, 89.2% were neutered, while 64.6% of dogs were neutered. Of cats, 83.7% were classified as shorthaired breeds, while 49.0% of dogs were large or giant breeds.

Of the consultations recorded, 67.4% of canine and 66.7% of feline consultations had a standard diagnosis coded during the consultation (13,534 and 7,543 consultations respectively). In dogs, the most common reasons for presentation included diarrhoea (845 consultations, 6.2% of coded consultations), lameness (792, 5.9%), otitis externa (761, 5.6%), vomiting (433, 3.2%), pyoderma (382, 2.8%) and conjunctivitis (344, 2.5%). In cats, the most common reasons for consultations included cat bite abscesses (371 consultations, 4.9% of coded consultations), feline lower urinary tract disease (FLUTD) (329, 4.4%), hyperthyroidism (310, 4.1%), dental disease (290, 3.8%), lameness (250, 3.3%), and anorexia (214, 2.8%).

Discussion

This work documents common reasons for companion animals presenting to veterinary practices for treatment and highlights the potential value of electronic patient records for animal disease surveillance. Diagnostic coding frequencies were relatively high in this pilot study and represent a feasible and efficient method of recording veterinary surgeon perceived disease across a number of clinical veterinary practices.

The reasons for consultation recorded here were broadly consistent with previous work in the UK and abroad [Hill *et al.*, 2006; Lund *et al.*, 1999]. The diagnoses recorded represent veterinary surgeon assessed disease and may not always accurately reflect actual disease distributions. Nonetheless, these data are of value as they highlight potential trends in disease prevalence and can alert to changing patterns of companion animal disease. Additional work is ongoing to link the clinical disease data to clinical and histo-pathological diagnoses where further diagnostic work-up has been undertaken.

In summary, this report highlights the feasibility of using private veterinary practice based data to report veterinary surgeon assessed disease. Work is now ongoing within the VEctAR project to enlarge the practice network across the UK.

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GIS application in veterinary medicine – A data warehouse-based decision support system for the management of disease surveillance programs

N. Ferrè[1*], M. Trolese[1], M. Mazzucato[1], M. Lorenzetto[1], M. Dalla Pozza[1] and S. Marangon[2]

Abstract

Veterinary surveillance strategy depends on a variety of epidemiological information, which enhances the complexity of such a decision-making task. A possible solution is the development of a decision support system aimed at retrieving data from different databases and information sources and analyzing them in order to provide useful and explicit information. On the basis of this concept, a data warehouse combined with a geo-data mart system is presented in this paper as a tool to support the surveillance strategy of the veterinary services of the Veneto Region in Italy.

Keywords: WebGIS, Geo Data mart, Online analytical process (OLAP)

Introduction

Veterinary surveillance strategy can take advantage from the availability of an integrated information system. This is also the case for the decision making processes or intervention strategies in case of an emergency situation or for the management of infectious diseases as avian influenza (AI), which requires real-time data on animal population, on the health status of the poultry population and on the evolution of the epidemic. When a new information system is developed, rarely is it possible to start from a clean slate. In most cases, already existing systems could have part of the information required, but to properly use this information, together with other data considered of relevance, an integration process becomes necessary. This became evident in north-eastern Italy for the management of AI epidemics occurred from 1997 to 2006 [2]. Until 2007, there was neither corporate vision of the AI epidemiological data necessary for intervention strategy definition, nor tools to facilitate the access, the processing and the dissemination of the relevant information among stakeholders. In addition, few poultry production data, characterized by low quality and scarce integration were available at that time.

The problems of identification of data gaps, monitoring of data quality, integrated analysis of livestock sector and information dissemination to stakeholders exist due to non-availability of digital centralized repository of information for the livestock sector. In the early 90's, *data warehousing* was proposed as a multi-purpose solution to the problem of satisfying management information needs. A data warehouse is a database which provides a single consistent source of information for reporting and analysis across the organization.

According to this database application technology, since 2007, a data warehouse based on AI epidemiological information was developed with the aim of providing the data necessary to monitor disease evolution and to support intervention measures in case of an epidemic.

Geography plays a major role in understanding the dynamics of an epidemic. For this reason, in recent years, an increasing number of veterinary organisations have sought to develop geographic information system (GIS) to store, share and publish disease data, and as a warning tool for emerging and re-emerging diseases [3]. The development of a GIS system is a complex process that must tackle a wide variety of critical issues, such as technological requirements, people, institutional frameworks, and inter/intra-institutional relationships [1]. Different combination of these factors can lead to different type of GIS. For some organizations, such as local governments, a GIS may constitute the foundation of their data which affects and ties together most of the organization's activities, whereas for others it may consist only of a simple tool addressed to the completion of a single task.

This paper outlines the technological solution that has been adopted to implement a GIS-based decision support system (DSS) developed by the Unit of Veterinary Epidemiology of the Veneto Region (CREV) based at the Istituto Zooprofilattico Sperimentale delle Venezie (IZSVe) in order to combine GIS technologies with an advanced database management system (DBMS), to allow users to access veterinary information with the support of computerised mapping technologies.

Materials and methods

The technological architecture chosen was a data warehouse structure combined with geo-data mart as "retail" level of the data warehouse [4, 5]. The dimensional model developed was structure into 3 tiers:

- data warehouse: the data "product" obtained from data "suppliers" (operational systems or external sources) is temporarily stored in a relational data "warehouse" (extract process).
- Geo-data mart: in the data warehouse the transformed data were loaded in several data marts (the load process) that contain subsets of specialised business data (that could be seen as "attributes" in a GIS environment) organised in a format that enables easy and efficient integration with the related feature entities (polygons, lines, or points).
- End-user components: data organised within the geo-data mart are then delivered via feature layer to data "consumers" (end users) to be visualised through GIS desktop viewers or WebGIS applications.

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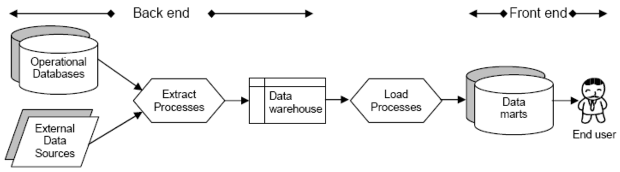
[1] GIS office, Veterinary Epidemiological Unit, Istituto Zooprofilattico Sperimentale delle Venezie, Viale dell'Università 10, 35020 Legnaro (Padova), Italy - *crev.nferre@izsvenezie.it

[2] Istituto Zooprofilattico Sperimentale delle Venezie, Viale dell'Università 10, 35020 Legnaro (Padova), Italy

Figure 1: The DSS architecture (rectangles indicate data stores, while circles indicate processes).



The data warehouse design

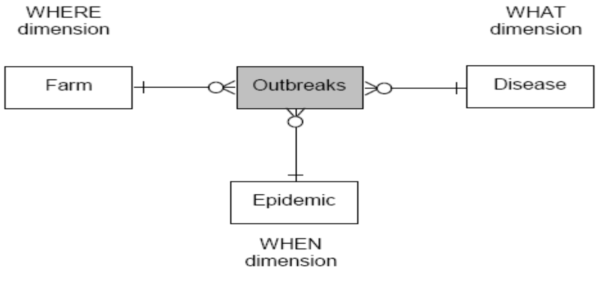
The relevant information is available within the following operational source systems:

- the Regional livestock holding database (Oracle 10g database, based at Vega Park in Venice-Italy);
- Laboratory Information and Management System (Firebird 2.0.6, database based at IZSVe, Legnaro (PD) - Italy);
- poultry farm restocking plans (information about the flocks restocked at a given time, Oracle 10g database, based at Vega Park in Venice-Italy);
- Animal Diseases Notification System (Oracle 10g or Access Microsoft XP, based at CREV, Legnaro (PD)- Italy);
- the National Cartographic Portal (Web Map services (WMS) and Web Feature Services (WFS)] managed by the Italian Ministry for Environmental Protection, Rome - Italy);
- the feature data sets (Oracle 10g combined with ESRI SDE as gateway, based in Ferrara - Italy).

The extraction process was a custom programmed module developed in Java and PHP that automatically acquires the available data from different sources through (i) dblink and Web Services from Oracle and Firebird databases, (ii) automatic replication from Access databases, and (iii) ArcSDE on Oracle synchronisation

The dimensional model adopted was the star schema based on 3 transaction entities ((i) farms: this entity records information related to livestock holdings of different animal species and their characteristics (*e.g.*, type of production, number of animals); (ii) outbreaks: this entity stores outbreak data and (iii) exams: this entity records detail on data generated by IZSVe diagnostic laboratories) and more than 40 component entities.

Figure 2: Simplified version of the fact table for the outbreak star schema



The geo-data mart design

This module processes and integrates I&T data into the geo-relational database by means of specific spatial table-views. The geo-relational database was configured as a decision support system with the Oracle server software supporting queries from direct client users and the ArcSDE supporting the application data server for spatial queries. In particular, the geodatabase can be broken down into three major components: (i) the spatially enabled data, (ii) the Oracle server process and (iii) the ArcSDE server process. Both ArcSDE and Oracle cooperatively process GIS application queries, while non-GIS queries were handled by Oracle alone.

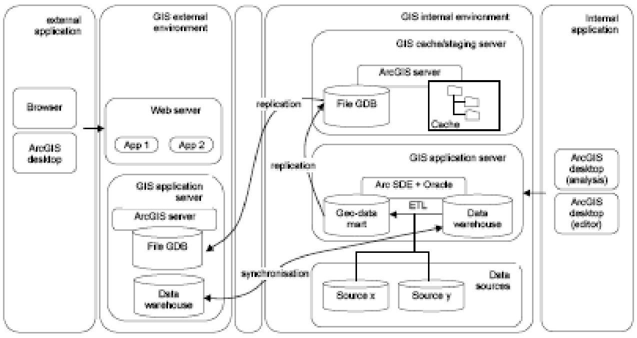
The end-user components

In order to publish the geo-data mart, two different modules were developed: one module, referred to as the "desktop module" (dedicated to managing activities for epidemic emergencies and surveillance), operates at the intranet level and was configured as a desktop section; the other module, a WebGIS platform, was dedicated to data dissemination and sharing.

The desktop module was based on ESRI ArcGIS descktop and extentions suite, and a set of procedures and GIS models developed with the ESRI model builder.

The WebGIS module is based on the ESRI ArcGIS Server - Oracle architecture that includes: (i) the internal application tier developed with ESRI model builder, (ii) GIS application server for the internal GIS environment developed with ESRI ArcSDE and Oracle 10g; (iii) GIS cache staging server based on ESRI file Geodatabase and ESRI ArcGIS Server; (iv) Firewall; (v) GIS application server for external production environment based on ESRI ArcGIS Server, File Geodatabase and Oracle 10g and the (v) Web client for external applications.

Figure 3: Conceptual reference architecture of the Web GIS module



Result

Two different categories of outputs were delivered: the geo-data marts and the WebGIS applications.

Geo-data marts

Three data marts were developed:

1. Farms, contains information on farm characteristics;
2. Outbreaks, contains information on outbreaks; and
3. Health status, contains information on surveillance and monitoring programmes.

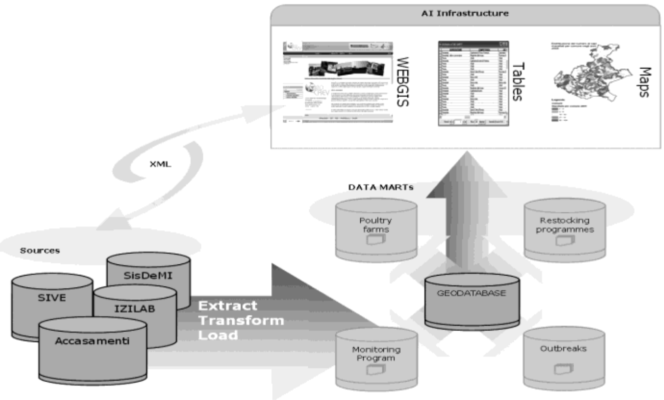
Each data mart was structured into logical layers, each based on a table-view that contains attributes (joined with the related spatial features) used for cartograms production. For the *Farms* data mart, the table-views were categorised according to species, production type and year; for the *Outbreaks* data mart, they were categorised by epidemic and year; and for the *Health status* data mart, they are categorised according to monitoring programmes, diagnostic techniques and disease.

This modular structure makes it easy to add new feature classes. If other internal or external data will be accessible, it should first be modeled into the data warehouse environment then processed and incorporated into the geo-relational data mart model to to be published by a new set of layers.

The WebGIS applications

Several types of layers were derived from the data published by the geo-data mart. These layers were published through the GeoCREV portal equipped with several standard ArcGIS tools (zoom in/out, pan, *etc.*) and query functions (identify, query, find and select). An additional enquiring tool was provided by the WebGIS: the navigator tool. This tool allows the user to explore the relevant epidemiological data related to a selected site (farm or outbreak), to visualise the laboratory results, the health status *etc.*, by navigating through the tables provided by the geo-data mart. A set of Web services connects the WebGIS to the data sources, enabling the retrieval of all the information collected by each original system in real time. This function is particularly relevant for the thematic accuracy and quality control task, since it allows the veterinary services to verify the original interpretation and value of data. Finally the system provides a set of WFS to share the epidemiological spatially related information with an authorised group of stakeholders.

Figure 4: The geo-data mart and the WebGIS links



Discussion

The DSS presented is a system designed to integrate geographic information and veterinary laboratory data. Differently from other WebGIS systems, this DSS system adopts data warehouse combined with a geo-data mart solution.

In response to data fragmentation, absence of regular updating and duplication of information and other common problems related to the collection of epidemiological data, data marts contributes to increase efficacy by focusing on a specific subject instead of creating a generic data warehouse. The geo-data mart solution has the advantage of structuring data in a more intuitive way and increasing the accessibility of information by the end users by means of GIS applications and visualisers.

The major benefit of a warehouse combined with a geo-data mart solution is that it focuses on faster implementations, a faster return on investment, and generally no drill-through requirement since all data is stored in the individual data mart (since the data marts contain both detail and summary data, users do not have to ‘drill through’ from a data warehouse to obtain detailed data). Moreover with a geo-data mart solution it is possible to design a system: (i) for non-technical users (the outcomes will be accessible to a wide variety of individuals who have little sophistication using data analysis tools); (ii) for an ease of use (the outcomes won’t require users to have prior knowledge of the complexity behind the system what they can see is a set of information easy to understand and self-explicative in order to make effective use of the data); for a decision-support purpose (the outcomes will provide a set of limited, basic and accurate decision-support information).

The DSS has been optimized to manage AI epidemiological data, but the design principles can be extended to other diseases or surveillance activities

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Data Visualization and Information Consuming: a Strategy to Collate and Disseminate Surveillance Information for Information Consumers

T. Herntier[1]*, J. Berezowski[1], J. Bystrom[1], S. Checkley[2], C. Christianson[1], R. Clarke[1], G. Hauer[1],
I. Jamal[3], J. Keenliside[1], C. Mainali[1], B. Miller[1], C. Morley[1], H. Ortegon[1], S. Otto[1],
J. Patel[1], D. Peters[1], S. Turner[1], J. Vance[1] and Y. Qu[3]

Abstract

Disease detection, response and information communication are key components to the Alberta Veterinary Surveillance Network (AVSN) [1]. A strategy for data collation and information dissemination is vital to the success of AVSN.

Keywords: Data collation; Data Visualization; Information Creation

Introduction

Getting information into the hands of information consumers is critical for any surveillance solution and involves a multi-phase process. The data must be extracted from the data capture source, transformed into a reportable and analytical format and made available to information consumers and decisions makers through reporting, analytical and data visualization tools.

Different stakeholders in a surveillance solution will have different requirements for visualizing and consuming surveillance information. Solutions for managing and distributing surveillance information must be robust enough to meet the requirements of all stakeholders.

The AVSN uses a specific architecture to support surveillance. Data is gathered through multiple disparate data sources. These data sources are then collated into a data warehouse. From the data warehouse, the data can be analyzed to create information and reported, or information can be created directly from the collated data and reported to multiple surveillance stakeholders (Figure 1).

This paper provides a brief description of the process used for the AVSN which collates previously collected surveillance data and disseminates information, enabling information consumers to make decisions.

Materials and methods

The AVSN was designed to enable early detection, notification and rapid effective response to emerging and re-emerging diseases of all livestock in Alberta. This paper will focus on information collating techniques, as well as reporting and visualization strategies used in AVSN, but are applicable to all surveillance initiatives.

Data Collation

For the purposes of the AVSN, data collation refers to gathering pre-collected data and transforming the data into a format more usable for reporting and analysis. Data collation is a three step process:

1. Extract
2. Transform
3. Load

Data collation is facilitated by software called an extract, transfer and load (ETL) tool

Extract

Data extraction is the ability to retrieve data from any data source. AVSN requires data extraction from internal and external disparate databases and comma delimited files, though extraction from any data source is possible.

Transform

Data transformation is the step where the bulk of work for data collation takes place. Data must be transformed into a format which makes it both easy to analyze and easy to report. Typically, this format is one record per observation. The one record per observation approach reduces the data to the smallest level of granularity; it ensures the data is in a format that will facilitate any data visualization and analytical requirements.

Load

Load takes the transformed data and stores it in a target data repository, typically a data warehouse.

After data collation, the data should be stored in a data repository easily accessible to analytical tools and data visualization tools.

Data Visualization

The requirements of data visualization for AVSN are as varied as the information consumers. Some information consumers, such as managers, require a high level snap shot of the information created from our surveillance infrastructure. Other information consumers, such as scientists, require the ability to see detailed information, as well as the ability to drill down into the data in order to answer questions that result from viewing the information. Generally, the AVSN uses the following reports to disseminate surveillance information:

- Daily Reports
- Dimensional Reports
- Detail Reports
- Ad hoc Reports
- Alerts
- Dashboards
- Advanced Visualization

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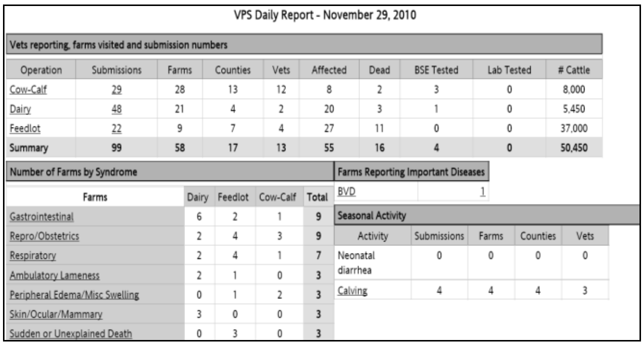
[1] Alberta Agriculture and Rural Development, Edmonton, Alberta, Canada - * travis.herntier@gov.ab.ca
[2] Department of Ecosystem Health, Faculty of Veterinary Medicine, University of Calgary, Calgary, Alberta, Canada
[3] AQL Management Consulting, Edmonton, Alberta, Canada

Daily Report
For the AVSN, a daily report consists of a snap shot of our surveillance data collected from the previous day. The information contained on the daily reported should be decided by those information consumers who use the report most frequently or make greatest use of the report. The daily report is an invaluable tool as it accomplishes:

- a single point of entry into the data visualization and reporting strategy
- allows drill through to subsequent dimensional reports to answer questions that arise from viewing the daily report.

For animal health surveillance initiatives, the daily report should display all information that consumers would like to view on a daily basis, typically the number of observations from the previous day, the disease state of the population under surveillance and any alerts or information of interested that occurred in the data collected from the previous day.

Figure 1: Partial example of a Daily Report



VPS Daily Report - November 29, 2010

Vets reporting, farms visited and submission numbers

Operation	Submissions	Farms	Counties	Vets	Affected	Dead	BSE Tested	Lab Tested	# Cattle
Cow-Calf	29	28	13	12	8	2	3	0	8,000
Dairy	48	21	4	2	20	3	1	0	5,450
Feedlot	22	9	7	4	27	11	0	0	37,000
Summary	**99**	**58**	**17**	**13**	**55**	**16**	**4**	**0**	**50,450**

Number of Farms by Syndrome

Farms	Dairy	Feedlot	Cow-Calf	Total
Gastrointestinal	6	2	1	**9**
Repro/Obstetrics	2	4	3	**9**
Respiratory	2	4	1	**7**
Ambulatory Lameness	2	1	0	**3**
Peripheral Edema/Misc Swelling	0	1	2	**3**
Skin/Ocular/Mammary	3	0	0	**3**
Sudden or Unexplained Death	0	3	0	**3**

Farms Reporting Important Diseases

BVD	1

Seasonal Activity

Activity	Submissions	Farms	Counties	Vets
Neonatal diarrhea	0	0	0	0
Calving	4	4	4	3

Dimensional Reports
A dimensional report is a summary of information across any dimension of the surveillance information. A dimension is an attribute of the data to which measures can be aggregated. Some dimensions in an animal health surveillance solution would consist of the participating veterinarian's name, animal production type and clinical diagnosis. There are typically a large number of dimensions in surveillance solutions. Therefore, it usually does not warrant a report for every dimension. Dimensional reports need only be created for dimensions identified by information consumers for which they wish to commonly view aggregated information.

Ad hoc Reports
Ad hoc reports answer general questions that information consumers want answered and do not fit into any single dimensional report. Often, the information compiled in an ad hoc report will be information summarized across multiple dimensions, or information from dimensions that do not warrant their own dimensional report. For the AVSN, only one ad hoc report is required, as it contains the ad hoc information identified by the information consumers that was not available via dimensional reports. More than one ad hoc report can result in confusion as to where the correct information is compiled.

Detail Report
A detail report is a report that displays a subset of the raw surveillance data. This is important for surveillance as it is impossible to create an information dissemination solution that will answer all possible surveillance questions. The detail report shows the data at the smallest level of granularity allowing scientists and other stakeholders to consume the data using any tool they prefer. Access to the detail report should be made available from the daily report, all dimensional reports, as well as the ad hoc report.

Alerts
Alerts are automated workflows that detect points of interest in surveillance data. Alerts are typically divided into a two step process:

1. Event
2. Tasks

The event is an occurrence that needs to be detected. For the AVSN, this can range from detecting data quality concerns, to detecting possible FMD observations in the surveillance data.

Tasks are the response to an event. An alert can have multiple tasks which occur when an event is detected. Conventional tasks include email notifications, running reports or notifying information consumers through news updates. As tasks are the action in response to the alert, and are what the information consumers receive, they should facilitate a response. Therefore, when information consumers are notified, the task should contain the information needed for the consumer to facilitate action. This is typically a name and a phone number of someone who can provide more information, or a link to a subsequent dimensional report.

Dashboards
A dashboard is an interactive summary report designed to display key measurement indicators (KPI) of a dataset. For animal health surveillance data, KPI's may include disease levels, number of observations and number of animals under surveillance. Dashboards are interactive allowing users to drill down to detail data, making them useful tools for mangers, as they can quickly see a summary of the most important measures of data, as well as retrieve detail information if necessary.

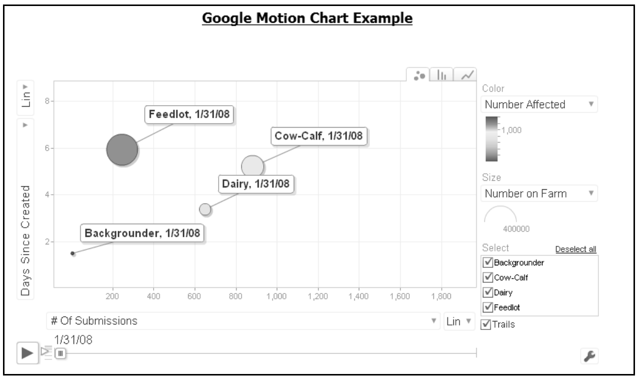
Advanced Data Visualization
For the purposes of the AVSN, advanced data visualization refers to data mining of large amounts of information visually. Typically, advanced data visualizations will use animations across a timeline, allowing information consumers to detect trends, as information is displayed over time. Advanced data visualization is useful in accomplishing:

- Discussion between multiple stakeholders
- Developing further surveillance data visualization concepts
- Demonstrating visually what has happened in the past to detect trends in the data that can be further investigated.

Results

The AVSN's data collation and information dissemination solution was developed and has been in use since 2009. The information dissemination solution consists of one daily report, six dimensional reports, one ad hoc report, five alerts and two advanced data visualization reports. The information dissemination solution is being used by scientists and management on a daily basis to view and query data coming into our databases from our surveillance system, as well as to generate surveillance information for reporting to other stakeholders.

Figure 2: Example of Advanced Data Visualisation - Google Motion Chart [2]



Discussion

Surveillance data is only valuable if pertinent information is created from the data. This information is only valuable if it is delivered to information consumers in a manner that is useful and can facilitate action. To achieve this, a data collation strategy must be implemented that is robust enough to handle current surveillance datasets, as well as scalable to allow for the integration of future surveillance datasets. Also, an information dissemination solution is required that facilitates decisions makers to access information quickly and in a medium that aids action.

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Collection of blood samples from slaughtered cattle for the surveillance of bluetongue in Denmark

A. Huda[1*], S. Mortensen[1] and T. Mørk[1]

Abstract

In 2009 and 2010, the Danish surveillance programme for bluetongue virus was based on blood samples collected from slaughtered cattle for antigen detection by PCR. The blood samples were collected on slaughter plants and represented all geographical areas of the country. Hand held barcode readers linked by the mobile network to a web based registration system was applied for recording the identification of the slaughtered animals that were sampled and the herd of origin. The registration system was an efficient tool for controlling the number of samples and the geographical coverage of the sampling. By a minimum of administrative work, the surveillance programme was representative of the Danish bovine population.

Keywords: Surveillance, bluetongue, blood samples, slaughter plants

Introduction

Bluetongue (BT) is a vector borne, notifiable disease transmitted to ruminants and camelids by *Culicoides* spp. midges. During 2007, Bluetongue virus serotype 8 (BTV8) continued to spread within the Netherlands, Belgium, Luxembourg, France and Germany. In the autumn 2007, BTV8 was diagnosed in Denmark for the first time. The following year Denmark experienced 15 outbreaks of BTV8. The last outbreak of BTV8 in Denmark was in November 2008. According to EU legislation, Member States must implement a BTV surveillance programme in as well as outside restricted zones [1]. The surveillance must be able to detect the circulation of BTV. In 2007 and 2008, the Danish Veterinary and Food Administration (DVFA) organized a bluetongue surveillance programme that was performed as serological examinations of blood samples and bulk milk samples. However, as a Danish vaccination campaign against bluetongue was initiated in 2008 and from 2009 covered the whole country, serological examinations was replaced by virus detection tests. A sampling strategy and registration system was organized in order to ensure the geographical coverage of the whole country.

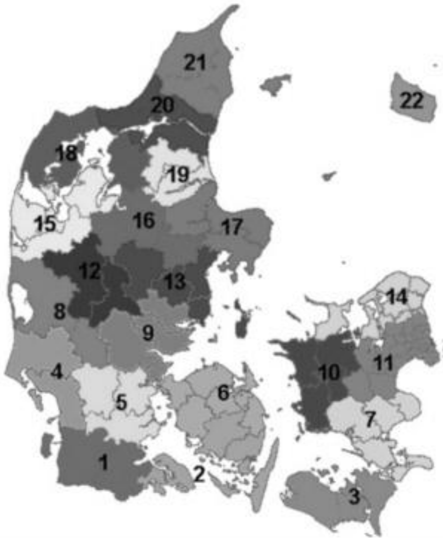
Materials and methods

In 2009 and 2010, blood samples were collected from slaughtered cattle on three slaughter plants by official veterinarians and technicians. Sampling period was from the mid of August to the end of November/beginning of December.

For the purpose of BTV surveillance, Denmark was divided into 22 geographical units, each of approximately 2,000 km^2 (see Figure 1). The surveillance programme aimed at getting a uniform coverage of samples across all geographical units.

Prior to the sampling period, the geographic distribution of herd origins of slaughtered cattle on each of the eight Danish cattle slaughter plants was estimated based on data extracted from the central herd register. Based on the result of this analysis it was decided to target three regional slaughter plants that jointly slaughtered animals from all 22 geographical units.

Figure 1: Map illustrating Denmark divided into 22 geographical units of approximately 2,000 km^2 each.



Using a handheld barcode reader device and a web based registration system that was developed by the Danish Meat Research Institute the samples were recorded online, with data sent over the mobile network. In this way, the identification of the blood sample tube (barcode label) instantaneously was linked to the identification of the slaughtered animal (barcode label) (see Figure 2). Each animal is linked to the herd of origin in the central herd database.

Throughout the sampling period, the geographical coverage of the survey was monitored and adjusted by the DVFA and the veterinary control staff as the number of blood samples from each geographical unit continuously was counted and displayed on a website of the surveillance programme.

A polymerase chain reaction (PCR) method to detect BTV was applied to pooled blood samples (five samples in one pool). The tests were performed by the National Veterinary Institute at the Technical University of Denmark.

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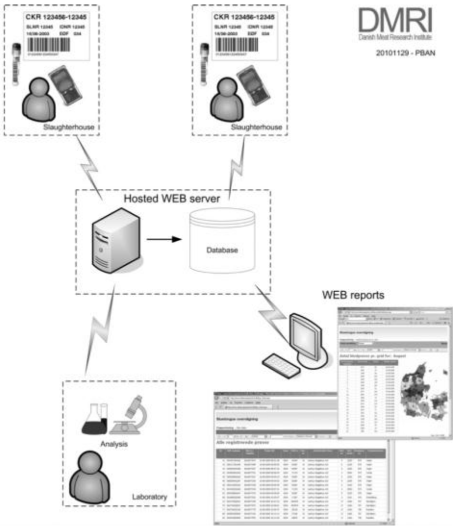
[1] Danish Veterinary and Food Administration, Centre for Veterinary Disease Control, Animal Welfare and Trade, Mørkhøj bygade 19, DK-2860 Søborg, Denmark. - *anxu@fvst.dk

Figure 2: Diagram illustrating the web based registration system for recording blood samples collected for the Danish bluetongue surveillance programme.



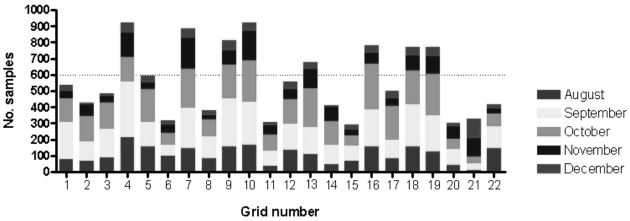
Results and Discussion

In the period from August to December 2009 and August to November 2010, approximately 13,500 and 10,000 blood samples, respectively, were collected. All samples tested negative for BTV.

By the use of the handheld barcode reader device and the web based registration system, the DVFA could reduce the costs for collection of samples by targeting the effort in three slaughter plants and minimize the administrative work related to identification of samples for the surveillance of BTV. As the number of collected samples per geographical unit and per month continuously was displayed on the website (see Figure 3), actions *e.g.* to increase the number could be simple and fast if the number was lower than desired.

This concept of collecting blood samples from slaughtered cattle may easily be transferred to other animal health surveillance programmes. A targeted surveillance programme may by the use of this concept efficiently be designed and controlled in such a way that the samples are representative for the population in an epidemiological relevant geographical area.

Figure 3: The number of blood samples collected per geographical unit (grid) per month in the Danish bluetongue surveillance programme in 2009.



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1. Commission Regulation (EC) No 1266/2007 of 26 October 2007.

Acknowledgements

The authors would like to thank Mr. Peter Bisgaard Andersen, Danish Meat Research Institute, for providing information on the web based registration system for the BT surveillance programme.

An integrated web system to support veterinary activities related to the management of information in epidemic emergencies

S. Iannetti[1], L. Savini[1], D. Palma[1], P. Calistri[1], F. Natale[2] and **A. Giovannini**[1]*

Abstract

The efficiency of management of public health emergencies is improved by quick, exaustive and standardized information flow of data on disease outbreaks. The efficiency of surveillance systems and disease control or eradication programmes is increased by using specific software for data analysis and collection.

In this context, the National Information System for the Notification of Outbreaks of Animal Diseases (SIMAN) was designed and developed to collect and share outbreaks notifications data in real time by using the World Wide Web. The system is part of the e-Government process that involves all public administrations of the European Union (EU) and refers to the use of information and communication technologies for the digital processing of documents in order to obtain simplification and interoperability of administrative procedures through the Internet.

Epitrace is a useful web application based on the Social Network Analysis (SNA) and on network epidemiological models. This software has been integrated in the BDN and gives the possibility of assessing the risk associated to holdings on the basis of their trade patterns and to target better risk management measures in case of an outbreak.

Keywords: cooperative tools, register data, real-time data, modelling, social network analysis.

Introduction

An efficient management of outbreaks can be obtained only if the competent authority has access to updated and reliable information. Therefore, it is critical to have an efficient information system that can:

- store all detailed information necessary for mandatory notifications to international institutions
- represent a valid and rapid alert system
- contribute useful information for risk analysis.

The immediate notification to the Competent Authority of information related to the onset of suspected outbreaks of animal diseases is essential for implementing control measures. Notification of disease outbreaks to the European Commission (EC) and to World Organization for Animal Health (OIE) is one of the obligations linked to membership in these international organizations.

Crucial factors with notification are the timeliness of the communication and the consistency of information transmitted along a number of different communication chains at national and international levels.

In epidemic emergencies, the main challenges faced by surveillance systems are the ability to expedite the process of collection and analysis of data and to provide the information required for a timely and efficient delivery of activities for the control and eradication of the epidemic.

The Istituto “G. Caporale” designed and implemented a tool (National Information System for the Notification of Outbreaks of Animal Diseases - SIMAN) for the notification of disease outbreaks and data management in case of epidemic emergency [1].

Another tool implemented by the Istituto “G. Caporale” is the integration of the EpiTrace module in the National Italian Animal Database (BDN), allowing the automatic performing of trace-back and trace-forward activities.

Materials and methods

SIMAN: SIMAN is a tool accessible through the World Wide Web, which collects data on notification and follow-ups of outbreaks of animal diseases as required by international authorities and institutions like EC and OIE.

The information system uses Relational Database Management System (RDBMS) Oracle 10g to store data.

Data of suspected or confirmed outbreaks are provided by the veterinary services and the laboratory results data are reported by the Public Health Institutes, using on line forms or Extensible Markup Language (XML) files. Moreover, SIMAN accesses BDN using web services for querying information about holdings and farms. SIMAN web application is based on Java 2 Enterprise Edition (J2EE) technologies. The web server is Apache on OS Unix.

SIMAN uses extensions of ESRI JavaScript API together with ArcGIS Server as a platform for Java. The result is an application that combines and advances the extremely dynamic features of Geographic Information System (GIS) software. It produces a flexible application with advanced Esri GIS functions and the high resolution of Google Maps cartographic database.

The jobs scheduler for data validation and processing, and e-mail notification uses the framework Quartz. SIMAN uses JasperReports and other open-source libraries for reporting data.

EpiTrace: EpiTrace module includes a search engine at the BDN, which calls a web service, and a Java applet for visualizing the networks on movement data and performing the epidemic simulations. It is also possible to explore dynamically the resulting networks, using a local application for network visualization.

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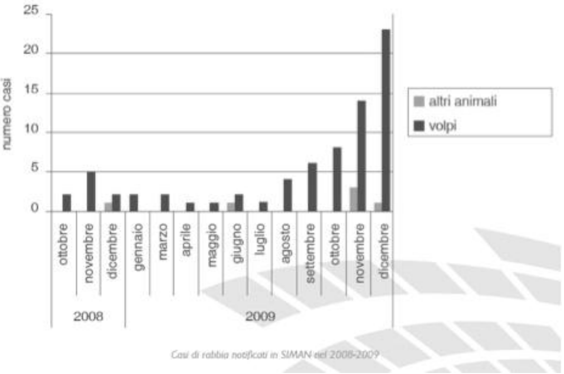
[1] Istituto G. Caporale, Teramo, Italy - * a.giovannini@izs.it
[2] Joint Research Centre, Ispra (VA), Italy

Results

SIMAN: SIMAN is available in the unique portal of veterinary information systems of the Italian Ministry of Health (https://www.vetinfo.sanita.it), together with BDN and other national information systems. Users can log in by entering user name and password or through a smart card with digital certificate.

SIMAN is accessed by veterinary services of the local and Regional levels, National Reference Laboratories, Italian Ministry of Health and Public Health Institutes. SIMAN is able to collect data produced at local level, using uniform procedures and templates for data input and output. Information about holdings is obtained using a BDN web service. The system reworks data collected to produce the periodical and immediate outbreak notifications required to fulfill the informative debt towards the international competent authorities. SIMAN provides automatically the report on the health status of livestock and is the source of information and data for the compilation of the National Veterinary Epidemiological Bulletin (Figure 1)

Figure 1



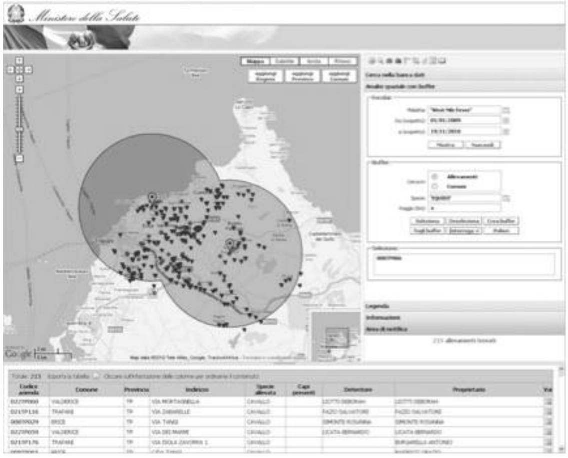
Finally, SIMAN produces reports and interactive thematic maps using GIS application. SIMAN can display data in table format or as thematic maps. Data aggregation may be customised according to user needs and territorial jurisdiction.

It provides the following information to authorized users:

- The veterinary legislation and the emergency plan for animal diseases, which are available in a specific section of the menu from which the users are allowed to download the documents.
- An automatic alert system via email is able to transmit in real time the suspect or the confirmation of a disease outbreak to the Competent Authorities.
- Data on outbreak notification to the national reference laboratories using web services.
- The WebGIS provides users with useful tools for map navigation and spatial querying of data (Figure 2).

EpiTrace: EpiTrace web module (http://epitrace.jrc.ec.europa.eu:80/) integrates the application of Social Network Analysis (SNA) and network based epidemiological models in relation to livestock movements from BDN, giving the possibility of quickly and more efficiently performing automatic trace-back and trace-forward activities, aimed at identifying the possible origin of a disease outbreak and possible secondary outbreaks (Figure 3). It also assesses the risk associated to all relevant holdings on the basis of their trade patterns.

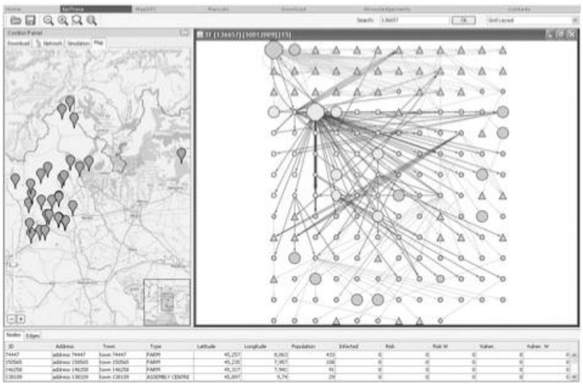
Figure 2: West Nile disease outbreaks map, buffer tool and table with the list of holdings in the buffer.



In this way, the veterinary service can plan the inspections of herds in contact with the outbreak according to their level of risk, so expediting the process of disease control and eradication. In more detail, EpiTrace performs the following activities:

- It 'downloads' livestock movement data by quering BDN remotely and in real time and also allows an interactive graphical exploration of the resulting networks (either backwards or forwards in time with respect to the suspect date of infection of a herd).
- It 'runs' two different network-based epidemic models in order to evaluate the different roles of holdings in respect of disease spread.

Figure 3: From tables and queries in BDN, EpiTrace generates in real time a graphical network representation of contacts and makes it available directly to local veterinary services



The first epidemic model is a generic network traversal, mirroring a disease flow (Disease Flow Centrality - DFC) model (Figure 4).

The DFC model takes into account the temporal dynamics of the livestock trade relations and reflects a disease flow process on a dynamic network. The calculation of DFC is based on the idea of traversing a network and counting the number of times each node (=herd) is reached and traversed ('vulnerability measure') or that is at the origin of this process ('risk measure' in spreading the disease) [2]. The second model is a meta-population SIR model on the basis of more specific disease parameters (Figure 5).

Figure 4

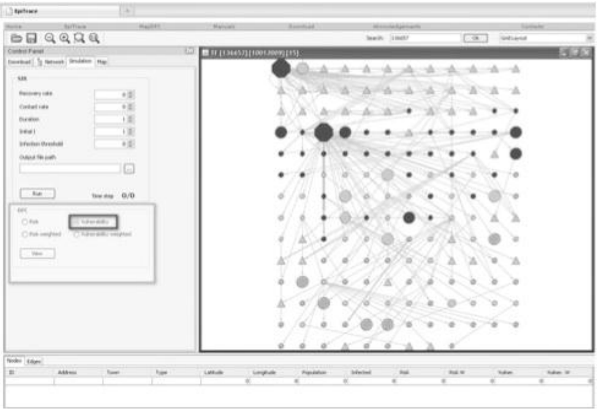
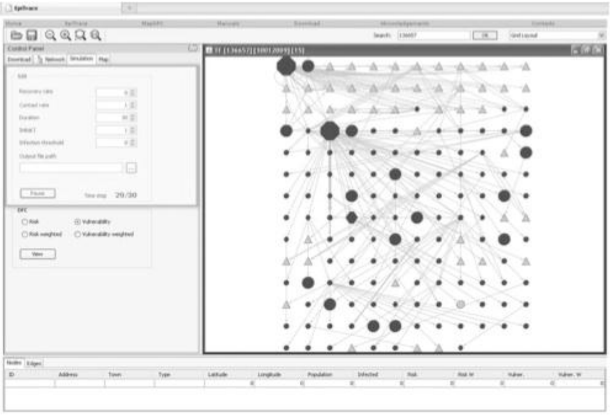


Figure 5



In the case of the SIR meta-population model, the epidemic spread in the network is modelled on the basis of specific disease parameters, using a combination of

- a component describing the epidemic dynamics at the single premise level (intra-population) and
- a transport component, describing the movement of animals and possibly of infected animals within the network structure (inter-populations) [3].

Discussion

SIMAN and Epitrace take advantage from using BDN information on farms and animals related to an outbreak. The quality of BDN information is granted by a lot of complex control routines that ensure correctness and consistency for all stored data.

The time notification of events in BDN is compliant to recommendations of EC, and since 2009 more than 85% of cattle movements are stored into BDN within 30 days.

In the past, data was collected at regional or municipal level, in the absence of any structured information systems. Therefore, data collection and reporting was open to delays, errors or omissions: the same information was often requested several times and in different ways, causing confusion for the lack of a unique data collection and reporting systems.

SIMAN is able to collect and report information concerning suspected or confirmed animal outbreaks in a consistent way, and allows the veterinary services to enter data electronically, instead of using paperworks, in the framework of the process of e-government and dematerialization of the administrative acts.

SIMAN is the official website for information on outbreaks. Data are immediately accessible for local and national authorities. The tool is actually implemented only in Italian version.

The system provides the national competent authorities with all relevant information for planning control measures in case epidemic emergencies.

SIMAN helps the veterinary services in carrying out epidemiological analysis, which are essential for surveillance and control of a wide range of animal diseases. SIMAN has been used for the emergency of West Nile Disease in Italy, since its beginning in 2009. Recently, the Ministry of Health has made exclusive and mandatory the use of SIMAN for the notification of outbreaks of Equine Infectious Anaemia.

Web-GIS Module and Epitrace give useful tools for emergency management. Network-based epidemic simulation models give a risk estimate for each node in the network, so that the competent authority has useful indications to target or to prioritise control actions.

EpiTrace is designed for bovine animal trade, therefore the veterinary services can use the system in case of emergency due to highly contagious diseases of bovines, such as those that were included in the OIE list A. Actually, such diseases are not present in Italy, so EpiTrace had to be tested through the simulation of a disease outbreak.

Caution should be adopted in interpreting the outcome of EpiTrace epidemic models, given the uncertainty of model parameters, the lack of or the delayed notification of some movements to national databases, and the possibility for disease to spread also through contacts not linked to animal transports. The epidemic simulations are intended as an aid in making a better use of traceability data and should not replace epidemiological investigations, which must take into account several other factors determining the spread of diseases.

The next step of implementation will be the integration of EpiTrace and other information systems in a single veterinary information portal, to obtain a more efficient use of all modules about outbreaks management.

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An Interated tool for Global Disease Surveillance Early Warning and Disease Control

J. Pinto[1*], C. Lockhart[1], S. Von Dobschuetz and C. Hamilton-West[1]

Abstract

Early warning for disease outbreaks at the global level and the communication of the spread of pathogens into new areas are essential elements to effectively contain and control transboundary animal diseases (TADs),including zoonoses. To enhance early warning and response to TADs and support their progressive control and elimination, FAO’s Emergency Prevention System (EMPRES) has developed a web-based platform, the Global Animal Disease Information System (EMPRES-i) to collect reliable information on animal disease outbreaks and surveillance activities of EMPRES priority diseases. Disease data can be stored in a standard format, analyzed and shared in a timely manner with FAO animal health officers, collaborating institutions, FAO partners and the public, through a public web-interface.

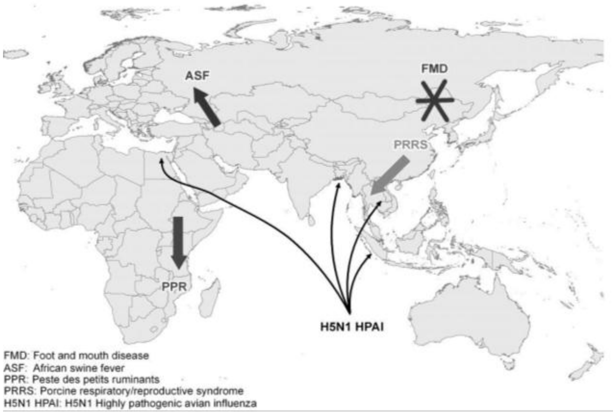
Keywords: disease surveillance, information system, data management.

Introduction

Major animal disease events continue to disrupt livestock production, rural economies and people’s livelihoods and food security. During 2010, a number of highly infectious animal diseases continued to spread in different regions of the world. This was largely due to the limited capacity of veterinary services to contain animal diseases in endemic settings, and to the presence of disease drivers such as highly intensive animal production systems, increased trade of animal and animal products and intensified contact between animal, human and wildlife populations. This significant increase in disease events included the rapid expansion of African swine fever (ASF) within Eastern Europe; the reoccurrence of foot-and-mouth disease (FMD) in the Korean peninsula, Japan and Mongolia; the rapid spread of peste des petit ruminants (PPR) within the Eastern African countries of Kenya and Tanzania, with potential risks to the entire Southern African Development Community (SADC) region; and the emergence of a new highly virulent strain of porcine respiratory and reproductive syndrome (PRRS) virus in Asia and potentially in Europe. Additionally, H5N1 highly pathogenic avian influenza (HPAI) continues to be a disease of concern due to a significant increase the number of reported outbreaks as well as overall the number of infected countries in 2010, compared with the last two years (Figure 1).

To provide updated information on global animal disease distribution and current threats at national, regional and global level, FAO’s EMPRES has developed a web-based platform, the Global Animal Disease Information System (EMPRES-i), to collect, analyze and to share information on priority animal diseases with the global community.

Figure 1: Main disease threats in 2010



Materials and methods

EMPRES-i is an information system built using open source technologies. There is a public web site where information can be accessed (figure 2).

Figure 2: EMPRES-i web-interface

Public users of EMPRES-i can access the following features:

- Disease outbreaks database: Under the “Disease Events” tab, EMPRES-i enables users to access and retrieve information on animal disease outbreaks/cases throughout the world according to the user’s criteria (disease, date, species, location, etc). Data can then be easily exported into two available formats (PDF and Excel) for further analysis.
- Mapping/graphing tools: These allow the selection of outbreaks/cases from the database and represent them graphically as charts (by time or by location) or geographically on a map that can be tailored by adding

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[1] Emergency Prevention System for Priority Animal and Plant Pests and Diseases/ Global Early Warning and Response System (EMPRES /GLEWS), Animal Health Service, Food and Agriculture Organization of the United Nations, Rome, Italy –
* julio.pinto@fao.org

optional layers, such as livestock population,biophysical layers, socioeconomics, animal health, trade, *etc*. These layers are created and maintained by the Global Livestock Production and Health Atlas (GLiPHA), is user-friendly, and can be highly interactive as the user can toggle on/off variables and statistics and is Key Indicator Data System (KIDS) based.

- Library: FAO technical material such as books, bulletins, reports, newsletters, manuals, guidelines, etc can be searched for in the Library section according to different criteria. It allows users to search for information related to the current situation, epidemiology, diagnoses and control of TADs by a number of criteria (document type, topic, language, date or free text).
- Directory: The Expert Directory section allows the search for contact information of FAO reference centres, FAO/OIE reference laboratories, and national authorities, including chief veterinary officers in each country. EMPRES-i users may search by a number of criteria (location, disease, category or free text).

EMPRES-i is integrated with other databases developed by FAO and external such as the UC Davis Bioportal, the Swiss Institute of Bioinformatics, GAINS, among others (figure 3).

Figure 3: Empres-i integration

Information on animal disease outbreaks is received from a wide range of sources, such as FAO in-country representations, project reports, field missions, partner Non-Governmental Organizations (NGOs), cooperating institutions, other United Nations agencies, government Ministries of Agriculture and Health, public domains, the media, web-based health surveillance systems and from the joint FAO/OIE/WHO Global Early Warning and Response System for major TADs, including zoonoses (GLEWS), an initiative to share information on disease outbreaks of common interest. Verification of suspected TADs outbreaks is achieved through FAO's worldwide network of field officers, personal contacts in other institutions or in national governments, OIE and WHO. All information gathered is fed into the EMPRES-i database and presented through a user-friendly and customizable interface, providing the perfect mechanism to increase awareness on TADs and zoonoses at the national, regional and global level. User access can be granted on different levels in order to protect un-verified, sensitive or confidential information.

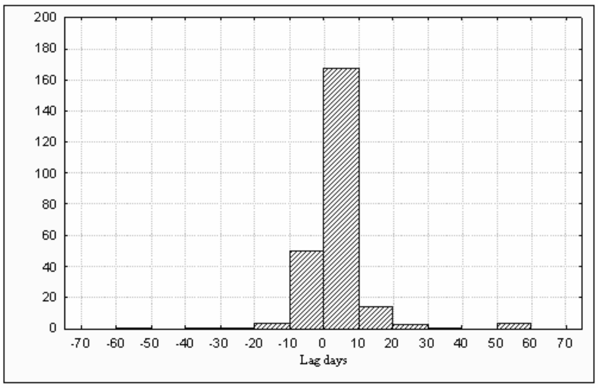
Recently, a new module was created within in EMPRES-i to collect information on animal disease surveillance. In its first stage, this module is expected to support FAO surveillance projects and joint projects with FAO partners.

The data collected is analyzed by the EMPRES team on a regular basis and used to generate periodical disease-specific status reports, *e.g.* daily Disease Updates (confidential), weekly HPAI Updates (limited distribution) and a monthly HPAI Overview (public), or early warning messages on disease threats.

Results

EMPRES-i was developed to gather and deliver timely and accurate situation updates on outbreaks of priority animal disease. Its ability to give early warning to communities could be highlighted through the analysis of the lag between the observation or reporting dates and the date when an outbreak is recorded in EMPRES-i. For instance, the lag between reporting dates of H5N1 HPAI outbreaks in countries affected during 2009, and the date when the information was included in EMPRES-i, was on average 4 days (figure 4).

Figure 4: Lag days between reporting date and inclusion in EMPRES-i, for H5N1 HPAI outbreaks in 2009



The EMPRES-i platform is an EMPRES initiative, conceived in response to the growing demand by users for animal health information, one-touch disease information gathering and sharing formula. Depending on a user's assigned privileges, there are different access levels in terms of the confidentiality and details of the accessed information.

Discussion

EMPRES-i is an important reference source for disease outbreak information and is currently used by international agencies, national governments, research institutions and scientists to follow up and study the global status and patterns of major animal diseases outbreaks.

EMPRES-i is a key tool for FAO early warning and disease response activities. In terms of the timeliness of reporting, results show an overall decrease in the time between outbreak and reporting date, along with a reduction in the variance, as the EMPRES-i system has evolved over time. This trend is encouraging and reflects improved data collection and reporting capabilities of EMPRES-i, along with suggesting an overall increase in the transparency and reporting capabilities of many countries affected by H5N1 HPAI.

These results support increased use of EMPRES-i data for developing and prioritizing disease response activities, as well as its use as an early warning tool for identifying areas at risk for new incursions. This use of EMPRES-i may encourage local animal health authorities to increase biosecurity and surveillance activities in locations near an ongoing outbreak [Farnsworth *et al.*, 2010].

Also EMPRES-i contributes to timeliness of disease early warning activities throughout the joint FAO/WHO/OIE GLEWS initiative (Global Early Warning and Response System) (figure 5)

Figure 5: Global Early Warning and Response System

The EMPRES-i system is under continuous development and new features are being added. One such feature is a module to collect information on active disease surveillance from FAO projects and joint projects with partners. In addition, a genetic module is currently being designed to integrate genetic data from virus sequences stored in open databases, such as Openflu for H5N1 HPAI viruses and FAO/OIE World Reference Laboratory Pirbright for FMD viruses. Currently, a mobile application prototype for smart phones is being developed, to be used to report disease data information into EMPRES-i from field activities. EMPRES-i, through specific agreements with key partners, is further integrating databases of other systems, such as the Global Animal Information System (GAINS), the FMD UC Davis BIOPORTAL, the Swiss Institute of Bioinformatics (SIB) and FAO Reference Centres. Certain EMPRES-i modules have been customized for use by other FAO groups, *e.g.* EMPRES food safety, ECTAD Asia and the Crisis Management Centre (CMC). EMPRES-i technology could be made available for the development of similar platforms, *e.g.* for an influenza gene observatory.

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Technical Overview of the Alberta Veterinary Surveillance Network Surveillance Information Management Systems Project

Y. Qu[1*], J. Berezowski[2], T. Herntier[2], I. Jamal[1], G. Zeng[1] and L. Zhang[1]

Abstract

The Alberta Veterinary Surveillance Network Surveillance (AVSN) has developed a software platform called the Surveillance Information Management System (SIMS) to provide services that are essential for surveillance including data collation, manipulation, analysis, reporting and visualization The SIMS application architecture comprises open source software that is robust and extensible and supports ongoing innovation in surveillance and analytics research.

Keywords: monitoring systems, syndromic surveillance, pattern recognition, early warning systems, multiple sources of data.

Introduction

Outbreak detection is an essential component of animal health surveillance. Recent technological and internet infrastructure advancements have allowed agricultural businesses and governments including surveillance agencies to generate timely data for business management purposes. Surveillance and livestock production data have value for identifying changes in the disease status of farmed livestock. Timely and accurate detection of outbreaks in surveillance data requires a robust software platform that can provide many services to users including data collation, manipulation, analysis, reporting and visualization. This paper provides a brief description of the processes and the analytical methods developed by the AVSN to support outbreak detection in surveillance data.

Materials and methods

The vision for the design of the SIMS was that of a software platform for data management, data analytics, reporting and visualization as an early warning system that detects, projects, reports and generates notification of potential disease outbreaks.

The architecture of the SIMS application is typical of surveillance systems and comprises layers of data integration, storage and directory; case and outbreak detection, notification and user interface with additional services of reporting, visualization, and projection [1]. The application was built from a collection of open and proprietary source software that provide a robust and extensible platform supporting ongoing innovation in surveillance and analytics research. The SIMS automated mode was built around sequential data workflows that process datasets in parallel.

The data processing engine is built using the Konstanz Information Miner (KNIME) [2], a user-friendly and comprehensive data integration, processing, analysis, and exploration platform developed at the University of Konstanz, Germany [2]. It is open source software that can be combined with multiple other open sources like R-project [3], a comprehensive statistical software, SaTScan [4] software for spatial, temporal, time and space data analysis, BIRT [5] a reporting software, Pentaho [6] a dashboard and other stand alone executable algorithms (*e.g.* text mining).

In the SIMS project, work flows were constructed with KNIME for both automated analysis and adhoc analysis. Automated analysis consists of system driven preprocessing and event detection algorithms that generate daily outbreak-detection reports. Adhoc analysis provides tools for user initiated explorations of the data such as drill down, development and use of additional outbreak-detection methods, ad-hoc reporting and adhoc data visualization.

The first phase of SIMS development focused on two datasets. The Veterinary Practice Surveillance (VPS) [7] for cattle dataset is extracted from a near real-time database that was designed and implemented by the AVSN for emerging disease surveillance of cattle in Alberta. Briefly, this is a voluntary surveillance system in which veterinarians submit data about cattle diseases to an AVSN database through a restricted access website. The Bovine Spongiform Encephalopathy (BSE) [8] dataset is similarly extracted from the near real-time database of information collected about cattle submitted for BSE testing in Alberta. These datasets generate daily case submissions that have varying temporal and spatial distributions.

These datasets are complemented by datasets from other domains such as environmental (*e.g.* weather, water quality) and economic (*e.g.* price) to broaden the scope and inputs of this early warning system. The AVSN is expanding to include VPS of other species and also to include complete supply chains (movement, processing, distribution, *etc.*). While the datasets are correlated within and between themselves, at this stage work is being done on the basis that the data can be analyzed as uncorrelated univariate time series. However, multivariate methods are under development. For example, the VPS cattle dataset is analyzed from 5 key dimensions for diseased cattle: type of cattle (cow-calf, dairy, feedlot, and back-grounder), clinical syndrome, clinical diagnosis, county of farm location and veterinary practice, yielding 374 time series subsets for event detection

Automated analysis comprises data collation (extract, transfer and load) to and from the data warehouse; data cleaning and preprocessing; analytical preprocessing; event detection; event projection; notification; data reporting and visualization (Figure 1)

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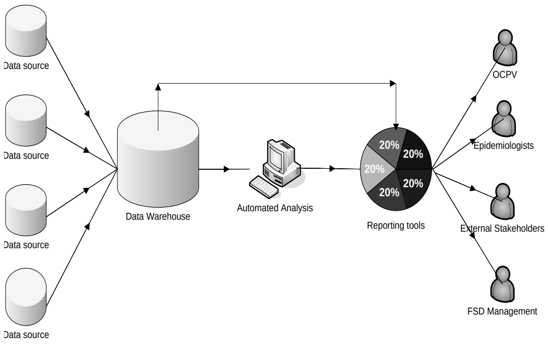
[1] AQL Management Consulting Inc, Edmonton, Canada - * yingqu@aqlmc.com

[2] Alberta Agriculture and Rural Development, Edmonton, Alberta, Canada

Figure 1: SIMS Architecture



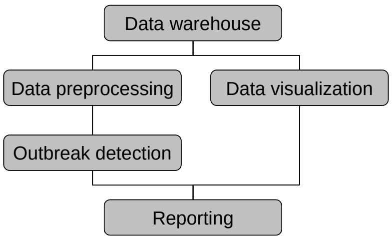
The first data preprocessing workflows clean, select and prepare the data for analysis. Thereafter data visualization workflows generate both time plots and spatial maps for all input subsets and for various time scales (*e.g.* daily, seven-day, seven-day rolling average, monthly) to display temporal trends and distribution patterns for reporting if required. The BSE dataset requires text mining to extract syndromes or clinical diagnoses from open data entry fields. This was done using a concept model generated in SPSS Clementine [9] which was validated with similar categories from the VPS dataset. The preprocessing workflows also allow adding innovative visualization methods. For example, the Symbolic Aggregate approximation (SAX) representation has been used for visualization of time series and for dimensionality reduction, clustering and indexing [10].

In the second step, analytical preprocessing workflows are used to remove linear trends and autocorrelations in the preprocessed data using methods such as Poisson regression [11] and autoregressive integrated moving average [12] models to generate near-normal distributed time series data which become input to the bank of event detection algorithms.

In the thirds step, automated temporal and spatial outbreak event detection algorithms are run daily. Stakeholders are notified of possible suspicious events by email or phone text messages, graphical and tabulated output is created, and the data warehouse updated. The algorithms include control chart (xbar – 13), classic cusum [14], EWMA [13] methods optimized for simulated “low”, “medium” and “fast” outbreaks. Simulated outbreaks were generated using the North American Animal Disease Simulation Model (NAADSM) [15], an application for epidemiologic simulation modeling of livestock diseases and inserted into training VPS data subsets. At the same time, both retrospective and prospective analysis from purely spatial and temporal-spatial cluster analysis is performed using SaTScan [16]. Other methods are being tested [*e.g.* 17].

Finally, the results are reported in a dashboard providing epidemiologists with an interface for more detailed analyses. Tools for multidimensional visualization and analysis are also being explored. Over time the dashboard is envisioned to be a portal to real-time and ad-hoc data and surveillance results from the overlapping domains of animal, human, environmental and economic health.

Figure 2: The structure of workflows



Results

Data and the results of analysis are too extensive for a comprehensive description in this short report. A few examples of results including descriptive and diagnostic charts, plots, maps, tables from the data preprocessing, manipulation, analysis and reporting and visualization (figures 3 to 8) are presented here. These tools are at various stages in development, testing and implementation.

Figure 3: Time plot of daily submission counts for syndrome Gastrointestinal

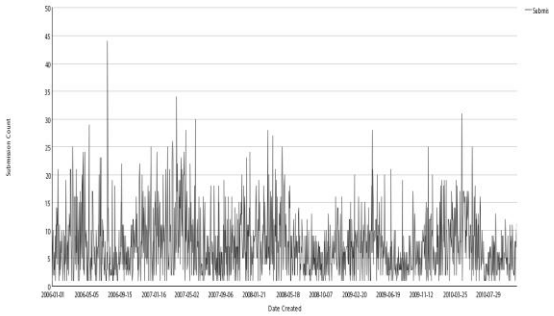
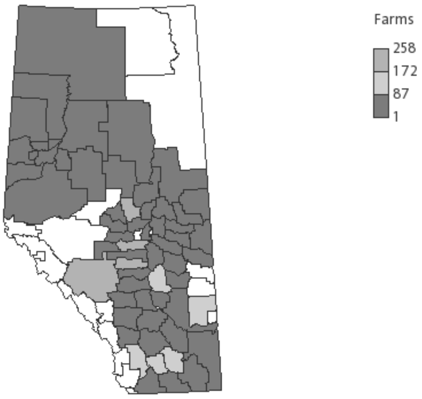


Figure 4: County map of submission counts for syndrome Gastrointestinal



Discussion

Modern surveillance systems generate large quantities of very complex data. Understanding, analyzing and visualizing these data requires more tools than are commonly found in an epidemiologist’s toolbox. The AVSN has committed to using surveillance and other data including production, carcass, weather and even commodity price data to understand and detect changes in the health of Alberta livestock populations. Many of the tools being tested are not familiar to epidemiologists. However they have been well used in other fields, especially process control, network analysis, supply chain management and data mining. The experience to this point would suggest that while these methods hold promise, their implementation needs to be supported by a strong multidisciplinary research, innovation and collaboration program that improves the seamless adaptation of these methods to animal health data.

Figure 5: Normality plot of pre-processed submission counts for syndrome Gastrointestinal

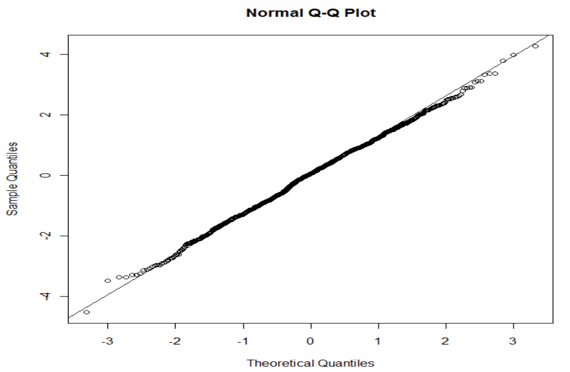


Figure 6: Autocorrelation function plot of pre-processed submission counts for syndrome Gastrointestinal

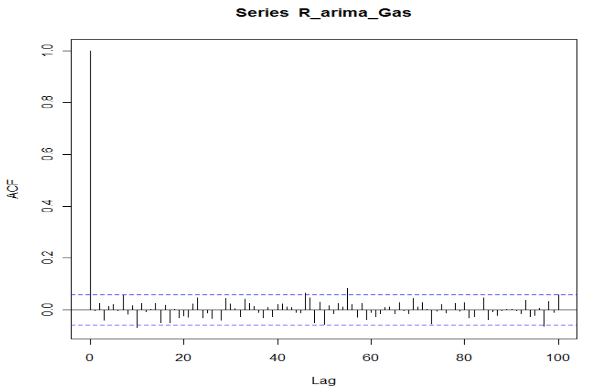
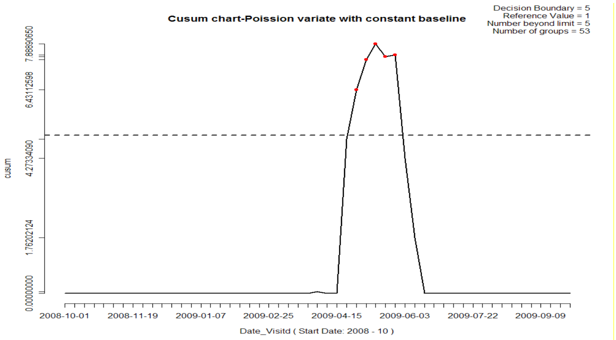


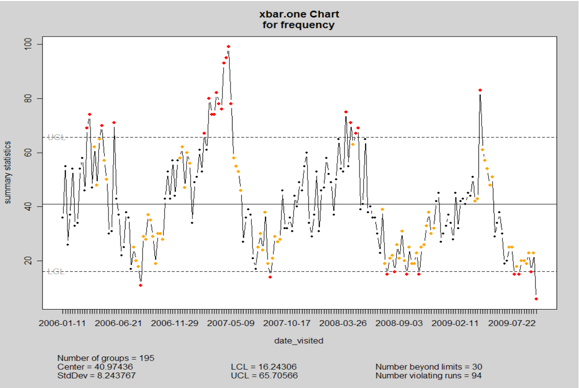
Figure 7: Poisson-Cusum chart for submission counts for syndrome Gastrointestinal



Methods for exploring, analyzing and reporting data have been explored in this project. However, there are many possible areas for further exploration and research. There are many potential temporal or spatial outbreak detection methods for both univariate and multivariate time series data. While there is no method that could be suitable for all datasets there is a need to refine existing and develop new algorithms that can be optimally applied within and across multiple datasets, particularly from overlapping health domains.

KNIME has been performed well as a robust and user-friendly software for data mining. It provides us with a platform for our development work. More importantly, as it is open source nature it could provide surveillance researchers and practitioners with a useful analytic toolkit to be expanded, shared and used.

Figure 8: Xbar chart for submission counts for syndrome Gastrointestinal



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Targeted surveillance of cattle trade using social network analysis tools

S. Rautureau[1*], B. Dufour[2] and B. Durand[1]

Abstract

Networks generated by live animal movements are the major support for the propagation of infectious agents between farms, and their structure strongly affects how fast a disease may spread. Structural characteristics may thus be indicators for targeting surveillance. The method proposed here is based upon the analysis of specific sub-networks: the giant strongly connected components (GSCs) considered as vulnerable structures for infectious diseases spread. Their disappearance when targeted nodes are removed allows studying how network vulnerability may be controlled. The method was applied to the cattle trade network in France, 2005.

Among several tested approaches, the most efficient procedure was based on the ranking of nodes by decreasing betweenness centrality (the proportion of shortest paths between nodes on which a specific node lies). GSC disappearance was obtained after removal of <1% of network nodes. A targeted surveillance on this small subset of holdings identified using centrality measures may thus help to control the spread of an infectious disease through the animal trade network.

Keywords: disease surveillance, network analysis, cattle, trade.

Introduction

Events following the introduction of foot-and-mouth disease (FMD) into United Kingdom (UK) in 2001 or classical swine fever epidemic in the Netherlands and Germany in 2003 clearly demonstrated that trade with disease-free countries is not 'risk-free' [1]. These events also underlined the vulnerability of national trade networks to the spread of an infectious disease.

The live animal trade can be represented by a network of linked holdings. Social network analysis (SNA) concepts and methods can be used to study these relationships. SNA has developed indicators of the centrality for nodes or for their relationship, and methods for the identification of cohesive structures (groups or individual clusters) [2]. The approach has been introduced in veterinary epidemiology studies only recently (reviewed by Dubé *et al* [3] or Martinez-Lopez *et al.* [4]). Livestock movements have been analyzed to evaluate the potential transmission of an infectious disease through the contact network, or to assess the impact of livestock movement regulations.

Network connectedness determines how fast and widely an infection may spread, and the existence of large connected components (beyond a certain size) could be the basis of network vulnerability. Strongly connected components (SCs) where connectedness is particularly high is defined by SNA as sub-networks for which every node can be reached from every other node via one (or several) directed path(s). A disease introduced into any holding of a SC can potentially reach any other holding in that SC. In a real network, a large connected component often emerges, known as the 'giant strong component' (GSC). For the French cattle trade network, a previous study has shown the existence of such large subset of holdings, widely spread all over the country, whatever the studied time scale [5]. It is also known that GSC size is a good predictor to assess the potential epidemic size [6, 7] .

A corollary to these results is that network vulnerability may be controlled by focusing measures on the holdings that play the role of 'hubs' and ensure the overall cohesion of animal trade network. Most of animal movement networks and in particular their GSCs have a scale-free structure [5, 7-9]. Scale-free networks have a great robustness but quickly break into many isolated fragments when nodes are not removed randomly but according to a targeting procedure based on network topology [10]. These structural properties can be used to target control or preventive measures and decrease the connectedness of the network.

The objective of the study was to evaluate network-based targeting procedures in order to identify subset of holdings in which targeted surveillance could be implemented. For this purpose, cattle movement between French holdings were studied at different time scales.

Materials and methods

Network construction: French cattle movement data were obtained from the National Bovine Database of Identification (BDNI) which is managed by the French Ministry of Agriculture. Individual cattle movements registered during year 2005 were selected (before movement limitations due to bluetongue epizootic). Three kinds of holdings were distinguished: farms, markets, and dealers. Markets and dealers are collectively named 'trade operators'.

The cattle trade network was built representing as a node each holding involved in any movement during a given period. All of the movements between two specific holdings during the time period were then consolidated into a single link. The method was applied for three different time scales; the year, the month (12 monthly networks) and the week (52 weekly networks). For each of these networks, the strongly connected components (SCs) and the size of the two largest SCs were determined. Both sizes were compared to qualify the largest SC as the 'giant' strongly connected component.

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[1] French agency for food, environmental and occupational health safety (ANSES). Maisons-Alfort, France - * severine.rautureau@anses.fr

[2] Alfort National Veterinary School (ENVA), Maisons-Alfort, France

The composition of GSCs by type of holding was determined. The main centrality measures were calculated for each holding in networks; the degree (number of nodes to which it is directly linked), the betweenness (the frequency according to which a node is on the shortest path between any pairs of nodes [11]) and the closeness (a measure of how closely a node is connected to any other node [12]).

Targeting procedures: For each network, four targeted node removal procedures were tested to determine the most efficient way leading to GSC disappearance. GSC disappearance was defined by the fact that, after node removal, the size of the largest SC had fallen below a predefined threshold. This threshold was set to the maximal size of the second largest SC observed in the yearly, monthly, and weekly networks (before any node removal).

The first node removal procedure was based on holding type: the sizes of the largest SCs were computed after the removal of markets, dealers, or both. The three other procedures used centrality measures: degree, betweenness, and closeness. For a given centrality measure, nodes with the highest value were removed; the centrality measure was then recalculated after removal, as well as the size of the SCs. These operations were repeated until GSC disappearance.

Network analyses were performed using the Igraph package (v 0.5.2, http://igraph.sourceforge.net) for R software [13].

Results

A large and widely spread strong component was observed in each of the studied networks (Figure 1). In the yearly network, this component included 45% of network nodes, this proportion being lower in the monthly (mean proportion: 8%) and weekly networks (mean proportion: 4%). However, the size of the other strong components was always $<10^{-3}$ lower (range: 4-51 nodes) than the size of the largest strong component. The latter was therefore considered as the ‘giant’ strong components (GSCs).

Even if GSCs were mainly composed of farms, trade operators were markedly overrepresented in these sub-networks. In the yearly network, the proportion of holdings involved in the GSC was 2.2 times higher for trade operators than for farms. This contrast was stronger in monthly and weekly networks with ratios of 12 and 22, respectively (Table 1).

The degree, betweenness, and closeness centrality appeared markedly higher in dealers and markets than in farms (Figure 2).

Removing the trade operators from the yearly network did not induce GSC disappearance. After node removal, the size of the largest strong component was reduced to 36% (41,588 nodes) of its initial size, but the GSC was still present. This node removal procedure based on holding type was successful in monthly and weekly networks, for which removing all of the trade operators always led to GSC disappearance (Table 2). This disappearance was not obtained if a single category of trade operators (markets or dealers) was removed from the network, even for the weekly scale time.

Figure 1: Spatial spread of holdings belonging to the giant strong component (GSC) for the smallest weekly cattle trade network (33th week) in France, 2005

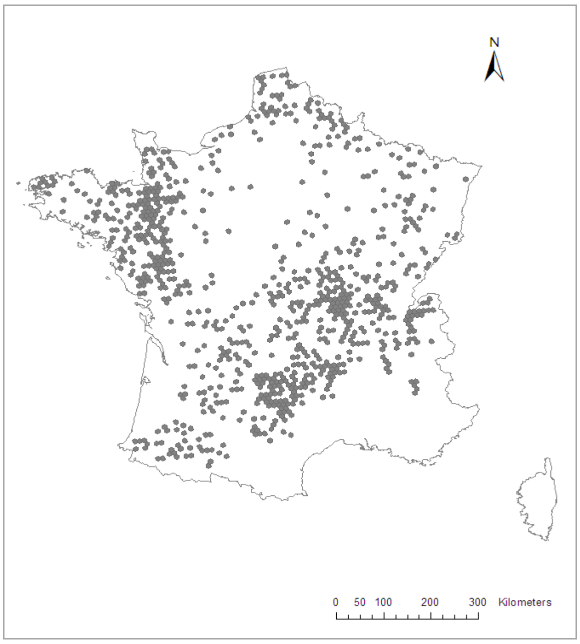
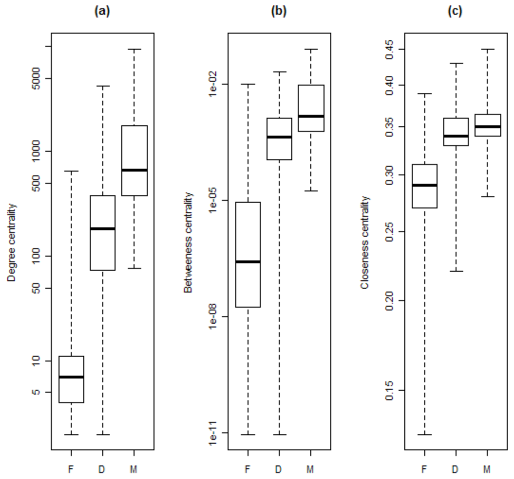


Table 1: Descriptive parameters for the giant strong components of the yearly, monthly and weekly cattle trade networks in France, 2005

	Annual network	Monthly networks mean data [range]	Weekly networks mean data [range]
Size	108,904	10,277 [7,254-12,652]	2,115 [885-2,657]
Farms	107,539	9,245 [6,277-11,622]	1,430 [524-1,885]
Dealers	1,289	964 [908-1,008]	633 [320-714]
Markets	76	69 [65-73]	52 [39-60]
Links	804,331	39,592 [29,726-47,581]	7,417 [2,655-9,485]

Figure 2: Distribution of degree (a), betweenness (b) and closeness (c) centrality measures in holdings belonging to the giant strong component of the yearly cattle trade, according to the holding type (farms: F, dealers: D and markets: M), France, 2005



Procedures depending on the centrality measure led to the removal of thousands nodes in the annual network (representing 1 to 2% of its size) and tens to hundreds nodes in weekly and monthly networks (representing 0.2 to 0.3% of their sizes) (Table 2). The betweenness centrality was the most efficient targeting measure, for which the number of removed nodes was the lowest: 2,866 nodes in the yearly network and, on average, 299 nodes in monthly networks and 82 nodes in weekly networks. The proportion of removed nodes was much higher for trade operators than for farms, particularly for markets.

Table 2: Number of node removals allowing to obtain the disappearance of the giant strong component in yearly, monthly and weekly cattle trade networks, France, 2005

Node removal targeting procedure	**Time scale**	**Number of removed nodes (%[a])**			
		Farms	Dealers	Markets	Total
Holding type[b]	Monthly	-	964 (86%)	69 (97%)	1,033 (0.8%)
	Weekly	-	633 (63%)	52 (79%)	685 (1.4%)
Degree centrality[c]	Yearly	2,322 (1.0%)	1,113 (85%)	75 (100%)	3,510 (1.4%)
	Monthly	3 -	351 (31%)	48 (68%)	403 (0.3%)
	Weekly	-	83 (8%)	29 (44%)	113 (0.2%)
Closeness centrality[c]	Yearly	2,805 (1.1%)	1,073 (82%)	75 (100%)	3,953 (1.6%)
	Monthly	55 -	295 (26%)	46 (65%)	396 (0.3%)
	Weekly	10 -	79 (8%)	24 (36%)	113 (0.2%)
Betweenness centrality[c]	Yearly	1,766 (0.7%)	1,035 (79%)	75 (100%)	2,866 (1.2%)
	Monthly	8 -	251 (23%)	40 (56%)	299 (0.2%)
	Weekly	1 -	59 (6%)	23 (35%)	82 (0.2%)

[a] Global and holding category-specific percentages of nodes removed from the network (average values are given for monthly and weekly networks).

[b] Removal of nodes representing trade operators (this procedure failed for the yearly network).

[c] The node with the highest centrality measure is repeatedly removed until the size of the largest strong component falls below 51 nodes (maximal size of the 2nd largest strong component in the studied networks).

Discussion

Animal movements form networks linking holdings. SNA methods can supply general indicators to evaluate network vulnerability to infectious diseases. As an example, the control of vulnerability of the French cattle trade network was studied at different time scales. The yearly time scale aimed at studying the vulnerability of the network to non-notifiable diseases: once introduced the pathogen agent would spread freely across the network. The monthly and weekly time scales were studied to focus on notifiable diseases, assuming that the epidemic would spread during one week or one month before the identification of the first infected premise.

We studied four targeting procedures either based upon holding type (farm, dealer, or market), or on node centrality measures. The efficacy of these targeting procedures was evaluated and compared. GSC disappearance was chosen as an indicator whether network vulnerability was under control. Studying the effect of trade operator removal on the GSCs was a natural choice because of their important presence in GSCs. The high values of their centrality measures also suggest that many of the trade operators could play the role of 'hubs'. Removing all of the dealers and markets led to GSC disappearance in monthly and weekly networks only. Removing only one type of trade operators (dealers or markets) never led to GSC disappearance. Targeting procedures based on centrality measures appeared more efficient as the removal of <1% of nodes always led to GSC disappearance. Among the removed nodes, markets (and, to a lesser extent, dealers) were markedly over-represented. Past studies already demonstrated the role of markets in disease spread [6, 7, 14]. Ortiz-Pelaez *et al.* [15] characterized their high betweenness centrality as key factors in the evolution of the initial phases of the foot-and-mouth outbreak in the UK in 2001. The efficacy of targeted control procedures of disease spread in networks based upon centrality measures have been also studied *in silico* for hypothetical diseases, either highly infectious [16] or endemic [8, 9].

This study illustrated by the French cattle trade network has shown that applying SNA tools to animal movement data may be useful for identifying a small subset of holdings in which targeted control or surveillance measures could be applied (sensitization to bio-security, clinical surveillance, measures such as suspending trade activities). Implemented by a near-real time traceability system, this method could be used for a continuous targeted surveillance and thus help to control the spread of an infectious disease through the animal trade network.

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Building emerging infectious disease intelligence in low-middle income countries: The potential role for mobile phone-based surveillance systems

K. Sawford[1*], C. Robertson[2], W. Gunawardana[3] and C. Stephen[1,4]

Abstract

The risk posed by infectious diseases is dynamic and increasing. There are limitations to diagnostic laboratory-based disease surveillance, especially in low-middle income countries. We propose that mobile phone-based emerging infectious disease (EID) surveillance could play a role in building EID intelligence.

Keywords: evaluation methods, decision-support systems, risk, syndromic surveillance, low-middle income countries.

Introduction

In 1998 the Centre for Disease Control (CDC) developed the Guidelines for Evaluating Public Health Surveillance Systems to 'ensure problems of public health importance are being monitored efficiently and effectively.' Though they have been updated over time, the system attributes simplicity, flexibility, data quality, acceptability, sensitivity, predictive positive value, representativeness, timeliness and stability remain the standard measures of performance [1]. These guidelines have played a vital role in the development, implementation and maintenance of many surveillance systems, and will continue to do so in the future.

It is worth noting that since inception of these guidelines the landscape of infectious disease risks has undoubtedly changed. A number of new infectious diseases have emerged, catching the global public health community off guard, and the rate of emergence has been increasing over the past forty years [2]. Further, it is estimated that close to 75 percent of new EIDs in humans have arisen in animals [2]. As the size of the global population increases so too will the forces driving disease emergence [2]. When the risk of future EID events is mapped, it is highest in areas at lower latitudes where many countries range from low to middle income. These countries have limited resources, and therefore little to allocate to EID surveillance [2].

Infectious diseases are deemed 'emerging' if they have only recently arisen or if they are previously known diseases that are increasing in incidence or geographic range [3]. Surveillance in the field of animal health has historically targeted submissions to diagnostic laboratories, much like in human medicine, where the aim is to make a definitive diagnosis. Within animal disease surveillance it is evident that laboratory-based surveillance fails to capture the information required to adequately forecast the risk posed by animal health related events.

As a result of the changing EID landscape and the limitations of laboratory-based surveillance, there is a desire to develop, implement, and evaluate surveillance systems that use other forms of animal health data to identify events that could forecast an emerging health risk to humans. This presents two challenges: firstly, there is a need to detect events. Secondly, there is a need to consider the event in context to determine its significance as a human health risk.

A number of surveillance systems that use animal health data have been developed, however the majority operate in high-income countries [4]. Very few have undergone a formal evaluation process, and most often only a subset of the CDC's system attributes is considered [4]. One of the challenges in evaluating these types of systems is the goals of surveillance systems on which the CDC's guidelines were based differ markedly from surveillance systems targeting the animal population: the CDC's guidelines are based on systems designed to identify human cases within human data. This objective is quite different from the need to identify an animal health related event, and determine its significance.

Work in the area of detecting a change in risk is not limited to the field of EIDs. With recently heightened concerns around terrorism, there has been extensive research and investment into characterizing risk in the area of military intelligence [5]. However, when comparing the research from the field of military intelligence to that from EID surveillance there are important differences to consider. In the field of military intelligence there is a distinction drawn between surveillance and intelligence [5]. Military surveillance equates to monitoring of any data that are collected from reconnaissance [5]. Military intelligence involves analyzing that data and transforming them into usable content for planning and decision-making [5]. In order to address EID risks more broadly, we need to shift to an intelligence-based approach.

In this paper we propose that mobile phone-based surveillance systems in low-middle income settings serve to supplement laboratory-based disease surveillance and consider their potential role in building EID intelligence. We present 10 years of animal laboratory data collected in Sri Lanka. We then present outputs from the Infectious Disease Surveillance and Analysis System (IDSAS), a mobile phone-based surveillance system that was piloted in Sri Lanka. Finally, we consider the position of laboratories and the IDSAS relative to animal health related events and their potential contributions to EID intelligence.

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[1] Faculty of Veterinary Medicine, University of Calgary, Calgary, Alberta, Canada - * kate.sawford@gmail.com
[2] Department of Geography and Environmental Studies, Wilfrid Laurier University, Waterloo, Ontario, Canada
[3] Faculty of Veterinary Medicine and Animal Science, University of Peradeniya, Peradeniya, Sri Lanka
[4] Centre for Coastal Health, Nanaimo, British Columbia, Canada

Materials and methods

Government Veterinary Services in Sri Lanka: The Department of Animal Production and Health (DAPH) is a national-level body responsible for control of livestock diseases, livestock research, animal breeding, and education in animal husbandry. Veterinary services are delivered through provincial-level DAPH councils and field offices. Provinces are made up of districts, which are further divided into divisional secretariat (DS). Each DS division is assigned a minimum of one field veterinary surgeon (FVS) that provide animal health services.

Diagnostic laboratory capacity in Sri Lanka: The DAPH carries out surveillance for listed World Organization for Animal Health (OIE) diseases and emerging animal diseases. The Veterinary Research Institute (VRI) operates under the DAPH and is the only national-level organization in Sri Lanka that provides veterinary diagnostic services. District-level laboratory diagnostics are provided by Veterinary Investigations Centres (VICs) located in the following districts: Anuradhapura, Badulla, Hambanthota, Chillaw, Jaffna, Matara, Peradeniya, Rannala, Polonnaruwa, Ratnapura, Vaunia, Welisara, Kegalla, Nuwara Eliya, and Dambulla. Means of making a diagnosis vary markedly between the VRI, VICs, and field offices (Table 1). One aim of the DAPH is to establish VICs in every district in Sri Lanka.

Diagnostic laboratory data are stored in paper format at the VRI and VICs. To permit analysis, laboratory data from DS divisions covered by FVSs participating in the IDSAS were electronically compiled. When available, for each submission fields included: date; location from which the sample was collected down to the division level; species; age of the animal(s); number of animals in the flock or herd; sex; number of samples collected; type of samples; test performed; result of the test; and agent identified. The laboratory data used in this study represent the period of January 1st 2000 through to December 31st 2009.

Description of the diagnostic laboratory data: In order to detail the current diagnostic laboratory-based disease surveillance system in Sri Lanka, descriptive statistics on the laboratory data are presented. We report the number of laboratory tests performed for the 40 participating DS divisions; the total number of cases; the average number of tests per year; and the range, mean, and median of tests per DS division over the 10-year period.

The IDSAS: The IDSAS was established in collaboration with the DAPH [6]. The system tracked syndromes and clinical diagnoses in cattle, buffalo, and poultry, in the four participating districts in Sri Lanka (Anuradhapura, Matara, Nuwara Eliya, Ratnapura). 40 FVSs participated as data collectors. Each survey submitted by a FVS represents one visit to a farm or one examination in clinic of at least one of the three species. Surveys were classified by routine visits (yes/no), presence or absence of an animal health issue, location of the case (clinic/on farm), diagnostic samples submitted (yes/no), and post mortem examination (yes/no). In the case of an animal health issue, cases were given a syndrome group and a clinical diagnosis. FVSs were given the option of classifying the cause of the health issue as unknown. There were a total of 17 syndrome groups for cattle and buffalo and 11 for poultry. Options for clinical diagnoses were based on the syndromic grouping selected. As each FVS is responsible for a known geographical area, geographic locations could be associated with each survey down to DS division. FVSs were asked to submit surveys via email to a surveillance database daily. Weekly reports were disseminated to project partners containing a list of cases. Robertson *et al.* [6] provides a detailed description of design and implementation of the IDSAS.

Finally, patterns of information flow identified in the datasets are presented in relation to their potential contribution to an EID intelligence-driven system.

Table 1: Veterinary diagnostic capabilities

Location	Diagnostic capabilities	Confirmable condition (if applicable)
Field offices	Clinical examination	
	Post mortem examination	
	California Mastitis Test (CMT)*	Mastitis
	Microscopy (+/- stain)*	Blood-borne parasites
VICs	CMT	Mastitis
	Microscopy (+ stain) and fecal flotation	Blood-borne parasites, intestinal parasites
	Aerobic bacterial culture	Bacterial infection
	Antibiotic sensitivity testing	
	Rose Bengal plate agglutination test	Brucellosis
	Rapid antigen detection	HPAI
VRI	CMT	Mastitis
	Microscopy (+ stain) and fecal flotation	Blood-borne parasites, intestinal parasites
	Aerobic and anaerobic bacterial culture	Bacterial infection
	Antibiotic sensitivity testing	
	Histopathology	
	Complement fixation test	Brucellosis
	Milk ring test	Brucellosis
	Antigen detection enzyme-linked immunosorbent assay (ELISA)	Foot and mouth disease
	ELISA	Classical swine fever
	Reverse transcription-polymerase chain reaction	HPAI
	Pathogen isolation by egg inoculation	Newcastle disease
	Serology	Infectious bursal disease Infectious bronchitis Reovirus infection Infectious laryngotracheitis

*Only a small number of offices have these diagnostic capabilities.

Results

Summary of the laboratory data: During the 10-year study period 2083 laboratory tests were performed on 1882 cases. This is equivalent to ~5.21 laboratory tests/DS division/year (0.43 tests per month). The tests per DS division ranged from 0 to 427, with a mean of 54.16 and a median of 22. Of the 2083 tests performed, 808 reported the age of the affected animal(s) (38.79%), 787 reported the sex (37.78%), and 129 included the number of animals present in the herd or flock (6.19%).

Summary of the IDSAS data: IDSAS operated for 365 days (January 1 2009 through to December 31 2009).

During this period, 5758 unique surveys were submitted to the system by participating FVSs. This is equivalent to ~144 surveys/FVS over a 12-month period (12 per FVS per month). Of the total number of surveys, 4639 cases were reported (*i.e.*, reported an animal health issue). The survey required entries in all fields prior to completion.

The relationship between IDSAS, diagnostic laboratories, and animal health related events: FVSs made a clinical diagnosis in 4402 cases, of which 247 had a post mortem examination performed. In 237 cases FVSs reported the cause of the case unknown, of which 18 had a post mortem examination performed (Figure 1).

Of the 4639 cases submitted to the IDSAS, 326 indicated that a sample submitted to a laboratory. During 2009 the VRI received samples from 21 cases and the VICs received samples from 298 cases. Though the IDSAS enabled FVSs to report sample submission to a laboratory, there was no way to track individual samples from FVSs to the VICs or VRI as indicated by the dashed lines in Figure 1.

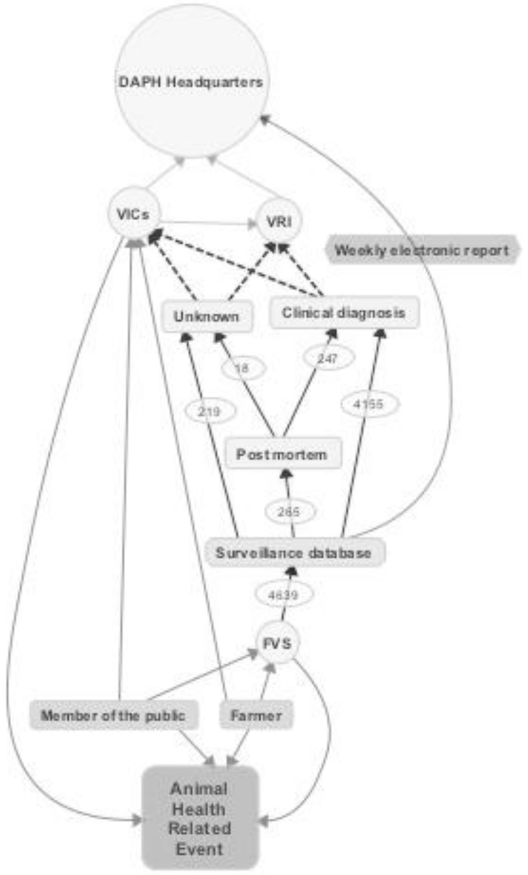
Discussion

The results demonstrate that few reports of animal health related events are being received by laboratory facilities in Sri Lanka. The IDSAS greatly increased the number of case submissions and reports were promptly available for review by high-level officials in the DAPH.

The IDSAS has the potential to contribute to EID intelligence in that it helps describe the context in which animal health related events occur. As the IDSAS is based on submissions from FVSs it provides more opportunities to observe change within the population: FVSs visit farms, interact with farmers, and can gather ancillary data. They are one step away from farmers, who most often report animal health related events. In addition, as the IDSAS requires all ancillary data be entered prior to survey completion, the contextual information more accurately reflects the animal health situation encountered by FVSs.

This study demonstrates the ability of a mobile phone-based system to engage FVSs. However, at this time the IDSAS is no longer in operation. Though it is being adapted to integrate with existing national disease surveillance in Sri Lanka, it terminated in the form presented here when the research ended and FVSs ceased to submit surveys. Part of the reason for this may be that though information flowed from FVSs to stakeholders in the DAPH, flow in the other direction was not built into the IDSAS, nor were VIC veterinarians or diagnosticians within the VRI included. In addition, though the IDSAS provided more numerous case submissions, there was no means of follow up in the system, which meant there was no opportunity for validation of clinical diagnoses. To achieve EID intelligence future systems need to build in the ability to follow up on signals, enabling a response in advance of an etiological diagnosis, as well as explore means of ongoing engagement of stakeholders at all levels.

Figure 1: The position of the IDSAS and laboratories relative to an animal health related event. The arrows describe flow of information



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Collection, Transmission and Management for animal disease surveillance in selected districts of Zambia

Y. Sinkala[1*] and C.M. Mundia[1]

Abstract

We present the application of the digital pen technology as a tool for data collection, transmission and management of animal disease data in Zambia. The technology has been tested and found to be working.

Keywords: data collection, transmission, management, digital pen technology

Introduction

Collection of surveillance and outbreak data is normally done manually by field officers, and then sent to district office. From the district office, the data is sent to provincial office and then captured manually onto a computer system. This process takes quite a lot of time when doing consolidation and does not provide timely information of diseases occurrence

The digital pen technology (DPT) is a tool that is being used to solve problems of lack of timely information flow from the various collecting sources, particularly veterinary camps that are mainly in remote areas, to decision makers at headquarters. It will enable appropriate decision-making commensurate with required timely effective action.

The technology has the potential to be used in early warning and reaction for transboundary animal diseases emerging and zoonotics.

This technology aims at networking, enhanced information flow as well as strengthening a regional surveillance network backed up by the Livestock Information Management System (LIMS) at national and regional levels.

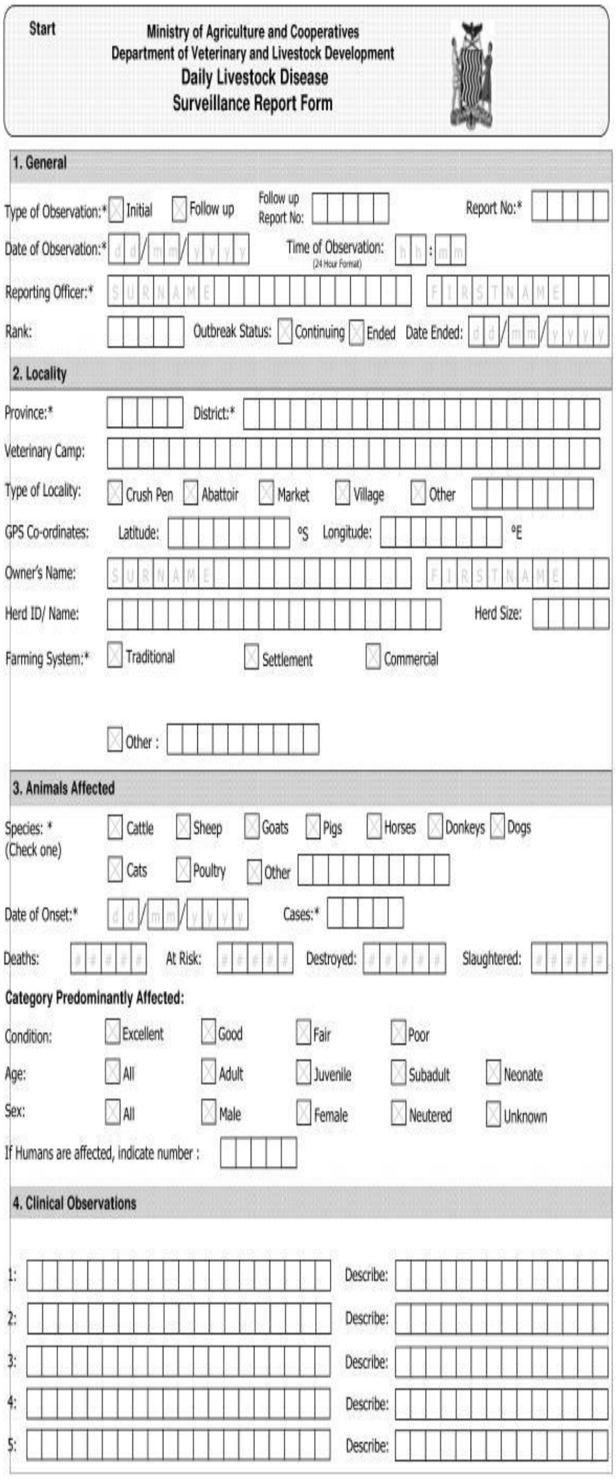
The challenge is to automate the capture of disease outbreak and surveillance data and provide information to predict the outbreak of diseases.

Materials and methods

An assessment was conducted of the information needed to address the surveillance objectives. This was then summarized in a form for collection of outbreak and general surveillance data. The forms was designed with a series of tick boxes, labels, textboxes and critical fields embedded into the form that work well with a Digital Pen solution. Lexicons were created for names of diseases, species and locations to be used by hand writing recognition engine to convert the pen strokes into ASCII characters. The information collected on digital form is then uploaded immediately via Bluetooth and GPRS technology to a central computer where they are stored.

A web based Form Utility and workflow application has also been developed which allows updating and approval of collected data.

Figure 1: Surveillance form for DPT



Start

Ministry of Agriculture and Cooperatives
Department of Veterinary and Livestock Development
Daily Livestock Disease
Surveillance Report Form

1. General

Type of Observation:* ☒ Initial ☒ Follow up Follow up Report No: Report No:*

Date of Observation:* d d / m m / y y y y Time of Observation: (24 Hour Format) h h : m m

Reporting Officer:* S U R N A M E F I R S T N A M E

Rank: Outbreak Status: ☒ Continuing ☒ Ended Date Ended: d d / m m / y y y y

2. Locality

Province:* District:*

Veterinary Camp:

Type of Locality: ☒ Crush Pen ☒ Abattoir ☒ Market ☒ Village ☒ Other

GPS Co-ordinates: Latitude: °S Longitude: °E

Owner's Name: S U R N A M E F I R S T N A M E

Herd ID/ Name: Herd Size:

Farming System:* ☒ Traditional ☒ Settlement ☒ Commercial

☒ Other :

3. Animals Affected

Species: * (Check one) ☒ Cattle ☒ Sheep ☒ Goats ☒ Pigs ☒ Horses ☒ Donkeys ☒ Dogs

☒ Cats ☒ Poultry ☒ Other

Date of Onset:* d d / m m / y y y y Cases:*

Deaths: # # # # # At Risk: # # # # # Destroyed: # # # # # Slaughtered: # # # # #

Category Predominantly Affected:

Condition: ☒ Excellent ☒ Good ☒ Fair ☒ Poor

Age: ☒ All ☒ Adult ☒ Juvenile ☒ Subadult ☒ Neonate

Sex: ☒ All ☒ Male ☒ Female ☒ Neutered ☒ Unknown

If Humans are affected, indicate number :

4. Clinical Observations

1: Describe:

2: Describe:

3: Describe:

4: Describe:

5: Describe:

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[1] Ministry of Livestock and Fisheries Development, Lusaka, Zambia - * sinkalay@yahoo.co.uk, corneliusm@hotmail.com

Figure 2: Digital Pen

Result

The timely collection and transmission of data by field officers has been observed to be working well. Previously it used to take 15 to 30 days for the monthly report to reach the epidemiology unit but now it takes 2 minutes on average.

Now surveillance and outbreak data can be available for viewing in couple of seconds at the offices by a web interface which can help in accessing the outbreak of diseases in a particular location.

Discussion

The system is still work in progress and at the moment we are not able to do comparisons because the data is yet to be validated by the District Veterinary Officers

The success of the DPT hinges on the Veterinary Assistants sending reports and DVO/PVOs editing and validating them.

Data collected is available in an instant which enables Decision Makers to take action and also predict outbreaks of diseases among animals in specific locations. Unlike other fully computerized systems, paper copies of the form still exist and can be filed as appropriate for reference.

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Acknowledgements

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Use of the Global Positioning System (GPS) to map the locations of affected farms in an outbreak of Porcine Reproductive and Respiratory Disease in Lao PDR

S. Sinthasak[1], P. Latthachack[2] and D. Bourn[3]*

Abstract

Knowing the geographical location and environmental characteristics of disease outbreak sites are essential for disease investigation studies, control strategy formulation and assessing the effectiveness of control measures.

This paper illustrates the use of hand-held, Global Positioning System (GPS) navigation devices and public domain mapping software to locate and map the positions of affected farms in a recent outbreak of Porcine Reproductive and Respiratory Syndrome (PRRS) in Lao PDR.

Keywords: Global Positioning System (GPS); Porcine Reproductive and Respiratory Syndrome (PRSS); disease investigation; Lao PDR

Introduction

An outbreak of Blue Ear Disease (Porcine Reproductive and Respiratory Syndrome - PRRS) around Vientiane, the capital of Laos, and adjacent districts in Thailand, provided a timely opportunity to demonstrate the use of hand-held Global Positioning System (GPS) navigation devices to obtain the exact locations of farms with suspected cases.

The outbreak in Laos is believed to have started on 16 June 2010 [1] and spread rapidly thereafter, with more than 2,000 mortalities on 23 farms in 6 districts around Vientiane over the next three months [2 and 3].

The Department of Livestock and Fisheries (DLF) convened various stakeholder meetings to determine how best to control the disease and coordinate activities to prevent it spreading. Strict movement controls were imposed and the outbreak has now been resolved [5]. The Government of China contributed 20,000 doses of anti PRRS vaccine and FAO contributed an emergency assistance fund, as well as technical support.

An active surveillance program was initiated with daily collection of samples and laboratory testing by the National Animal Health Center, Epidemiology Unit, with technical assistance and reagents for real-time polymerase chain reaction laboratory testing from FAO.

The Laos component of the Environmental Animal Health Management Initiative (EAHMI), an FAO project funded by the Italian government, provided technical assistance in collecting the precise geographical coordinates of infected farms using hand held Global Positioning System (GPS) navigation devices, and preparing computer generated Geographical Information System (GIS) maps, showing the location of infected districts and farms. This enabled better targeting of disease control interventions by strategically focusing the surveillance during and after the outbreak around the affected areas.

Materials and methods

Field work involved collaboration between staff of Vientiane Capital Agriculture and Forestry Office, who provided information on the names of affected farms and outbreak records; and the Department of Livestock and Fisheries' Environmental Animal Health Management Initiative, who provided access to GPS navigation devices; with technical training and information technology support provided by staff of the Faculty of Environmental Science, National University of Laos.

The geographical coordinates of suspected outbreak farms, together with the tracks of the routes travelled, were down-loaded from the GPS navigation device to computer using standard data transfer and mapping software [5], such as:

This data was then merged with other farm specific data and exported to a .kml or .kmz files (for small or large amounts of data, respectively), which can easily be run and transferred on ubiquitous public domain mapping software [6 and 7].

Results

Figure 1 shows the precise geographical coordinates (Longitude and Latitude) of each of the affected farms visited. The figure also shows the exact tracks of survey vehicle routes to farms, which is very useful to know if repeat, follow-up visits are required, possibly with a different survey team and driver.

Figures 2, 3 and 3 show various views of the uploaded kml data file of the suspected PRRS farm locations around Vientiane on Google Earth and Google Maps. Figure 5 also shows the result of clicking on one of the farm display pins, which opens a data display box of farm details.

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[1] Affiliation: National Focal Point Officer, Environmental Animal Health Management Initiative in Laos - * Corresponding author email: david.mackenzie.bourn@gmail.com

[2] Affiliation: Faculty of Environmental Sciences, National University of Laos

[3] Affiliation: Project Coordinator, Sub-regional Environmental Animal Health Management Initiative in South East Asia

Figure 1: Coordinates of affected farm and access tracks

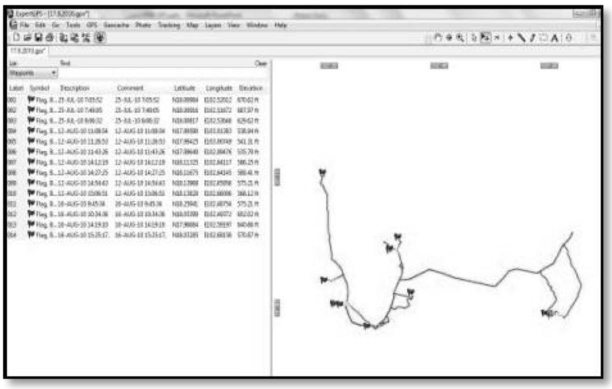


Figure 2: Regional view of locations on Google Earth

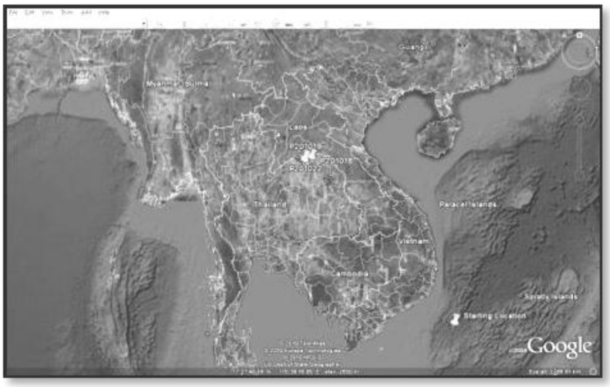


Figure 3: Local view of locations/tracks on Google Earth

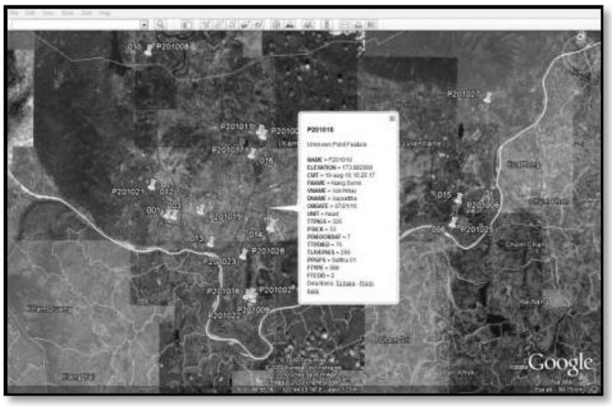
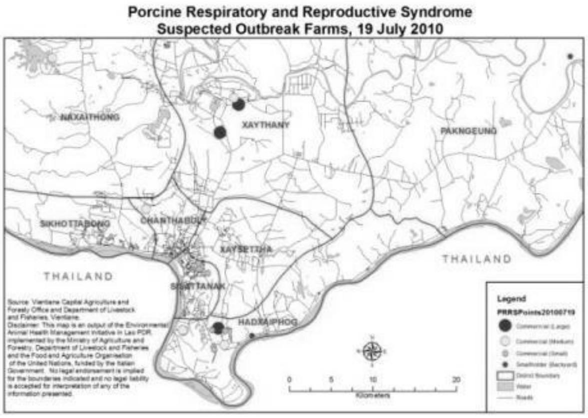


Figure 4: Local view of locations/tracks on Google Maps

Figure 5: Farm locations and types, and road network



Discussion

The utility of hand-held, GPS navigators to track movements and fix the precise locations of suspected disease outbreaks (or other sites of interest) for transfer to computer for mapping, reporting and analysis, as illustrated in the maps presented in this paper, enabled the government to focus their surveillance strategically. It also gave information on how to limit and manage animal movement. Proper tracking of outbreaks enabled the government to efficiently use their resources. To date, the PRRS outbreak has been controlled, but surveillance continues around the outbreak areas.

Further capacity building and institutional strengthening to promote this capability at both national and provincial level in Laos is a major priority and focus of attention of the Department of Livestock and Fisheries for future disease investigations, and more general recording and reporting of animal production and disease data, supported by FAO's Environmental Animal Health Management Initiative in Laos.

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Linking Surveillance Systems and Diagnostic Laboratories Worldwide - A Suggested Approach Based on the NAHLN Experience

S.E. Weber[1]

Abstract

The United States Bioterrorism Act of 2002 called for the US to implement an agricultural bioterrorism early warning system by enhancing the capability and coordination between the existing State veterinary diagnostic laboratories, Federal and State Agricultural facilities and public health agencies. This coordination was needed not only to increase laboratory capacity for diagnostic testing in the event of a large scale animal disease outbreak, but also to assure consistency in tests performed and the results reported. The timeliness of the reporting was of concern as well and was addressed through the implementation of information standards to allow results from diverse surveillance databases and laboratory information management systems to be quickly aggregated for analysis.

The enhanced coordination, now known as the National Animal Health Laboratory Network (NAHLN) began with five pilot diagnostic laboratories in 2003, has proven successful, and now incorporates more than 50 laboratories in the United States. The same concept could be considered to enable surveillance and disease control response to transboundary diseases on a regional basis and even on a broader international level for analyzing transmission and adaptation of disease agents. An approach to achieve these benefits is proposed.

Keywords: informatics, surveillance, Laboratory Information Management Systems (LIMS), NAHLN.

Introduction

Concern about the ability of the United States to effectively identify and quickly control a large scale outbreak of a foreign animal disease increased after the events of September 11. The US quickly responded to the new public health threats and created a comprehensive public health response network coordinated through the Centers for Disease Control and Prevention but a similar effort was needed for the animal health sector. The Bioterrorism Act of 2002 provided the basis for funding that effort. In addition, the October 2002 outbreak of Exotic Newcastle Disease Virus in California and the resulting numbers of samples which had to be quickly tested and reported, underscored that increased cooperation between State level animal health diagnostic laboratories and the USDA APHIS National Veterinary Services laboratory could facilitate the diagnostic testing necessary during disease outbreaks.

Even though advances in diagnostic methods such as real time reverse transcriptase-polymerase chain reaction (RRT-PCR) allowed for much faster processing of the samples collected during the surveillance and control phases of the outbreak, delays occurred when reporting and analyzing the results due to the time required for entry and transmission of the information associated with the collected samples. In addition to the standardization in laboratory diagnostic protocols needed to assure consistency in the test results obtained by multiple laboratories when testing samples collected from a specific outbreak, it was hoped that standardization in the associated epidemiologic information would be key to decreasing the amount of time needed for reporting of the results of individual sample tests and overall analysis of the status of the outbreak.

However, a lack of standardization existed. It was recognized that electronic reporting procedures were not synchronized or standardized across the nation, nor was there single federal information system or process in place to consolidate information and to enable the analysis of data collected during an emergency outbreak. Finally and probably of most impact on the timely reporting of diagnostic information, there was significant variation in information management capabilities and technologies in use by the state and university veterinary diagnostic laboratories expected to be members of the NAHLN. It would have been costly and disruptive to the on-going responsibilities of participating laboratories to mandate a single laboratory information management system (LIMs), instead another approach was needed.

Methods

The solution decided on built on the existing NAHLN concept of agreed upon validated standard operating protocols for diagnostic methods and extended that concept to the information and format through which information was to be exchanged between the participating laboratories. Three key standards were chosen to support the transfer of a consistent set of information relating to the origin and type of sample collected, the type of diagnostic tests requested from the participating laboratory, and the results of the diagnostic testing performed.

The three international standards chosen as the basis for consistency in data transferred were already used extensively in the electronic transfer of public health data but had not been used collectively on a broad basis for the transfer of animal health information. The three standards were: **S**ystematized **No**menclature of **Med**icine-**C**linical **T**erms (SNOMED) for establishing consistency in epidemiological data; **L**ogical **O**bservation **I**dentifiers **N**ames and **C**odes (LOINC®) for standardization in identifiers and diagnostic results; and Health Level 7 (HL7) as a standardized template for formatting the electronic messages containing the SNOMED, and LOINC terminology. The adaptation of

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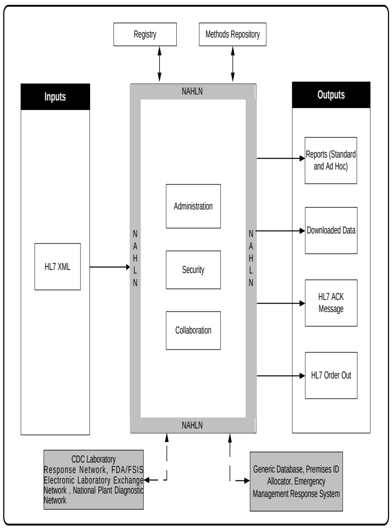
[1] USDA, APHIS Veterinary Services- Centers for Epidemiology and Animal Health, Ft. Collins, CO USA - steve.weber@aphis.usda.gov

these standards and this approach allowed the participating NAHLN diagnostic laboratories to retain their current LIMS systems by developing mapping routines between the standardized information required and the data fields contained in their current database. The data mapping routines accommodated incoming electronic messages containing sample information (order messages) and outgoing electronic messages containing the subsequent results from the diagnostic testing (result messages).

The ability to process information quickly was further enhanced through the use of handheld computers to record data in the field at the time the sample was collected and to electronically transmit that information to the testing laboratory (order message) while the sample was brought or mailed to the laboratory. A central database was developed to accept the diagnostic results (result message) facilitating the reporting of information and permitting the ability to subsequently analyze standardized current and retrospective outbreak results. Thus the objectives of the desired reporting system could be achieved.

Figure 1: A schematic of the NAHLN IT System



Result

Although the scope of the National Animal Health Laboratory Network was anticipated to include many diagnostic laboratories in the United States, a pilot project involving only five laboratories was initiated to test the concept in 2003. Within a year, the standardized terminology, messages, and database had been developed and piloted, proving that the approach was sound and the desired objectives could be achieved without requiring the participating laboratories to adapt to one specific laboratory information management system. Since the initial pilot, over 50 diagnostic laboratories are now participating in the NAHLN utilizing multiple LIMs and reporting standardized and consistent surveillance information and diagnostic test results for several animal diseases.

Discussion

Just as it was not considered practical to require multiple diagnostic laboratories in the United States to utilize a specific laboratory information system to process samples and quickly report results while attaining the consistency in information needed for successful implementation of the National Animal Health Laboratory Network, it would be far less feasible to necessitate a single approach for multiple laboratories in many countries involving several languages. However, the approach that has been described could be utilized on a regional or even worldwide basis to achieve even far greater results.

Imagine a consistent set of standardized international animal disease surveillance data which could be effectively analyzed to demonstrate trends in epidemiologic factors associated with the transmission of diseases of concern; identify potential changes in disease expression based on spatial considerations; and the ability to modify laboratory diagnostic test parameters to increase sensitivity or specificity as a result of significant numbers of standardized test results. Imagine the capability of examining the occurrence of transboundary diseases in adjacent countries and based on that analysis of consistent information an increased possibility to develop effective disease control programs. Imagine the ability of adjacent countries to assist with increased laboratory capacity when large outbreaks of disease occur, and to quickly report the results of the tests to the affected country.

These benefits and more could be achieved through the implementation of a similar approach for specific animal diseases on an international basis.