PROCINORTE

Animal Health Task Force Workshop Report

"Rapid Efficient Response to High Consequence Animal Diseases"
December 1 - 3, 2015
NH Hotel, Mexico City, Mexico

Submitted July 14, 2016, to the PROCINORTE Board of Directors

Animal Health Task Force
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Contents

Executive Summary

Representatives from Mexico, Canada, and the United States met in Mexico City December 1-3, 2015. The objectives of the workshop were to review and exchange information on priority diseases that impact animal agriculture, with particular emphasis on rapid and efficient response to high consequence animal diseases. The workshop started with a brief overview of PROCINORTE, including the objectives of the Animal Health Task Force (AHTF). This was followed by three scientific sessions on swine viral diseases, avian viral diseases, and other emerging animal diseases of concern in North America. The workshop concluded with proposals by the workshop participants on potential areas of collaborations that could be implemented to address the issues and research priorities presented during the scientific sessions.

Overview of PROCINORTE and the Animal Health Task Force

PROCINORTE is an important mechanism to facilitate the institutional and technical integration of the Unites States, Canada, and Mexico under the umbrella of the Inter-American Institute for Cooperation on Agriculture's (IICA) Northern Regional Center. PROCINORTE is a cooperative program in research and technology with four task forces (Animal Health, Plant Health, Tropical and Sub-Tropical Fruits & Genetic Resources) that determine common research priorities. Setting work priorities is a major task, because they are strategically important to guarantee the allocation and effective use of national and international resource availability, and they also are important in developing effective collaboration efforts to take advantages of the opportunities of multinational research, especially in those research fields where there is a need to optimize research resources, avoid duplication of efforts, and optimize the use of facilities, and equipment and to facilitate a broad environmental validation of results. PROCINORTE objectives are to:

1. Promote dialogue to identify priority research issues common to the three countries and to influence the regional, hemispheric and global agendas.
2. Facilitate the exchange of experiences, information and training through the building of linkages among public and private country institutions of the Northern region (PROCINORTE) and between the major research and technology transfer actors in the region, hemisphere and the world.
3. Facilitate the collaboration among the countries to solve problems of mutual interest.

Potential mutual benefits from collaborations include:

a) Perform strategic research for agricultural development.
b) Development of technologies for agribusiness benefit.
c) Strengthen technological exchange.
d) Development and use of methodologies for the establishment of standard norms for common use in commodities trade.
e) Provide solutions to common problems and challenges to help the countries to cover their present population needs more efficiently.
f) Develop scientific solutions to agricultural problems, to increase profitability for farmers preserving their land and natural resources.

The PROCINORTE Animal Health Task Force (PAHTF) is comprised of leading government scientists from the three member countries. The PAHTF meets face-to-face at least once a year by holding scientific workshops on animal diseases deemed to be priorities for North America. The primary goal of these workshop is to determine the disease situation and available countermeasures to control and respond to animal diseases that impact agriculture in the three member countries. The ultimate goal of the workshops is to provide scientists the opportunity to get to know each other and establish research collaborations that will advance research to enhance animal health in the three member countries.

The PAHTF identified the following criteria for prioritizing areas of research:

1. Diseases that impact the movement of animals between Canada, U.S, and Mexico.
2. Diseases that have significant economic and/or public health impact.
3. Diseases that are national priorities for either Canada, U.S, or Mexico.
4. Diseases that are endemic in one or two of the three countries where the disease free-country will benefit from the expertise of the endemic country, including the ability to work directly with a foreign animal pathogen, expert scientists, and pathogen-dedicated facilities.
5. Areas of expertise in one country may complement expertise in another country enhancing the formation of multi-disciplinary research teams.
6. Opportunities to enhance the impact of limited financial resources.
7. Opportunities to develop control measures such as diagnostics and vaccines that can be applied within the three countries, resulting in uniform diagnostic tools and control measures.
8. Opportunities to bank and share samples for diagnostic validation and future research.

The expected results from the activities of the PAHTF include:

1. Sharing of research activities and potential changes in high consequence animal disease control program policies, procedures and techniques.
2. Coordination of research activities to promote collaborations between the US, Canada and México.
3. Development of an understanding of measures used in the US, Canada and México for the control and eradication of high consequence animal diseases and harmonization (where appropriate) of policies and procedures.

Swine Viral Diseases

Presentations from the member countries were provided for the following priority swine viral diseases.

Porcine Epidemic Diarrhea Virus (PEDV)

United States
In April 2013, porcine epidemic diarrhea virus (PEDV) was detected for the first time in the United States and within months it spread throughout all major swine producing regions of the US. The virus caused severe diarrhea in young piglets leading to high mortality. Within the first year of the epidemic about 50% of the sows in the US became infected resulting in a 7-8% loss in total pig

production. During the second year the incidence of new cases declined dramatically raising hope this new disease would fade away and current control strategies might be adequate. Concurrent with the PEDV outbreak in the US was the emergence of porcine deltacoronavirus, another novel swine enteric virus. Fortunately, this virus has not had the impact that PEDV has, but the industry is still cautious. The unexplained emergence of this and other swine viruses in the US demonstrates the constant need for disease surveillance and a better understanding of the epidemiology of transboundary diseases.

Mexico
Swine producers and veterinarians first reported July 2013 clinical cases characterized by the presence of diarrhea, consistent with clinical signs suggestive of infection by PEDV. The official diagnosis was recorded on May 22, 2014; however, the phylogeny of the virus present in Mexico has not been analyzed to define the origin of the infection. Accordingly, studies were initiated with the objective of developing molecular diagnostics to enable the rapid and accurate detection of PEDV. The molecular characterization of PEDV was achieved through the partial sequencing of gene S and phylogenic analysis to identify the origin of PEDV in in Mexico. The sequencing results confirmed the presence of PEDV in test samples and determined that the most related viruses strains were in the United States and Korea.

Ebola Virus (EBOV)

Canada
The Foreign Animal Disease Diagnostic Laboratory on Plum Island in the United States isolated EBOV-Reston from pig samples collected during an outbreak of PRRSV in Philippines in 2008. The identity of the virus was confirmed by CDC, Atlanta, USA. Subsequent sero-survey in farm workers indicated that there was transmission of the virus to humans. Although EBOV does not caused disease in humans, this raised concern by WHO and FAO about pursuing intensification of swine production in Africa in regions endemic to EBOV species Zaire, Sudan and Bundibugyo - all three with case/fatality rate in humans of 40 - 90%.

Public Health Agency of Canada (PHAC) and CFIA conducted series of collaborative experiments to investigate susceptibility of swine to EBOV-Zaire (ZEBOV). These experiments determined that pigs are susceptible to infection with ZEBOV, will replicate the virus to relatively high titers in the respiratory tract contributing to shedding of infectious virus by an airborne route. Considering anticipated difficulties with licensing and production of veterinary vaccine for EBOV, it was suggested that interferon biotherapeutics (offering temporary partial protection) should be investigated as a tool to assist with depopulation in outbreak control (to allow more time required for the depopulation).

Vesicular Stomatitis Virus (VSV)

United States
Vesicular Stomatitis Virus (VSV) remains as an important animal pathogen, causing outbreaks in the Southwestern US and Mexico as recently as 2015. In cattle and swine, its clinical signs are indistinguishable from foot-and-mouth disease (FMD), a devastating transboundary disease of

livestock. Additionally, VSV is the most common vesicular disease reported in livestock in the Americas, particularly now that FMD is almost eradicated from this South American. VSV strains causing outbreaks in the southwestern US are closely related to certain viral lineages circulating in enzootic areas of Mexico. The means of transmission and introduction into the US remain unclear. Host, vector, viral and ecological factors influencing clinical presentation and transmission are poorly understood. Further research on the natural mechanisms of virus maintenance and transmission is necessary not only to establish effective control programs but also help with its approval as vector for vaccines and cancer therapy. Since VS is a common problem that affects Mexico and the US (and can potentially spread to Canada) it is important to take research approaches in both countries to better understand the problem and find potential solutions.

Porcine Reproductive and Respiratory Syndrome Virus (PRRSV)

Mexico
Studies conducted in Mexico were implemented to determine the infection frequency and genetic variability of porcine reproductive and respiratory syndrome virus (PRRSV) in farms with suggestive clinical data located in seven states of the Mexican Republic. To determine genetic variability primers amplifying 809 bp from ORF5-ORF6 were used. To differentiate between American and European strains, two sets of primers that separately amplify 337 bp and 241 bp from ORF7 were employed. Puebla, Veracruz, Mexico, Guanajuato, Michoacan, Queretaro, and Jalisco States had PRRSV seropositive farms with 45-100% frequencies, and 20-98% of positive animals. Phylogenetic analysis showed high variability for PRRSV, and co-existence of genetically different isolates within herds. Differential RT-PCR detected only American strains.

Avian Viral Diseases

Presentations from all three member countries were provided for avian influenza.

Avian Influenza

United States
Beginning in December 2014, Canada and the United States have experienced an unpreceded outbreak of H5 Gs/GD-lineage HPAI as the first intercontinental spread of a Eurasian HPAI virus (HPAIV) to North America. Initially, a reassortant H5N2 clade 2.3.4.4 HPAI virus appeared in British Columbia, Canada, and within a few days the original Eurasian H5N8 and the reassortant H5N2 HPAIV appeared in a wild duck and gyrfalcon in Washington state, respectively, Subsequently these H5 HPAIV spread through the Pacific Flyway and to the Midwest USA. Molecular analysis indicated that the infected premises (backyard and commercial) in Western and initial premises in Midwestern USA were point source introductions from wild birds, while most cases in the Midwest had secondary spread from common sources. In total, the H5 HPAIV outbreaks has affected 21 states, with detections in 4 captive wild birds, 75 wild birds, 21 backyard flocks and 211 commercial flocks, totaling over 48 million birds. In the USA, the eradication effort cost more than $1 billion and the negative economic impact was over $3.2 billion. Experimental

studies in chickens, turkeys, pheasants, guinea fowl, partridges, and Japanese quail indicated quail were the most susceptible poultry species to infection and death, followed by other minor poultry species.

Canada

Canadian surveillance of Avian Influenza in wild waterfowl started in 2005 as a response to a highly pathogenic H7N3 outbreak in BC poultry in 2004, which caused large economic losses as well the emergence of Eurasian highly pathogenic H5 in Asia starting in 1997 causing mortality in wild waterfowl and the possibility of intercontinental spread lead to continuation of yearly wild bird surveillance. The purpose of the national surveillance was to make an inventory of Influenza A viruses occurring in Canadian wild birds; sufficiently characterize Influenza A viruses so that it will be possible to associate future outbreaks with viruses circulating in wild birds; monitor Canadian wild bird populations for the presence of particular Influenza A viruses; establish an archive of Influenza A virus strains from Canadian wild birds to permit rapid retrospective analysis in response to diseases outbreaks and to build and maintain an integrated, multi-agency field, laboratory, regulatory and communications capacity to carry out Influenza A virus sampling, identification, and molecular characterization. In December of 2014, HPAI caused by novel reassortant H5N2 virus was detected in commercial turkey and chicken farms in Fraser Valley, British Columbia (BC) and in February 2015, HPAI caused by novel reassortant H5N1 virus was identified in backyard chicken layer flock. Progenitor EA H5N8 and novel reassortant H5N1 viruses were also isolated from wild birds at the same time in the same area. An Eurasian H5N8 virus was also isolated from frozen hunter killed duck tissues and was the progenitor for the H5N2 and H5N1 outbreaks. Both viruses were pathogenic to juvenile Muscovy ducks and adult Chinese geese and the disease was able to transmit to naïve contact ducks and geese and cause mortality

Mexico

HPAI was detected in June 2012 in the Highlands of Jalisco, affecting 22.4 million breeding and commercial laying birds, also impacting Aguascalientes, Guanajuato, Puebla among others on a smaller scale states; contra epidemics measures and strategies to prevent, mitigate, control and eradicate the outbreak were implemented. The main actions against epidemics were: sanitary situation diagnosis and regionalization, foci inactivation with final implementation of quarantine at production units and their immediate depopulation; sanitary disposal of carcasses; strengthening epidemiological surveillance in backyard poultry, birds of fighting, endemic and migratory wild birds; strengthening biosafety procedures, verification of cleaning, washing and disinfection activities of farms; verification for thermal treatment of excreta, increased movement controls and preventive vaccination. An inactivated vaccine was developed from an avian influenza Low Pathogenicity strain isolated of a duck in Cienega de Lerma, State of Mexico, in 2006, making a first batch 10 million doses in the first month to date we have applied more than one billion doses. This strategy contributed to avoid the spread of the virus to more states, as observed in other affected countries. Currently, Mexico is working on lines of research to evaluate the protection conferred by avian influenza H7N3 vaccine, to demonstrate the vaccine antibodies have the ability to neutralize virus field, establishing their physicochemical characteristics and immunogenicity, perform sequencing studies to find possible mutations and antigenic changes.

Other Emerging Diseases

Presentations from the member countries were provided for the following emerging or re-emerging diseases of concern.

Emerging Pestiviruses

United States
When the pestivirus genus was first recognized it was thought to be composed of 3 species, bovine viral diarrhea virus (BVDV), border disease virus of sheep (BDV and hog cholera virus (later renamed classical swine fever virus or CSFV). Viruses were segregated into these three "classic" species based on host of origin. This segregation proved unsatisfactory as each of the three recognized species could replicate in multiple hosts. Subsequently this genus has expanded with BVDV being divided into two different species, BVDV1 and BVDV2, and the addition of 5 putative species (Giraffe, Bungowannah, Pronghorn, HoBi-like viruses and atypical porcine pestivirus). It has become evident that clinical presentations associated with classic pestiviruses, such as BVDV1 and BVDV2, can also be caused by pestiviruses genetically and antigenically distinct from classic pestiviruses such as HoBi-like viruses. Regardless of species designation the hallmark of pestivirus infections are immune suppression and the ability to cross the placenta and cause congenital defects including persistent infections. It now appears that the disease presentations collectively known as bovine viral diarrhea (which includes reproductive, enteric and respiratory disease) can be caused by three different species of pestivirus, BVDV1, BVDV2 and HoBi-like viruses. Further testing needs to be completed to determine the bovine pestivirus status for U.S., Canadian and Mexican cattle herds.

Bovine Papillomavirus

Mexico
Papillomas occur more commonly in animals, especially in cattle compared with other domestic animals. The causal agent of bovine papillomatosis is a virus that belongs to *Papillomaviridae* family. In Tamaulipas México, the virus is considered a serious problem that has caused economic losses by impeding the exportation or cattle to the US. In Mexico, the information about papilloma viral subtypes that infect cattle is limited. Recent studies showed that 52.6% of cattle were positive for BPV-1 and 47.4% for BPV-2.

Trichinella

Canada.
Trichinella is an intracellular nematode parasite of muscles of mammals, birds and reptiles. Transmission occurs by the ingestion of infected meat of wild or domestic animals that are predators or scavengers. The genus comprises of 12 species or genotypes and all can infect humans by the ingestion of raw or inadequately cooked meat. The domestic pig is the primary food animal that can serve as a reservoir host and a source of infection for consumers, rodents and other animals. However, only few species of *Trichinella* are capable of establishing infection in pigs, the primary risk in North America being *Trichinella spiralis*. Although *Trichinella* infection is included in the

OIE list of diseases for multi-species animals, clinical disease occurs only in humans. Nevertheless, there is a need for effective on-farm control programs as well as post-slaughter measures.

Potential Research Collaborations

Vesicular Stomatitis Virus

Vesicular stomatitis virus is a disease of livestock which causes severe vesiculation and ulceration in infected animals. The disease, which is transmitted by insect bite, has an important impact on the economy due to direct losses that it causes in infected herds and the imposition of quarantine restrictions that affect animal trade. The United States is regularly affected by VSV incursions, which originate from enzootic areas in southern Mexico. This research project seeks to generate knowledge on the ecological and epidemiological factors associated with VSV risk and to conduct epidemiological and molecular characterization of the strains causing epidemics to contribute to the surveillance systems in both USA and Mexico.

Specific objectives include:

1. Identify VSV lineages that are prevalent in Southern Mexico that are most likely to cause epidemics in Northern Mexico and USA using molecular information
2. Identify the genetic lineages of VSV circulating in endemic and non-endemic regions of Mexico.
3. Determine the patial and temporal distribution of VSV outbreaks in Mexico.
4. Improve diagnostic tests for the detection of VSV RNA and VSV serum antibodies in field samples.

Ebola Virus in Swine

Ebola virus (EBOV; family *Filoviridae*) are zoonotic viruses infecting both humans and swine, with often fatal outcome in the humans. Transmission of EBOV from swine to humans was documented for Ebola-Reston virus in Philippines. An introduction of this virus into a swine population in North America would be difficult to detect immediately, as this virus does not cause severe and/or typical disease in swine. The likelihood of its wide spread prior to its detection, very likely through human cases, is very high. The outbreak control by depopulation (assumed; note – this would be a CFIA or USDA program decision) would represent enormous logistical difficulties due to the nature of human infection, and require time to execute.

EBOV infects porcine immune cells and causes downregulation of IFN-alpha and as a consequence delays in the immune responses, allowing for its initial replication in the porcine host, and shedding of the virus via respiratory tract. The amount of the airborne virus is sufficient to infect other pigs and very importantly also humans. Consequently, a swine vaccine able to abolish virus shedding is of veterinary and human health interest.

The Special Pathogens Unit (SPU), Canadian Food Inspection Agency has tested so far three vaccine candidates for swine (Weingartl et al., 2006; unpublished). All require a several weeks to reach protective antibody levels.
ARS at USDA has developed a biotherapeutic strategy to control FMD. Inoculation of swine with an adenovirus vector expressing interferon (IFN), Ad5-IFN-alpha can offer protection against disease as soon as 1 day post administration and lasting for approximately 5 days (Moraes 2003, Dias et al., 2012). Moreover it has been demonstrated that administration of Ad5-IFNalpha has an adjuvant effect when used in combination with an Ad5-FMD vaccine (de Avila Botton 2006).

The hypothesis to be tested is that the administration of vectors expressing IFN will offer almost immediate protection against EBOV, and abolish or significantly reduce initial virus shedding. This would permit better and safer outbreak control.

The specific objective of the research is to determine protective effect of the vectored interferon administration prior to the inoculation with Ebola-Zaire virus.

Next Steps

The PAHTF agreed to explore the possibility of funding the proposed research collaborations on VSV and EBOV and to review progress made at the next PROCINORTE workshop.

Appendix I

Participants

MEXICO:

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Appendix II

Agenda

PROCINORTE Animal Health Task Force Workshop

"**Rapid Efficient Response to High Consequence Animal Diseases**"

(December 1 - 3, 2015; NH Hotel, Mexico City, Mexico,

Tuesday, Dec. 1

Participants arrive to Mexico City airport. Taxi/Van transfers from International airport to NH Hotel.

Wednesday, Dec. 2

Introductions and Overview of previous PROCINORTE´s AHTF workshops

9:00 Introductions and Welcome (Dr. Fernando Flores Lui, General Director, INIFAP)

9:15 **Introduction to PROCINORTE** (Dr. Audia Barnett, Executive Secretary of PROCINORTE, IICA Representative in Canada)

9:30 **Overview of previous PROCINORTE's AHTF workshop including Action Items and Objectives / Purpose for PROCINORTE´s AHTF Workshop 2015** (Dr. José López, National Manager, Animal Health Research & Partnerships, Canadian Food Inspection Agency) .

10:00 **Break**

Swine Viral Diseases Session -

(Ricardo Flores, CENID-Microbiology, INIFAP, and Cyril Gay, ARS-USDA to Lead Discussion)

10:30 **"Update on Swine Enteric Coronaviruses in United States".** Kelly Lager, National Animal Disease Center (NADC), ARS, Ames, Iowa,

11:00 **"Epidemiological surveillance of Porcine Epidemic Diarrhea virus in Mexico".** Luis Gabriel Figueroa Martinez, Dirección de Epidemiología y Análisis de Riesgo (DEAR), DGSA, SENASICA.

11:30 **"Molecular characterization and pathogenesis of porcine epidemic diarrhea virus in the Mexican Bajio region".** José Francisco Rivera Benítez, CENID-Microbiología, INIFAP.

12:00 **"Epidemiological surveillance of porcine reproductive and respiratory syndrome (PRRS) in Mexico".** Assad Heneidi Zeckua, Coordinator, Technical Certifying Committee on Epidemiology, CONCERVET.

12:30 **"Epidemiology of porcine reproductive and respiratory syndrome virus in several states of the Mexican republic".** Fernando Diosdado Vargas, CENID-Microbiología, INIFAP.

13:00 – 14:45 **Lunch**

Swine Viral Diseases Session – *(Continuued)*

15:00 "**Ebola Virus in pigs**" - Hana Weingartl, National Centre for Foreign Animal Disease, Winnipeg.

15:30 **"Eradication of classical swine fever and Aujeszky's disease in México".** Julio García Ángeles, Mexican-American Commission for Foot and Mouth Disease eradication (CPA), SENASICA.

16:00 **"Epidemiology of VSV in the United States".** Luis Rodriguez, Plum Island Animal Disease Center. Orient Point, ARS, New York.

16:30 "**User-friendly technologies for the rapid detection and typing of high consequence viruses**" Oliver Lung, CFIA Lethbridge Laboratory.

17:00 **"The U.S diagnostic program for foreign animal diseases."** Mike Mackintosh, Foreign Animal Disease Diagnostic Laboratory (FADDL), APHIS, Plum Island Animal Disease Center. Orient Point, New York.

17:30 **Summary of key points.** Ricardo Flores and Cyril Gay

18:00 **Adjourn**

Thursday, Dec. 3

Avian Viral Diseases Session *(Ricardo Flores, CENID-Microbiology, INIFAP, and José López,* AHR&P, CFIA *to Lead Discussion)*

9:00 **"Presence of low pathogenicity avian influenza virus (H5N2) in wildlife".** Elizabeth Loza Rubio, CENID-Microbiología, INIFAP.

9:30 "**Avian Influenza Virus in Wildlife**". Shawn Babiuk, National Centre for Foreign Animal Disease, Winnipeg.

10:00 **"Diagnostics and vaccines for control of highly pathogenic avian influenza virus"**. David Suarez, Southeast Poultry Research Laboratory, ARS, Athens, Georgia.

10:30 **"Current situation of highly pathogenic avian influenza, subtype H7N3, in Mexico".** Julio García Ángeles, Mexican-American Commission for Foot and Mouth Disease eradication (CPA), SENASICA.

11:00 **BREAK**

11:30 "**Disinfection and Decontamination of Premises, Vehicles and Supplies During and After an Outbreak**". Jiewen Guan, Ottawa Animal Health Laboratory.

12:00 **"New animal health legislation for avian influenza in México".** Karla Delgado Rodríguez, DGSA, SENASICA.

Other Emerging Diseases Session

12:30 **"Emerging pestiviruses: Surveillance and impact".** Julia Ridpath, National Animal Disease Center (NADC), ARS, Ames, Iowa.

13:00 **"Detection and phylogenetic analysis of bovine papillomavirus in cutaneous warts in cattle of Mexico"**. Edith Rojas Anaya, CENID-Microbiología, INIFAP, Mexico City, Mexico.

13:30 "**Outbreaks of *Trichinella* Infection in Food Animals: A priority for Public Health and Animal Health**" - Dr. Alvin Gajadhar, Centre for Food-Borne & Animal Parasitology, Saskatoon.

14:00 – 15:45 **Lunch**

General discussion and Wrap-up (Organizers to Lead Discussion)

APPENDIX III

Abstracts

Abstracts - Mexico

"New animal health legislation for avian influenza in México"

Due to the health, economic, social, commercial and political implications that Avian Influenza (AI) involves, SENASICA need to implement the following animal health measures:

Zooning: SENASICA will recognize and determine two zoosanitary status for AI: 1) Low prevalence 2) Free zone, for this zone a preventive and temporal vaccine program will be allowed prior a risk analysis and the authorization of SENASICA.

Recognition of compartments free of IA: for the recognition and maintenance of compartments the sampling required is the next:

Zootechnical function	Sample	Specifications	Resampling
Breeder Layer	60[1]	Preferably 2 to 3 weeks before the laying onset or at the beginning of it	Every 4 months
Broiler	60[1]	Up to 3 weeks before its release to market	Each lot that enter
Fighting birds Other domestic birds	60[2]	Any age	Every 4 months
Programas sociales	60[1]	Any age before thir movilization	Every 4 months

The compartment will be cessated in case that a positive test of hemagglutination inhibition is detected and the compartment will be cancelled if a viral isolation and sequencing is confirmed.

Diagnose: The official diagnosis tests for AI will be: hemagglutination inhibition, virus isolation in embryonated chicken and IVPI.

Mobilization: For mobilization of goods and live birds, farmers can use a Mobilization zoosanitary certificate or an announcement of mobilization.

Vaccination: Vaccination will be allowed in areas of low prevalence (vaccines emulsified, vectored and recombinant) in breeders, layers, broiler and turkey. For free zones that apply the vaccine preventively only
vaccines vectored, recombinant and new technology vaccines may be used (breeder and layers). The farms that vaccine should have sentinel birds.

Implementation of contra epidemic measures: Includes the implementation of quarantine, depopulation, disposal of carcasses and avian products and byproducts, sanitary fallow, vaccination, sentinels, repopulation, epidemiological investigation, cleaning, washing and disinfection, inactivation of organic and inorganic wastes, specific epidemiological surveillance in the affected premise or under risk and control of mobilizations.

Biosecurity and good farming practices: All farms must have programs for the training of workers, prohibit entry to outsiders, a perimeter fence, a binnacle for the income people, drive through disinfection bath and spray pump, a program for the control of wild birds and vermin, warehouses for equipment, food, biological and pharmaceutical, the source of water should not be contaminated, the incineration, sanitary burial or composting mortality, mobilize manure in a covered vehicle or bagged and cleaning and disinfection programs.

Implementation of distance between production units and other premises: The distance between any poultry farm to a SPF or breeders farms is from 10 km; between broiler, layers, turkey farms, hatcheries and feed mills are 5 km and from plants that process or sift manure to any other farm are 15 km.

Epidemiologic surveillance: Active and passive surveillance.

All this work should be done between the Federation, the municipal and state governments, for the prevention of spread control and eradication of the AI virus. That is the reason why SENASICA is in the process of updating the legislation for IA.

CENTRO NACIONAL DE INVESTIGACIÓN DISCIPLINARIA EN MICROBIOLOGÍA ANIMAL
INSTITUTO NACIONAL DE INVESTIGACIONES FORESTALES, AGRICOLA Y PECUARIAS
PROCINORTE Animal Health Task Force Workshop
December 1-3, 2015;
Abstract

Molecular characterization and pathogenesis of porcine epidemic diarrhea virus in the Mexican Bajio region

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Porcine epidemic diarrhea (DEP) is a highly contagious viral infectious disease of pigs. In the United States of North America the epidemic diarrhea virus swine (VDEP) was identified at the end of April 2013, bearing an identity nucleotide of 99.5 % with the AH2012 strain that caused problems in China. In Mexico, at the beginning of July 2013, producers and veterinarians dedicated to swine clinic reported clinical cases characterized with the presence of diarrhea, consistent with clinical signs suggestive of infection by the VDEP. The official diagnosis was recorded on May 22, 2014, however, the phylogeny of the virus present in Mexico, has not been analyzed to define, in a preliminary way, the origin of the infection. The objectives of this study were: to implement the molecular diagnosis for a fast and accurately detection of the VDEP; the partial sequencing of the gene S and to analyze the phylogeny to identify the origin of the VDEP present in Mexico. Samples of small intestine, large intestine and fecal material from piglets with acute diarrhea, suggestive to the VDEP pictures, from full-cycle farms were analyzed. The RT-PCR technique was used for the detection of the VDEP using a pair of oligonucleotides that amplify a fragment of 503 pb of the S of the VDEP gene. The VDEP amplification products were purified with the kit (Wizard SV Gel and PCR Clean-Up System) and sequenced. The sequence analysis was conducted with the Blast and Mega 5 program. A total of 13 samples were analyzed and the presence of the VDEP was detected in 11 of them. The analysis of the sequences revealed an 99 % homology with the strain USAColorado2013 of the United States, also identified three partial sequences belonging to genotype 2a (virulent classic), however in a sample (Fig. 2) important variations were detected. The sequences were recorded in GenBank with the following access numbers: KJ906601, KJ906602, and KJ906603. One of the samples identified with differences in the sequence was amplified by RT-PCR in real time for the detection of variant strains. Once identified as Strain INDEL, the experimental infection in lactating piglets carried out, the results of this process permitted to reproduce the clinical picture reported for the virulent strains. The sequencing results confirmed the presence of the VDEP in the samples, determining that most related viruses are strains of United States and strains Korean, the study of the pathogenesis determined that the circulating strain with insertions and deletions maintains a high virulence

Epidemiology of porcine reproductive and respiratory syndrome virus in several states of the Mexican Republic

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The aim of this study was to determine infection frequency and genetic variability of porcine reproductive and respiratory syndrome virus (PRRSV) in farms with suggestive clinical data located in seven states of the Mexican Republic. Sixty two farms were visited to collect blood and tissue samples, on a convenience transversal approach, from animals slaughtered for decreased weight gain. Specific serum antibodies were measured by ELISA. Viruses were isolated from macerated tissues filtered and applied onto MARC-145 cells, or detected by RT-PCR using specific primers to amplify 300 bp from the viral ORF7. To determine genetic variability primers amplifying 809 bp from ORF5-ORF6 were used. To differentiate between American and European strains, two sets of primers that separately amplify 337 bp and 241 bp from ORF7 were employed. Puebla, Veracruz, Mexico, Guanajuato, Michoacan, Queretaro, and Jalisco States had PRRSV seropositive farms with 45-100% frequencies, and 20-98% of positive animals. In positive farms PRRSV was detected by RT-PCR in at least a tissue sample. Phylogenetic analysis showed high variability for PRRSV, and co-existence of genetically different isolates within herds. Differential RT-PCR detected only American strains. PRRSV was isolated in three from seven sampled states. We conclude that PRRSV frequency in Mexican farms is similar to those reported for previous years, and PRRSV Mexican isolated have great variability.

Detection and phylogenetic analysis of bovine papillomavirus in cutaneous warts in cattle of Tamaulipas, Mexico

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ABSTRACT

Papillomas occur more commonly in animals, especially in cattle compared with other domestic animals. The causal agent of bovine papillomatosis is a virus that belongs to *Papillomaviridae* family. In Tamaulipas México, the virus is considered a serious problem that has caused economic losses by impeding the exportation or cattle to the US. In Mexico, the information about papilloma viral subtypes that infect cattle is limited. The aim of this study was to determine the subtype of bovine papillomavirus of cattle in Tamaulipas Mexico. A total of 52 wart samples were analyzed by PCR using bovine papillomavirus (BPV) primers able to differentiate BPV 1-2 subtypes, and subsequent sequencing. Sequencing quality was determined using MEGA 6.0. Similarity analysis was performed with BLAST programs to assess the identity with known BPV types. The results showed 52.6% were BPV-1 and 47.4% BPV-2. The distribution of both subtypes was homogenous in cattle. This study demonstrates the presence of BPVs in Tamaulipas cattle. BPVs 1 and 2 were the most frequent viral types . These data suggests that several BPV types are circulating in cattle in Mexico.

SITUATION OF AVIAN INFLUENZA TYPE A H7N3 IN MEXICO

It was detected in June 2012 in the Highlands of Jalisco, affecting 22.4 million breeding and commercial laying birds, also impacting Aguascalientes, Guanajuato, Puebla among others on a smaller scale states; contra epidemics measures and strategies to prevent, mitigate, control and eradicate the outbreak were implemented.
The National Emergency Animal Health (DINESA) was activated as part of strategy, under the terms of article 78 of Animal Health Federal Law, to perform field operations needed to address the contingency.

The main actions against epidemics were: sanitary situation diagnosis and regionalization, foci inactivation with final implementation of quarantine at production units and their immediate depopulation; sanitary disposal of carcasses; strengthening epidemiological surveillance in backyard poultry, birds of fighting, endemic and migratory wild birds; strengthening biosafety procedures, verification of cleaning, washing and disinfection activities of farms; verification for thermal treatment of excreta, increased movement controls and preventive vaccination.
Every episode of avian influenza in any country, has many variables that make it unique, Mexico made an efficient monitoring and control of mobilization, boosting actions in record time to develop a vaccine that confers good immunity, allowing contain the spread of the virus.
This inactivated vaccine was developed from an avian influenza Low Pathogenicity strain isolated of a duck in Cienega de Lerma, State of Mexico, in 2006, making a first batch 10 million doses in the first month to date we have applied more than one billion doses. This strategy contributed to avoid the spread of the virus to more states, as observed in other affected countries; if we had opted for massive depopulation of farms, we would have affected the national supply greatly and economic losses have been considerable.

Currently they are working on lines of research to evaluate the protection conferred by avian influenza H7N3 vaccine, to demonstrate the vaccine antibodies have the ability to neutralize virus field, establishing their physicochemical characteristics and immunogenicity, perform sequencing studies to find possible mutations and antigenic changes.

The sanitary work in collaboration with producers has been successful, at the time we have a pretty significant reduction in virus quarantined farms and we note they have extended winter periods in which it has been a progressive decrease in number of cases brought. It continues with a strict surveillance field to identify potential reservoirs of viral circulation, in order to remove them and have less risk of infections sources.

The national objective pursued is to achieve its eradication; collaboration among poultry farmers, authorities, private and official veterinarians, is the best option to address this and other diseases. SENASICA has implemented a series of agreements and programs to promote the modernization and competitiveness of the poultry industry at national and regional level:

1. BINATIONAL AGREEMENT MEX-USA
Establish a framework for technical and scientific reference that promotes operational cooperation and information exchange.

2.- MEMORANDUM OF UNDERSTANDING OF POULTRY HEALTH
Protect poultry health in region and address commercial situations with technical-scientific basis and participation of producers' associations in the three countries.

3.- NATIONAL PROGRAM OF HEALTH AND POULTRY PRODUCTION
Set objectives, strategies and action lines for a new modern health policy and production in industry to improve their health status and competitiveness.

4.- AGREEMENT OF DISTANCES BETWEEN POULTRY PRODUCTION UNITS
Foster the relocation and re-engineering of poultry industry for benefit of good production practices and biosafety.

5.- AGREEMENT OF NOTIFIABLE AVIAN INFLUENZA
Update of plans and control programs for avian influenza under efficient legal, regulatory and operational framework.

Abstracts - Canada

Outbreaks of *Trichinella* infection in food animals: A priority for public health and animal health

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Trichinella is an intracellular nematode parasite of muscles of mammals, birds and reptiles.

Transmission occurs by the ingestion of infected meat of wild or domestic animals which are predators or scavengers. The genus comprises of 12 species or genotypes and all can infect humans by the ingestion of raw or inadequately cooked meat. The domestic pig is the primary food animal which can serve as a reservoir host and a source of infection for consumers, rodents and other animals. However, only few species of *Trichinella* are capable of establishing infection in pigs, the primary risk in North America being *Trichinella spiralis*. Although *Trichinella* infection is included in the OIE list of diseases for multi-species animals, clinical disease occurs only in humans. Nevertheless, there is a need for effective on-farm control programs as well as post-slaughter measures. Recent international regulations and scientific guidelines for establishing national control programs including testing practices have been developed collaboratively by the World Organization for Animal Health (OIE), Food and Agriculture Organization (FAO), World Health Organization (WHO), Codex Committee on Food Hygiene (CCFH), and International Commission on Trichinellosis (ICT). These guidelines are complementary for use in developing a comprehensive program to help mitigate risks from animal production to food consumption. Recommendations include the establishment and maintenance of controlled housing negligible risk compartments, testing requirements, and knowledge of the occurrence of *Trichinella* species and genotypes in all susceptible food animals and wildlife. The need for communication and coordination of control strategies between Veterinary Authorities and Public Health agencies are emphasized. The recent guidelines are intended to provide science-based standards to facilitate international trade in pork, food safety and public health confidence. This presentation provides background information on *Trichinella* from perspectives of both animal control and public health control, examples of disease outbreaks, and discusses the gaps in knowledge to address recent international regulations and opportunities for research collaboration.

User-friendly technologies for detection and typing of high consequence viruses

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Current diagnostic tests for detection and subtyping of high consequence livestock and poultry viruses are inefficient in many ways. For example, most diagnostic tests are for detection of a single virus, the tests must be performed in centralized laboratories by highly trained staff, and further testing is required to obtain subtype information. Furthermore, molecular tests used for nucleic acid detection typically require multiple manual handling steps and pieces of instrumentation. Two types of novel technology platforms that can simplify the diagnostic workflow for detection and subtyping of veterinary pathogens will be presented. 1. Development of fully automated assays that does not require user intervention after sample introduction for a) detection and simultaneous H or N-typing of avian influenza viruses, b) simultaneous detection of FMDV, SVDV, VSV, CSFV and ASFV, as well as other multi-pathogen assays for detection of bacterial and viral pathogens will be discussed. 2. Examples of user-friendly, insulated isothermal PCR (iiPCR) assays performed on simple, compact , field-deployable instrument that automatically displays “+” or “-“ results without user interpretation within an hour using either extracted nucleic acid or low volume of neat clinical material will also be described.

Disinfection and Decontamination of Premises, Vehicles and Supplies During and After an Outbreak

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Animal disease outbreaks often occurred at cold seasons and it is important to study decontamination at freezing temperatures for controlling disease spread. Commercial disinfectants including Accel, Virkon, bleach and surface disinfection foam (SDF), and antifreeze agents including propylene glycol (PG), methanol (MeOH) and calcium chloride ($CaCl_2$), were evaluated at a laboratory setting using quantitative carrier tests for inactivating of *Geobacillus stearothermophilus* spores, infectious bursal disease virus (IBDV), Newcastle disease virus (NDV) and avian influenza virus (AIV) under light and heavy organic challenges. At -20 ºC, bleach, Virkon and SDF supplemented with PG caused less than a 2.0 $\log_{10}$ reduction of spores under both organic challenges with 24 h contact time. With NDV, at -10 ºC the three disinfectants under both organic challenges achieved a 5-$\log_{10}$ reduction within 5 minutes. Results with SDF were similar at -25 ºC and -10 ºC. To achieve comparable reduction with Virkon and bleach at -25 ºC, contact periods up to 2 or 24 h, respectively, were required. With IBDV, to achieve a 5-$\log_{10}$ reduction by treatment with Virkon or SDF at -20 ºC, contact periods of 2 h or 24 h, respectively, were required under both organic challenges. With AIV, Virkon and Accel supplemented with PG, MeOH or $CaCl_2$ inactivated 6 $\log_{10}$ AIV within 5 min at -20 ºC. PG and MeOH alone did not kill AIV, but the $CaCl_2$ solution alone inactivated 5 $\log_{10}$ AIV within 10 min. Four field trials were conducted to evaluate processes for decontamination of vehicles. Results indicated that thorough cleaning and washing to remove organic matters prior to disinfection was significantly important for effective decontamination in the field. Findings indicated that effective decontamination at cold temperatures would require efforts in reducing organic challenges and extending disinfection contact time.

In addition, we evaluated the effect of absolute humidity (AH), a combined factor of temperature and relative humidity (RH), on inactivation of an H9N2 and an H6N2 AIVs on porous and non-porous surfaces, based on the time required to obtain a $\log_{10}$ reduction of virus (D-value). At AH of 5.2 g/m^3 (23ºC & 25% RH), both viruses survived up to 14 days on the porous surface and for at least 28 days on the non-porous surfaces. The corresponding D-values for H9N2 and H6N2 were 1.49 and 6.90 days on the porous surface and 7.81 and 12.5 days on the non-porous surfaces, respectively. In comparison, at AH of 9.9 g/m^3 (35ºC & 25% RH) or 11.3 g/m^3 (23ºC & 55% RH), the D-values for H9N2 and H6N2 dropped to $\leq$ 0.76 day on the porous surface and to $\leq$ 1.81 days on the non-porous surfaces. As the AH continued to rise from 11.3 to 36.0 g/m^3, the D-value for both viruses decreased further. The relationship between D-value and AH followed a form of $y = ax^{-b}$ for both viruses. The D-values for H9N2 virus were significantly lower ($P < 0.05$) than those for H6N2 virus. The findings give evidence that increasing the AH in poultry buildings following an outbreak of disease could greatly reduce the length of time required for their decontamination.

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Ebola virus (EBOV) in pigs

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FADDL, Plum Island, USA isolated EBOV-Reston from pig samples collected during an outbreak of PRRSV in Philippines in 2008. The identity of the virus was confirmed by CDC, Atlanta, USA. Subsequent sero-survey in farm workers indicated that there was transmission of the virus to humans. (Fortunately EBOV-Reston does not cause disease in humans.) This raised a concern by WHO and FAO about pursuing intensification of swine production in Africa in regions endemic to EBOV species Zaire, Sudan and Bundibugyo - all three with case/fatality rate in humans of 40 - 90%.

Public Health Agency of Canada (PHAC) and CFIA conducted series of collaborative experiments to investigate susceptibility of swine to EBOV-Zaire (ZEBOV). We have determined that pigs are susceptible to infection with ZEBOV, will replicate the virus to relatively high titers in the respiratory tract contributing to shedding of infectious virus by an airborne route. While older piglets developed severe respiratory distress, younger piglets had mild or no clinical signs, while shedding the virus and transmitting ZEBOV to co-housed contact piglets, and very importantly to non-human primates without direct contact.

As a response to the ZEBOV outbreak in West Africa in 2014-2015, and the potential role of pigs in transmission of ZEBOV, SPU CFIA developed a diagnostic capability for detection of EBOV infection in swine. Assays for virus detection include: virus isolation, RT-PCR (importantly in oral and nasal samples), and immunohistochemistry in tissues. Antibody detection assay comprise: microtiter PRNT (in 4-5 days using immunostaining) and indirect ELISA (NP antibodies) with confirmation by PRNT and/or immunoblot.

Considering anticipated difficulties with licensing and production of veterinary vaccine for EBOV, interferon platform (offering temporary partial protection) should be investigated as a tool to assist with depopulation in outbreak control (to allow more time required for the depopulation).

Avian influenza in Wild Birds

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Waterfowl are the natural reservoir of all influenza A viruses. Virus representatives of all 16 hemagglutinin (HA) and all 9 neuraminidase (NA) subtypes have been isolated from waterfowl. Influenza A viruses in aquatic birds have been in a state of evolutionary equilibrium. Canadian surveillance of AI in wild waterfowl started in 2005 as a response to a highly pathogenic H7N3 outbreak in BC poultry in 2004 which caused large economic losses as well the emergence of Eurasian highly pathogenic H5 in Asia starting in 1997 causing mortality in wild waterfowl and the possibility of intercontinental spread lead to continuation of yearly wild bird surveillance. The purpose of the national surveillance was to make an inventory of Influenza A viruses occurring in Canadian wild birds; sufficiently characterize Influenza A viruses so that it will be possible to associate future outbreaks with viruses circulating in wild birds; monitor Canadian wild bird populations for the presence of particular Influenza A viruses eg. Eurasian H5N1; establish an archive of Influenza A virus strains from Canadian wild birds to permit rapid retrospective analysis in response to diseases outbreaks and to build and maintain an integrated, multi-agency field, laboratory, regulatory and communications capacity to carry out Influenza A virus sampling, identification, and molecular characterization. The majority of HA and NA subtypes were identified with the exception of HA14 and HA15. In December of 2014 HPAI caused by novel reassortant H5N2 virus was detected in commercial turkey and chicken farms in Fraser Valley, British Columbia (BC) and in February 2015, HPAI caused by novel reassortant H5N1 virus was identified in backyard chicken layer flock. Progenitor EA H5N8 and novel reassortant H5N1 viruses were also isolated from wild birds at the same time in the same area. An Eurasian H5N8 virus was isolated from frozen hunter killed duck tissues and was the progenitor for the H5N2 and H5N1 outbreaks. We performed risk assessment of the novel reassortant H5N2 and H5N1 viruses in different animal models. Both viruses were pathogenic to juvenile Muscovy ducks and adult Chinese geese and the disease was able to transmit to naïve contact ducks and geese and cause mortality.

Abstracts – United States

Tools for rapid detection of foreign and emerging animal diseases
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The FADDL serves to protect American agriculture through diagnosis of foreign animal diseases with a focus on high-consequence diseases of livestock. Though investigations to rule-out vesicular diseases such as foot-and-mouth disease (FMD) and surveillance for classical swine fever (CSF) are central to the mission, the FADDL has the capacity to diagnose a broad list of economically important diseases of ruminant livestock and wildlife. The FADDL further serves as a World Organization of Animal Health (OIE) and United Nations Food-and-Agriculture Organization (FAO) reference laboratory for FMD and as and as a foreign animal disease reference laboratory to the National Animal Health Laboratory Network (NAHLN), a large network of state veterinary diagnostic laboratories throughout the US. Integrated within the FADDL, is the North American FMD Vaccine Bank that is maintained in collaboration with Mexico and Canada as a stockpile of inactivated FMD virus (FMDV) antigens to be used for formulation of FMD vaccine should an outbreak occur. As viral diseases of livestock emerge, re-emerge and evolve the FADDL develops and improves reagents and diagnostic tools to ensure a rapid response to disease outbreaks. Development and validation of disease detection tools, development of new reagents, and training veterinary service practitioners and diagnosticians form the foundation of the FADDL's research and capacity building projects. Safe defective bacteriophage displaying molecular signatures of foreign animal disease viruses have been developed and are now routinely used by the FADDL to support PCR-based testing in other laboratories within the NAHLN or outside the US. Projects to develop panviral microarrays and next-generation sequencing have further enabled the detection and characterization of viruses associated with emerging or complex animal disease investigations. Still other projects are aimed at developing tools and experience to address recent trends such as the use of rope collected swine oral fluids as a herd sample, multiplexing of disease detection tests to streamline investigations, or development of new tests to address more frequent occurrences of certain FMD look-a-like diseases, including bluetongue and epizootic hemorrhagic disease (peaking in 2014), bovine popular stomatitis (peaking in 2013 and 2014), vesicular stomatitis in cattle and senecavirus associated disease in pigs (both peaking in 2015). Among such projects are the developments of a multiplex realtime RT-PCR as a herd test for rapid detection of CSF, FMD and African swine fever from rope collected swine oral fluids and a portable microfluidics PCR platform for differential detection of FMDV and bovine popular stomatitis virus at the penside. It is hoped that inter-American partnerships might be leveraged with some of these existing initiatives to enhance the development and sharing of new tools and strategies to detect and counter foreign and emerging animal diseases.

Epidemiology of Vesicular Stomatitis Virus in North America : A Re-Emergent Arbovirus
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Vesicular Stomatitis (VS) is a viral disease of horses, cattle and swine caused by an arthropod-borne virus (VSV) of the family Rhabodviridae, genus *vesiculovirus*. Laboratory strains of are among the best studied RNA viruses and modified VSV strains are being utilized as viral vectors for vaccines and cancer treatment. However, VSV remains as an important animal pathogen, causing outbreaks in the Southwestern US and Mexico as recently as 2015. In cattle and swine, its clinical signs are indistinguishable from foot-and-mouth disease (FMD), a devastating transboundary disease of livestock. Additionally, VS is the most common vesicular disease reported in livestock in the Americas, particularly now that FMD is almost eradicated from this South American. VSV strains causing outbreaks in the southwestern US are closely related to certain viral lineages circulating in enzootic areas of Mexico. The means of transmission and introduction into the US remain unclear. Host, vector, viral and ecological factors influencing clinical presentation and transmission are poorly understood. Further research on the natural mechanisms of virus maintenance and transmission is necessary not only to establish effective control programs but also help with its approval as vector for vaccines and cancer therapy. Since VS is a common problem that affects Mexico and the US (and can potentially spread to Canada) it is important to take research approaches in both countries to better understand the problem and find potential solutions.
Research questions:
How do new lineages of VSV emerge?
What mechanisms mediate expansion beyond endemic focus?
What determines epidemic transmission?
Where does virus overwinter?
Why lineages become extinct?
Can we predict epidemics?
Can we mitigate the impact of VS epidemics?

Emerging pestiviruses

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When the pestivirus genus was first recognized it was thought to be composed of 3 species, bovine viral diarrhea virus (BVDV), border disease virus of sheep (BDV and hog cholera virus (later renamed classical swine fever virus or CSFV). Viruses were segregated into these three "classic" species based on host of origin. This segregation proved unsatisfactory as each of the three recognized species could replicate in multiple hosts. Subsequently this genus has expanded with BVDV being divided into two different species, BVDV1 and BVDV2, and the addition of 5 putative species (Giraffe, Bungowannah, Pronghorn, HoBi-like viruses and atypical porcine pestivirus). This genus expansion has occurred for the following reasons. It was recognized that clinical presentations, not historically associated with pestivirus infections, such as porcine myocarditis syndrome in pigs (Bungowannah virus), porcine congenital tremors (atypical porcine pestivirus) and hemorrhagic syndrome in cattle (some strains of BVDV2) were caused by pestiviruses that were genetically and antigenically distinct from classic pestiviruses. In addition, it has become evident that clinical presentations associated with classic pestiviruses, such as BVDV1 and BVDV2, can also be caused by pestiviruses genetically and antigenically distinct from classic pestiviruses such as HoBi-like viruses.

Regardless of species designation the hallmark of pestivirus infections are immune suppression and the ability to cross the placenta and cause congenital defects including persistent infections. Further, while pestiviruses are economically significant pathogens worldwide, different geographic regions have different mixes of pestivirus species. The success of regional pestivirus control programs rests in correctly identifying the pestiviruses present in the region and designing vaccines and diagnostic based on those pestiviruses. As a case in point, it now appears that the disease presentations collectively known as bovine viral diarrhea (which includes reproductive, enteric and respiratory disease) can be caused by three different species of pestivirus, BVDV1, BVDV2 and HoBi-like viruses. BVDV1 is the most widespread of the three species and can be found in every continent but Antarctica. HoBi-like viruses are the most geographically limited being found, thus far, only in Asia, South America and Europe. It is hypothesized that HoBi-like viruses were introduced into Europe via the importation of contaminated fetal bovine sera from South America. In order to confirm the absence of HoBi-like viruses in US cattle, researchers at the NADC conducted surveys of fetal bovine serum (FBS) for the presence of the virus and surveys of adult cattle sera for the presence of antibodies. The approximately 2000 samples of adult cattle sera were randomly selected from the sera collected as part of the US brucellosis testing at slaughter program. These samples were collected over the course of 12 months and included samples from cattle originating in the 48 contiguous states. While both BVDV1 and BVDV2 were found in FBS originating in the US, no sample was contaminated with a HoBi-like virus. Similarly, no serum samples were identified that had antibodies specific to HoBi-like viruses. These results indicate that bovine pestivirus control programs in the US focus on vaccines that control BVDV1 and BVDV2 and that requirements for international commerce in cattle and cattle derived products include testing for HoBi-like viruses. Further testing needs to be completed to determine the bovine pestivirus status for Canadian and Mexican herds.

Update on Emerging Swine Diseases in the United States

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Abstract
Perhaps the most volatile cost in livestock and poultry production is animal health where dramatic losses can occur almost overnight due to emerging, or re-emerging diseases. This update describes recent disease concerns that has affected the US pork industry and directly or indirectly the health of Mexican and Canadian swine. In April 2013, porcine epidemic diarrhea virus (PEDV) was detected for the first time in the United States and within months it spread throughout all major swine producing regions of the US. The virus caused severe diarrhea in young piglets leading to high mortality. Within the first year of the epidemic about 50% of the sows in the US became infected resulting in a 7-8% loss in total pig production. During the second year the incidence of new cases declined dramatically raising hope this new disease would fade away and current control strategies might be adequate. Concurrent with the PEDV outbreak in the US was the emergence of porcine deltacoronavirus, another novel swine enteric virus. Fortunately, this virus has not had the impact that PEDV has, but the industry is still cautious. Senecavirus A is a porcine virus that was first discovered in the US about 20 years ago and has only been detected rarely since then. When found, it has been associated with cases of idiopathic vesicular disease. Beginning in July 2015, senecavirus A has been detected in a number of cases of vesicular-like disease suggesting this virus could cause vesicular disease in swine. Although this was confirmed in recently completed studies at the National Animal Disease Center, it is not yet clear why this “mini” epidemic of vesicular disease suddenly appeared. The unexplained emergence of these viruses in the US demonstrates the constant need for disease surveillance and a better understanding of the epidemiology of transboundary diseases.

Avian influenza virus and its impact on agriculture

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H5 or H7 highly pathogenic avian influenza (HPAI) has caused 39 epizootics in poultry since 1959. The H5 Goose/Guangdong (Gs/GD)-lineage HPAI, which originated in China in 1996, has been the largest epizootic. It has caused deaths in wild birds, poultry and humans in 70 countries in Asia, Europe and Africa, and recently in North America. The severity, size and broad geographic distribution of GS/GD epizootic merits the term panzootic. Beginning in December 2014, the Canada and USA have experienced an unpreceded outbreak of H5 Gs/GD-lineage HPAI as the first intercontinental spread of a Eurasian HPAI virus (HPAIV) to North America. Initially, a reassortant H5N2 clade 2.3.4.4 HPAI virus appeared in British Columbia, Canada, and within a few days the original Eurasian H5N8 and the reassortant H5N2 HPAIV appeared in a wild duck and gyrfalcon in Washington state, respectively, Subsequently these H5 HPAIV spread through the Pacific Flyway and to the Midwest USA. Molecular analysis indicated that the infected premises (backyard and commercial) in Western and initial premises in Midwestern USA were point source introductions from wild birds, while most cases in the Midwest had secondary spread from common sources. In total, the H5 HPAIV outbreaks has affected 21 states, with detections in 4 captive wild birds, 75 wild birds, 21 backyard flocks and 211 commercial flocks, totaling over 48 million birds. In the USA, the eradication effort cost more than $1 billion and the negative economic impact was over $3.2 billion. Experimental studies in chickens, turkeys, pheasants, guinea fowl, partridges, and Japanese quail indicated quail were the most susceptible poultry species to infection and death, followed by other minor poultry species. Chickens and turkeys require high doses of virus to become infected. Mallards and domestic ducks were very susceptible to infection but without illness or death; supporting the initial observation that the H5 HPAIVs were adapted to wild waterfowl and had reduced adaptation to poultry, but later viruses in Midwest had increased adaptation to chickens and turkeys.