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Dr. Villa earned his undergraduate degree in electrical engineering at the University of Baja California. He was awarded Master in Computer Science from the Center of Scientific Research and Higher Education of Ensenada, and he obtained his Phd in Bioinformatics from George Mason University. He has been a research scientist at the Engineering Institute of the University of Baja California since 2002. From his more relevant work: he participated in the International Bovine HapMap Consortium, characterizing the genetic structure of the *Bos Taurus* and *Bos Indicus* evolutions of Cattle, and generating a Haplotype Map of the Cattle Genome. The results of his research have been published in major journals as Science and BMC Genetics. In 2009 he receives the award “Outstanding Research in Bioinformatics” given by the College of Science of the George Mason University. Nowadays, Dr. Villa is collaborating with the Functional Genomics Laboratory of the USDA in Maryland, developing computational algorithms for the analysis of information of the Last Generation DNA Sequencers, and the analysis of High Density Genotype data from the Bovine Genome. He is the responsible researcher of the “Iniciativa Mexico 2010” for the implementation of Genomic Selection in Dairy Cattle from The State of Baja California. And he is coordinating the work for the creation of the first Mexican Bioinformatics Resource Center for Biodefense.

In 2011 Dr. Villa joined to the USA-Mexico One Border One Health consortium, as co-chair of the informatics workgroup. This consortium is working in the design and implementation of the first operational prototype for disease surveillance and response using One Health paradigms in the U.S./Mexico border. Dr. Villa and collaborators are developing a web-based Hybrid Geographic Information System which uses mathematical models to simulate how pathogens could spread in the border region and permits to visualize contingencies for different scenarios including information from past events such as pandemic H1N1 and other emerging and reemerging pathogens affecting surrounding areas of the USA-Mexico frontier.

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PROGRESS ON A ONE BORDER ONE HEALTH BINATIONAL, MULTI-SECTORAL, COLLABORATIVE SYSTEM

for Simulating the Spread of Pathogens at the USA – Mexico frontier

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Abstract

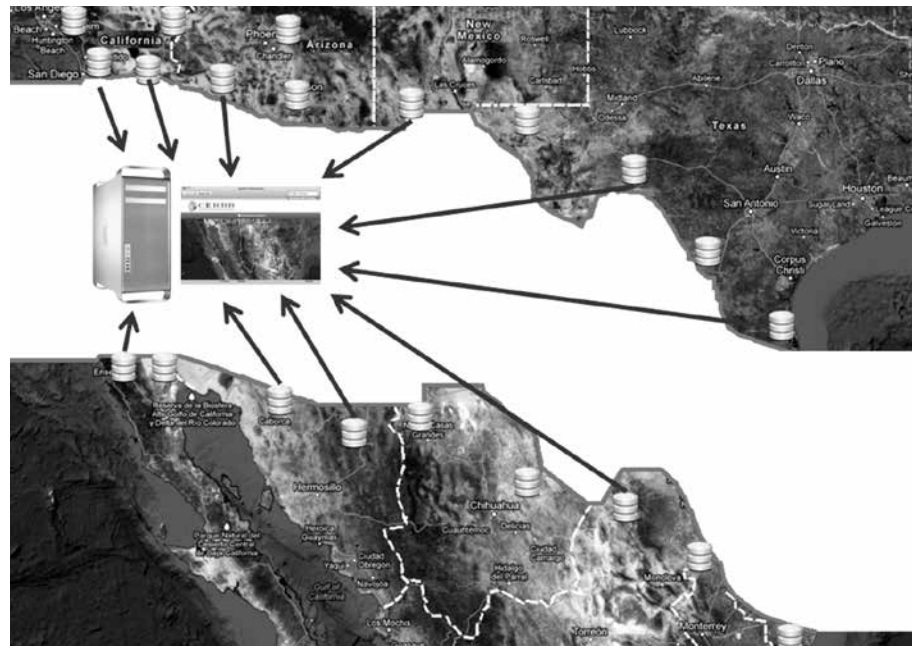
One Border One Health (OBOH) is a binational, multisectoral initiative to build more resilient and healthy border communities by creating sustainable solutions to health risks at the human – animal – environmental interface along the California/ Mexico border. The coalition consists of over 50 institutions – >30 from the USA and >20 from Mexico – from government, military, public, private and academic sectors. Created in 2011 OBOH has organized into three committees - Surveillance, Informatics, and Training & Outreach – that are cooperating to design and implement the first operational prototype for disease surveillance and response using One Health paradigms. In this background paper, we present the progress in the development of a bioinformatics collaborative system for administering and doing research on multi-sectoral-relational databases to be fed and shared by the coalition. This web-based Hybrid Geographic Information System uses mathematical models to simulate how pathogens could spread in the border region and will assist in the design of binational strategies for controlling the spread of infection. The model input includes environmental, ecological, biological, socioeconomic, and

demographic factors and is validated by data from historical disease outbreaks in the region. This is the first model of its kind to be used at the U.S./Mexico border. It models an area with large disparities between health systems, cultures, languages, socioeconomics, politics, animal management strategies, industries and ecosystems. The versatility of the system will permit us to visualize contingencies for different scenarios including information from past events such as pandemic H1N1 and other emerging and reemerging pathogens affecting surrounding areas of the USA – Mexico frontier.

Background

Mexico and USA are two countries with large disparities: both have evolved within a very different culture, language and kind of government. However, both have evolved sharing the same problems in their frontier. The risk of emerging and reemerging pathogens affecting population in both sides of the frontier is latent. While the Mexican population is vaccinated at early age for some pathogens (e.g. Tuberculosis), the USA population is vaccinated for others (e.g. Diphtheria). However,

Figure 1. A Web-based Geographic Information System Server will administer connectivity of databases from ten states along the Mexico-USA frontier.



both populations are in jeopardy for different pathogens, in addition to those against which none of the population is protected. In recent years, emerging and reemerging infections have proliferated due to yet undiscovered reasons. In 2009 the H1N1 pandemic outbreak and an eruption of Rickettsia caused infection and deaths of many people in both sides of the Mexico-USA frontier [1-3]. These events uncovered our vulnerability in biodefense aspects, and helped us to establish as maximum priority to do research for designing operations to increment national security. OBOH is an initiative of collaboration for protecting, through surveillance, the surrounding areas of the Mexico-USA border line, adopting a One Health paradigm [4]. OBOH joins more than 50 institutions from both countries and is organized by three committees- surveillance, informatics, and training -that are cooperating to design and implement the first operational prototype

for disease surveillance and response using One Health paradigm. This prototype input includes environmental, ecological, biological, socioeconomic, and demographic factors and is designed to be validated by data from historical disease outbreaks in the region. This is the first model of its kind to be used at the U.S./Mexico border. It models an area with large disparities between health systems, cultures, languages, socioeconomics, politics, animal management strategies, industries and ecosystems. In the following sections we present a description of the system.

General concept

The system is being designed for hosting a set of relational multisectoral databases distributed all along both sides of the Mexico-USA frontier.

These databases belong to the members of OBOH. A Web-based Geographic Information System Server (WGISS) will administer connectivity for information access and sharing. The collaborative participation of members is achieved through targeted designation of specific information regarding the sector. The Web server for example, which is administered by academics, permits all members, through a personalized password, to access accounts for feeding, uploading, and running simulation of pathogens of interest. This web-based GIS uses mathematical models to simulate how pathogens could spread in the border region and will assist in the design of binational strategies for controlling the spread of infection.

The system will allow access from the general public with restricted capabilities and is designed to offer, besides the capabilities for OBOH members, a platform for notification and overcome the general confusion of who to contact regarding unusual infectious diseases in humans, companion animals (pets) and livestock animals. The first prototype is being implemented in two states (California from USA and Baja California from Mexico), but, as shown in figure 1, the main goal is to interconnect databases from four USA frontier states- California, Arizona, New Mexico, and Texas – and six Mexico-frontier states - Baja California, Sonora, Chihuahua, Coahuila, Nuevo Leon, and Tamaulipas.

Simulation platform

The simulation platform input includes environmental, ecological, biological, socioeconomic, and demographic variables and is validated by data from historical disease outbreaks in the region. The state health departments from

both countries are allowed to upload information of public health and clinical status. Information regarding socioeconomic, geographic, and demographic is provided by government dependencies of statistics and geography. Transportation information is provided by urban planning and transportation departments, and pathogens information is provided by health and vector departments. Each member of the consortium will have access to the system under a password and is able to upload information for running specific simulations restricting access to her/his results as a convenience. Academic institutions do research in the data, generate epidemic models and update information needed to run simulations.

Figure 2 shows the simulation platform. Information is fed by members and the system administrator. Given the pathogen of interest, an epidemic model is selected for computing infected, susceptible, recovered, deaths, and immune people, through time. An interaction network model in conjunction with demographic information is used to estimate the affected area. As part of the Web-based GIS system, a projection will be done in Google maps for selecting the city and the number of initial cases, along with the projection of the affected area.

Overall strategy

In its current version, the system is executed on the web-based GIS, integrating tools from Google maps V3, different layers of information provided by the Mexican Institute of Geography and Statistics (INEGI) [5], and three different epidemic models capable of implementing

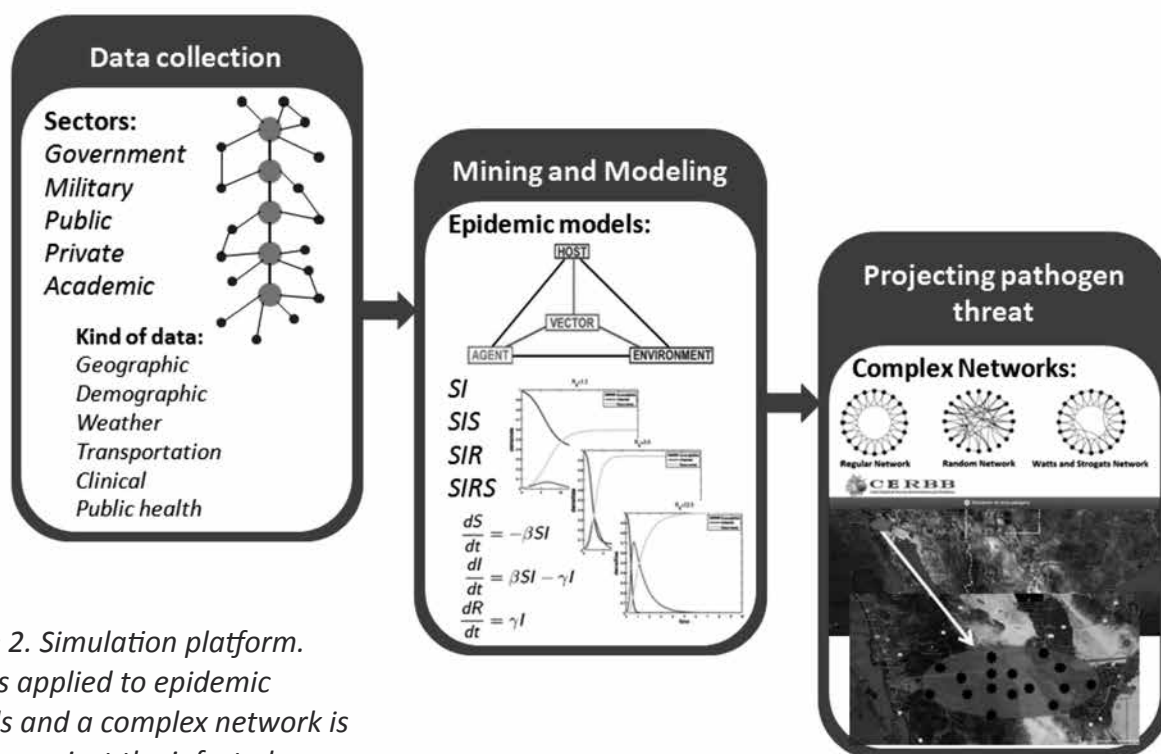
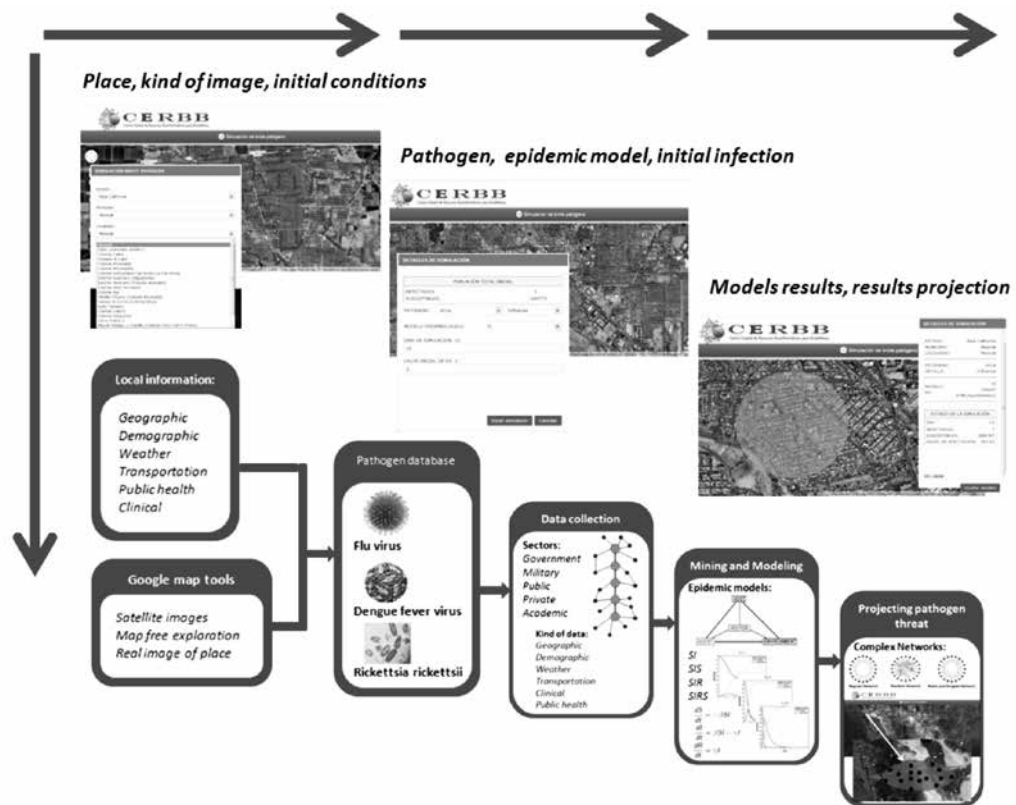


Figure 2. Simulation platform. Data is applied to epidemic models and a complex network is used to project the infected area.

vector-borne diseases. It can simulate the spread of pathogens all across the state of Baja California, Mexico. It is in process the inclusion of the state of California, USA. After this first stage is running and being used by the consortium, the next step is to gradually include the rest of states. As shown in Figure 3, a simulation starts with the selection of the place in which the infection would be simulated, along with the kind of Google maps image, and initial conditions of the place. Then, the pathogen is selected from a list which includes H1N1, Rickettsia, and Dengue. After this, the simulation is executed and the epidemic models along with an interaction network provides the number of people infected, recovered, and susceptible, and how they are distributed in the region around the initial infection.

Preliminary conclusion

This is the first model of its kind to be used at the U.S./Mexico border. The versatility of the system will permit us to visualize contingencies for different scenarios including information from past events such as pandemic H1N1 and other emerging and reemerging pathogens affecting surrounding areas of the USA – Mexico frontier. Integration of web-based tools, information systems and mathematical modeling helps to reconcile disparities between health systems, cultures, languages, socioeconomics, politics, animal management strategies and ecosystems, and design strategies for controlling the spread of infection in surrounding areas of the USA-Mexico frontier.



One Health strategies for combating zoonoses effectively requires interdisciplinary collaborative models for prevention and control of infectious disease epidemics, as well as chronic illnesses. Physicians, veterinarians, ecologists, environmental scientists, laboratory animal specialists, and other health science-related disciplines are getting involved in this work, equally without regard to “turf” barriers. We aim to accelerate the rate of change in surveillance, research, prevention, and control measures for cross-species infections like influenza and dangerous bacteria emerging from antibiotic resistance, with the design and implementation of this kind of collaborative models in which experts can share, access, and manage information from both sides of the USA-Mexico Frontier.

Figure 3. A Web-based GIS integrates all resources necessary for executing complete simulations, and provide a projection for results in a Google map based form.

^[1] Mexican Health Department. Official site. <http://portal.salud.gob.mx/contenidos/noticias/influenza/estadisticas.html>

^[2] Epidemic Department. Mexican Health Department, ‘Rickettsia en Baja California’. <http://www.dgepi.salud.gob.mx/boletin/2010/sem6/pdf/edit0610.pdf>

^[3] Centers for Disease control and Prevention. ‘2009 H1N1 Early Outbreak and Disease Characteristics’. <http://www.cdc.gov/h1n1flu/surveillanceqa.htm>

^[4] One Border One Health. Official site. <http://www.oneborderonehealth.com/>

^[5] National Institute of Statistics and Geography. Official site. <http://www.inegi.org.mx/>

ROLE OF SENTINEL SURVEILLANCE

in the Detection of Emerging Infectious Diseases
at the Human-Animal Interface, Nigeria

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BACKGROUND

Climate change and global warming has altered the process and outcome of infectious diseases worldwide. This alteration in the environment and increase in urban agriculture in response to population growth cause intensification of livestock farms in confine feeding operations (CAFO) thereby contributing to emerging diseases at the animal-human interface. This is both an economic and public health risk to the society. However early detection and control of these emerging diseases hinged on effective surveillance system is important for sustainable development. Unfortunately disease surveillance is poorly organized in developing countries of Africa.

OBJECTIVE

Despite present challenges with the spread of infectious diseases in developing countries especially, there are no effective and sustainable

national surveillance for early detection of emerging diseases at the human- animal interface in Nigeria. It in this presentation, I outline how adoption of sentinel surveillance had served effectively in the detection of emerging infectious diseases of both economic and public health importance at the human-animal interface in Nigeria.

MAIN MESSAGE AND LESSON LEARNED

Swine farming is one of the fastest growing sources of meat protein in the world today with 40% of the world meat protein consumption derived from pork and pork products and millions of metric tons traded across international borders. Nigeria accounts for about 30% of pig production in Africa and pig farms are widely spread in the country with higher concentrations in the Southern and Central agro-ecological regions, providing meat protein for Africa's most populous nation. The industry has witnessed gradual growth over the years with the promotion of peri urban intensive farm estates but

not without a number of challenges that ranges from diseases, nutrition to reproductive losses.

The recent pandemic of influenza A/H1N1 said to originate from swine is a cause for concern in the pig industry because pigs play significant role in the epidemiology of swine influenza and the emergence of pandemic virus. Constant monitoring of emerging virus among the animals and in persons occupationally exposed provides data for better public health policy.

Sentinel surveillance was designed and implemented in an intensive urban piggery production operation with over 5000 human concentration and 1 million pigs in a single site for over 24 months. Clinical specimens were collected from case presentation of swine influenza and human exposure. This was transported on ice to the laboratory for virus detection and isolation. Data on biosecurity practices were also collected with structured questionnaires and analyzed.

It was observed that the biosecurity practice in farm is far below acceptable standard. This obviously would encourage easy circulation and spread of swine influenza intra and inter species. Analyzed specimen confirms the circulation of human strain of swine influenza virus in pigs which may have been contracted from the farmers.

ADVANCEMENT OVER PREVIOUS SYSTEM

Previous national surveillance in livestock is bedeviled by weak veterinary infrastructure, poor capacity and political will. This surveillance

expended less resources, ensure close monitoring and took advantage of the peculiarity of the operation system.

This to my knowledge is one of the first effective surveillance at the human-animal interface in Nigeria where both animals and animal handlers were taken into consideration.

PRACTICAL RECOMENDTION

Epidemiology surveillance programme in developing countries should in addition to National surveillance be designed as focus groups of sentinel surveillance that would address unique terrain, culture, farm operation, diseases and population groups and observed over a period of time which is more effective in the detection of emerging infectious diseases.

The observation that human can readily be infected by viruses circulating in animals and vice versa, requires that diseases control measures such as biosecurity and vaccination should be targeted at this occupationally exposed group.

JOINT LIVESTOCK, Wildlife and Public Health Investigation of Q fever in Chiang Mai, Thailand

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BACKGROUND

Q fever, a zoonosis caused by *Coxiella burnetii*. In animal, the majority of cases, abortions occur at the end of gestation without specific clinical signs until abortion is imminent. But in human, the acute disease appears like a flu-like infection, usually self-limiting illness accompanied by myalgia and severe headache. Complications, such as pneumonia or hepatitis, may also occur. Endocarditis in patients suffering from valvulopathy, as well as premature delivery or abortion in pregnant women, is the main severe manifestations of the chronic evolution of the disease. [1]

Q fever in Thailand is an emerging disease. There were nine clinical cases in a prospective study in patients with acute febrile illness who were admitted to four hospitals in northeastern Thailand were reported in 2003. [2] In 2011, a study in Khon Kaen focusing on zoonotic causes of endocarditis in humans identified four confirmed cases of Q fever endocarditis. All case-patients had a history of contact with farm animals such as dairy and beef cattle. [3] Little information exists on the

incidence and prevalence of Q fever in animals. A serological survey in 1967 in Thailand showed seroprevalence of *Coxiella burnetii* of 28.1% in dogs, and seroprevalence in goats, sheep, and cattle varied from 2.3% to 6.1%. [4]

The One Health concept, the collaborative effort of multiple disciplines to attain optimal health for people, animals and the environment [5] is adapted in this study.

MATERIALS AND METHODS

Based on the strategic framework of the One Health concept, its achievement involves the strengthening of animal, public health and environment surveillance. (Figure 1) Sharing information between each surveillance system is practical for response, prevention and preparedness system at the provincial level.

The public health authorities are including Chiang Mai Public Health Office, District Public Health Offices, Sub-district Health Promotion Hospitals

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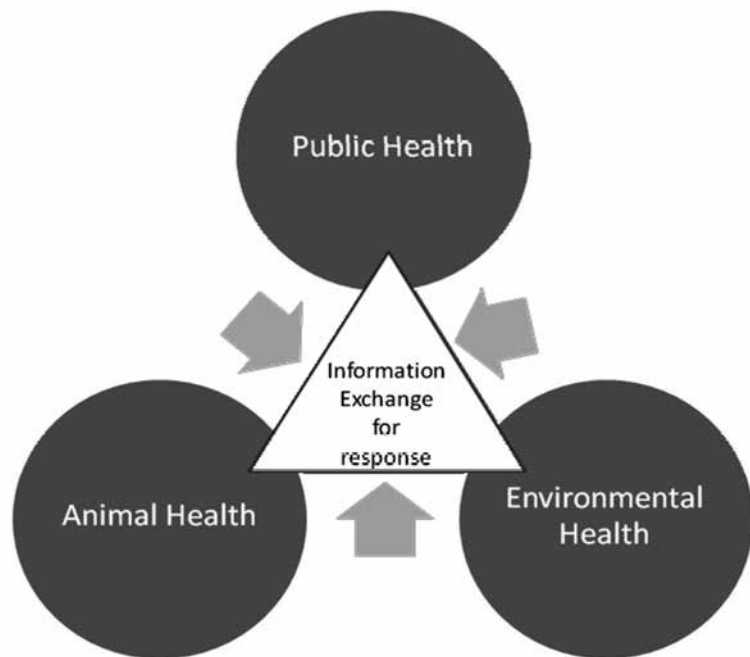
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Figure 1: The animal, public health and environment surveillance with sharing information for response



and National Institute of Health. The animal health authorities are including Chiang Mai Livestock Office, The Fifth Regional Livestock Office and National Institute of Animal Health. Chiang Mai Zoo and Chiang Mai Night Safari are representatives for environmental health.

The joint surveillance and investigation of Q fever was conducted to develop network of animal health and public health surveillance and response at provincial level.

RESULTS

A joint investigation of Q fever by livestock, wildlife and public health authorities aimed to determine the prevalence and risk factors of Q fever in animals and animal care takers in Chiang Mai, Thailand.

The One Health team was established at first in Chiang Mai provincial level. (Figure 2) The team is comprised with human and animal health, zoologist, epidemiologist and laboratorian as well as other professionals, would be charged with joint surveillance for Q fever and disease response.

The Q fever surveillance and investigation were set up. Blood samples from 271 dairy cows, 61 deer, 1 camel and 1 Indian bison were collected at two Chiang Mai zoos, Chiang Mai Zoo and Chiang Mai Night Safari, and ten dairy farms in April 2012. Three cow placenta and three buffalo placenta were also sampled from the fresh market in Chiang Mai during the same period. (Figure 3) Animal sera were tested for antibodies against *Coxiella burnetii* by ELISA at the National Institute of Animal Health.

Figure 2:
One Health Team



Of the animals tested, 22/334 (6.59%) had antibodies to *C. burnetii*: 22/271 (8.12%) in dairy cows. There is no antibody positive against *Coxiella burnetii* in zoo animal and cow placentas and buffalo placentas.

The response for Q fever in dairy farmer has been monitored. The blood samples will be collected after any symptom related to Q fever. Joint investigation will be conducted by the One Health team in order to prevent and control the disease.



Figure 3: Placentas collection from the fresh market in Chiang Mai

DISCUSSION

The results of these animal surveys will be used in conjunction with the results of the ongoing zoonotic endocarditis study in Khon Kaen to develop and implement effective surveillance models for Q fever in humans and animals. This model of joint investigation can also be applied to other zoonotic diseases to strengthen collaboration among livestock, wildlife and public health officers working in the same area. Human laboratory test result will be reported once they are confirmed.

1. Rodolakis A. Q fever, state of art: epidemiology, diagnosis and prophylaxis. *Small Ruminant Res* 2006 Mar; 62(1) 121–4.
2. Suputtamongkol Y, Rolain JM, Losuwanaruk K, Niwatayakul K, Suttinont C, Chierakul W, et al. Q fever in Thailand. *Emerg Infect Dis* 2003 Sep;9(9):1186-7.
3. Pachirat O, Fournier PE, Pussadhamma B, Taksinachanekij S, Lulitanond V, Baggett HC, et al. The first reported cases of Q fever endocarditis in Thailand. *Infect Dis Rep* 2012;4:e7.
4. Sankasuwan V, Pongpradit P, Bodhidatta P. *Seato Medical Research Study on Rickettsial Diseases in Thailand*.1967:449-04
5. The American Veterinary Medical Association. One Health Initiative Task Force. "One Health: A New Professional Imperative" [online]. 2008 [cited 2012 July 15]. Available from https://www.avma.org/KB/Resources/Reports/Documents/onehealth_final.pdf.