CRWAD
conference of research workers in animal diseases

Dedicated to
Dr. Yehia Mohamed (Mo) Saif

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NORTH AMERICAN PRRS SYMPOSIUM 2015 CHICAGO

North American PRRS 2016 Symposium

2016 CRWAD Tabletop Exhibitors

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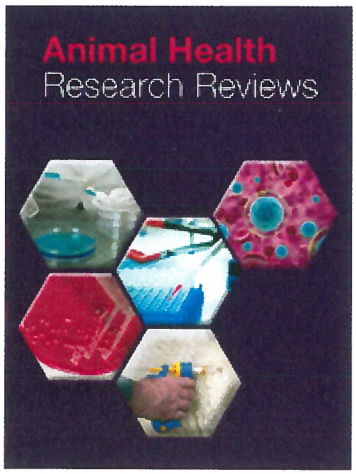

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2016 CRWAD Dedicatee

Yehia Mohamed Saif, DVM, PhD

Dr. Yehia Mohamed (Mo) Saif was born in Egypt and received his veterinary degree from Cairo University. He practiced avian and large animal medicine following graduation. Dr. Saif then matriculated to the The Ohio State University to pursue his PhD. In 1968 he became an assistant professor in the Department of Veterinary Sciences, at the Ohio Agricultural Research and Development Center (OARDC). Dr. Saif retired in 2013 from his position as Head of the Food Animal Health Research Program and Assistant Dean, College of Veterinary Medicine, OARDC, The Ohio State University. His research accomplishments include: the first demonstration of the interspecies transmission of influenza viruses and coronaviruses; elucidating the molecular basis of interspecies transmission of influenza viruses; first demonstration of the diversity of antigenic types of infectious bursal disease viruses; discovery of several avian enteric viruses and defining their pathogenesis and epidemiology; providing first description of the production and metabolism of the 3 turkey immunoglobulins; elucidating the pathogenesis and epidemiology of Mycoplasma meleagridis including its venereal route of transmission; establishment of a specific pathogen free turkey flock in 1964 that still exists for use in experimental studies; demonstrating the effect of relative humidity on the pathogenesis of aspergillosis. Dr. Saif is a past president of the American Association of Avian Pathologists (AAAP) and a Diplomate and past Chair of the Board of Governors of the American College of Veterinary Microbiologists (ACVM) and the American College of Poultry Veterinarians. He is currently Editor of Avian Diseases and was Editor-in-Chief of the textbook*, Diseases of Poultry*. He is a highly regarded expert on avian pathology and an advisor to the World Animal Health Organization (OIE) and his laboratory is an official OIE reference laboratory. He is author or coauthor of 170 peer reviewed scientific articles, 28 book chapters and 264 abstracts and popular articles and he mentored 31 graduate students. Dr. Saif has received numerous awards including AAAP Life Member and Special Service Award, the ACVM Distinguished Veterinary Microbiologist Award, an honorary diploma from the American Veterinary Epidemiology Society, and was elected an inaugural member of the Hall of Honor of the World Veterinary Poultry Association. He has received the research excellence awards from OSU College of Veterinary Medicine (CVM), OARDC, AAAP, American Veterinary Medical Association, and graduate teaching excellence award from OSU CVM. He serves as the AAAP representative to the AVMA's House of Delegates and he has been appointed as a board member to the recently formed USDA Foundation for Food and Agricultural Research. Dr. Saif retains his title as Professor and Head Emeritus of the Food Animal Health Research Program of the Ohio Agricultural Research and Development Center (OARDC) at The Ohio State University (OSU).

CRWAD Council Keynote

Sunday, Dec 4 Salon A/B/C/D
5th Floor 5:30 – 6:30 PM

Genome Editing for PRRSV Resistance and Beyond

Randall S. Prather, Curators' Professor
Director National Swine Resource and Research Center
Division of Animal Science, National Swine Resource and Research Center, University of Missouri, Columbia, MO

Genetic engineering has been a staple of food production, at least on the plant side. The applications have resulted in decreased pesticide and herbicide usage thus resulting in cleaner water in both rural and metropolitan communities. Recent development and application of gene editing technologies will result in even more significant applications in the plant world. The gene editing technologies include zinc-finger nucleases, TAL effector nucleases, and the CRISPR/Cas9 system. All three of these technologies have permitted genetic edits that range from the addition or removal of a single nucleotide to replacing a small region or swapping complete protein domains. What is notable is that the CRISPR/Cas9 system is relatively to use. It requires a guide RNA and the Cas9 protein. The guide RNA can easily be designed and assembled in a few days. This ease of construction is in contrast to the laborious task of assembling modules for zinc-finger nucleases and TAL effector nucleases. Not only are the guides easy to assemble they, like the other editing technologies, are highly efficient. Generally, it is thought that when the editing molecules cut the DNA the cut strand is repaired; but since the editing molecule is still there editing molecules continue to cut the DNA until a mistake is made in the repair mechanism and non-homologous end joining results. Since an error is made in the repair, the editing mechanism no longer cuts the DNA because the target sequence no longer exists. If a repair template is included at the time of editing, often the cut DNA will incorporate that molecule into the repair.

The CRISPR/Cas9 system has been used to edit *CD163* to make pigs resistant to Porcine Reproductive and Respiratory Syndrome Virus. The edits included both non-homologous end joining and repair by using a template to swap out domain 5 of the CD163 protein. In addition to *CD163*, use of a repair template has permitted introducing an Angus allele for the polled phenotype into Holstein cattle, and to introduce a sequence specific for Warthogs into domestic pig *RELA* potentially to provide resistance to African Swine Fever. Another proposed use of the editing technology would be to change a single amino acid in *CD18* in cattle to provide resistance to bovine respiratory disease caused by *Mannheimia haemolytica*.

The relative ease at which edits can be introduced into the genome of domestic animals ensures that additional applications in domestic animals for agriculture will be made to address disease resistance, animal welfare, productivity, and carcass composition. But not only agriculture will benefit, this same technology can be used to make, the pig for example, better models for studying human disease.

2016 CRWAD Session Keynote Speakers

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Bacterial Pathogenesis – Michael Federle – Monday, Dec. 5th 10:45 AM
"*Microbial Wikileaks: Intercepting Pathogen Conversations To Understand (and Disrupt) Interactions with the Host"*
Medicinal Chemistry and Pharmacognosy, University of Illinois at Chicago, Chicago, IL

Biosafety and Biosecurity – Karyn Havas – Monday, Dec. 5th 3:00 PM
"*A biosecurity assessment of U.S. animal production systems"* Diagnostic Services Section, USDA Foreign Animal Disease Diagnostic Laboratory, Greenport, NY

Companion Animal Epidemiology – Dan O'Neill- Monday, Dec. 5th 1:15 PM
Schwabe Award Winner
"Primary-care vet data: the final frontier"
Royal Veterinary College, University of London

Immunology – Subramaniam Srikumaran – Monday, Dec 5th 1:15 AM
AAVI Immunologist of the year
"Genetic engineering of disease-resistant animals: a fantasy or reality?"
Department of Veterinary Microbiology and Pathology, College of Veterinary Medicine, Washington State University, Pullman, WA

Pathobiology of Enteric and Foodborne Pathogens – Rodney Moxley – Monday, Dec. 5th 8:45 AM
"*Shiga toxin-producing Escherichia coli: key scientific discoveries and challenges that remain"*
School of Veterinary Medicine & Biomedical
Sciences, University of Nebraska-Lincoln, Lincoln, NE

Respiratory Diseases – Suresh Mittal - Monday, Dec 5th 3:45 PM
"*Emerging Avian Influenza Viruses: Their Implications and Control Strategies"*
Purdue University, College of Veterinary Medicine, West Lafayette, IN

Vector-Borne and Parasitic Diseases – Kelly Brayton – Monday, Dec. 5th 10:00 AM
"*How genomics has facilitated vaccine development for Anaplasma marginale"*
Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA

Viral Pathogenesis – Key Note speaker in memory of Prem Paul,
ACVM Microbiologist of the year – Dan L. Rock, - Tues, Dec 6th 10:00 AM
Challenges for African Swine Fever Vaccine Development – "…perhaps the end of the beginning."
Department of Pathobiology, College of Veterinary Medicine, University of Illinois at Urbana-Champaign, Urbana, IL
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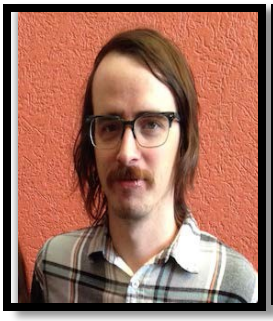

2016 Mark Gearhart Memorial Graduate Student Award

Salon A/B/C/D – Monday, Dec 5th 2:00 PM – 2:15 PM

CRWAD Presentation No. 357

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The Case-Control Design in Veterinary Sciences: A Survey

Jonah N. Cullen[a] , Jan M. Sargeant[b,c], Kelly M. Makielski[d], Annette M. O'Connor[a]

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[d] Department of Veterinary Clinical Sciences, College of Veterinary Medicine, Iowa State University, 1720 Vet Med, Ames, Iowa 50010, USA

The case-control study design is deceptively simple. However, many design considerations influence the estimated effect measure. An investigation of case-control studies in the human health literature suggested that some of these considerations are not described in reports of case-control studies. Our hypothesis was that the majority of veterinary studies labeled as case-controls would be incident density designs, and many would not interpret the effect measure obtained from those studies as the rate ratio rather than the odds ratio. Reference databases were searched for author-designated case-control studies. A survey of 100 randomly selected studies was conducted to examine the different design options described and estimated effect measures. Of the 100 author-identified case-control studies, 83 assessed an exposure-outcome association and, of those, only 54 (65.1%) sampled the study population based on an outcome and would thus be considered case-control designs. Twelve studies were incidence density designs but none used this terminology. Of the studies that reported an odds ratio as the effect measure, none reported on additional considerations that would have enabled a more interpretable result. This survey indicated many case-control-labeled studies were not case-control designs and among case-control studies, key design aspects were not often described. The absence of information about study design elements and underlying assumptions in case-control studies limits the ability to establish the effect measured by the study and the evidentiary value of the study might be underestimated.
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2016 American College of Veterinary Immunologists – Veterinary Immunologist of the Year

Subramaniam (Sri) Srikumaran

Dr. Srikumaran graduated from the University of Sri Lanka with a BVSc Degree in 1972 and served as a Government Veterinarian in the Department of Agriculture in Sri Lanka from 1974 to 1979. He migrated to the United States where he received an MS and PhD from the University of Maryland in Immunology in 1981 and 1982, respectively.

After receiving his PhD he was a Post-doctoral Research Associate in the Department of Biology at Amherst College, Amherst, MA. He became an Assistant Professor in the Department of Veterinary and Biomedical Sciences, University of Nebraska Lincoln in 1984, was promoted to Associate Professor in 1990 and Professor in 1996.

In 2004 he was named the Professor and Dr. Rocky Crate-Wild Sheep Foundation Endowed Chair in the Department of Veterinary Microbiology and Pathology at Washington State University. He retired from that position in 2016 and is currently Professor Emeritus, School of Veterinary Medicine and Biological Sciences, University of Nebraska- Lincoln and College of Veterinary Medicine, Washington State University.

Dr. Srikumaran has received several honors and awards including: Senior Fogarty International Fellowship NIH (1991-1992); he was a panel manager in 2002 for the Binational Agricultural Research Development Fund (BARD); NIH-NIAID Special Emphasis Panel on Food and Water-borne Diseases Integrated Research Network 2003; Consultant in Veterinary Biotechnology for Madras Veterinary College National Agricultural Technology Project 1999-2004; Outstanding Scientific Achievement Award from Wild Sheep Foundation in 2010 and he was inducted into the Wild Sheep Biologist Hall of Fame in 2015.

Sri has been a leader in understanding the immunology of infectious diseases in large and wild animals. He has especially been recognized for his work on Bighorn Sheep over the past decade. He has 90 refereed journal publications, Over 100 presentations and published Abstracts, adviser 16 PhD and 11 MS students and 12 Post-doctoral Research Associates. He has received over $3 million in research funding during his career.

In recognition of his many accomplishments he has been recognized by the American Association of Veterinary Immunologists as the AAVI Veterinary Immunologist of the Year.

2016 American College of Veterinary Microbiologists – Microbiologist of the year Prem S. Paul

Dr. Prem Paul's career began in Hissar, Haryana, India as a veterinary medicine student. After receiving his DVM (BVSc) from the Panjab Agricultural University College of Veterinary Sciences in 1969, then moved to the United States where he received a PhD in veterinary microbiology at the University of Minnesota in St. Paul, Minnesota in 1975, and in 1977 became a diplomate in the American College of Veterinary Microbiologists.

Prem began his career at the University of Minnesota as a research associate in the Department of Large Animal Clinical Sciences. Later he served as a veterinary medical officer at the USDA National Animal Disease Center for seven years. In 1987, Dr. Paul joined the faculty of Iowa State University as a member of the Veterinary Medical Research Institute. At ISU he served as director of graduate education (1991-1992), professor-in-charge (1992-1993) and associate director (1993-1999) of the Veterinary Medical Research Institute; assistant director of the Iowa Agricultural and Home Economics Experiment Station (1996-2000); associate dean for research and graduate studies for the College of Veterinary Medicine (1993-1999); and associate vice provost for research (2000-2001). In 2001, Dr. Paul accepted the position of dean of graduate studies and vice chancellor of research at the University of Nebraska–Lincoln in Lincoln, Nebraska. His title changed in 2008 to vice chancellor for research and economic development to reflect new responsibilities.

Dr. Paul's scientific expertise is in animal virology. He has authored more than 100 papers in refereed publications, has edited two books, 11 book chapters and holds more than 20 U.S. and international patents. Dr. Paul has been extremely proactive in advancing student exposure to research. He was instrumental in developing the Merial Veterinary Scholars Program, a national program that funds student research at veterinary schools and hosts a national symposium where students present their findings.

His impact on animal health/disease research can be measured in part by the accomplishments of his former students, which include a number of nationally and internationally renowned scientists at educational institutions and with government agencies in the United States and abroad.

He is a Charter Fellow of the National Academy of Inventers and a fellow of the American Association for the Advancement of Science. He has served on review panels for NIH, the USDA and the NSF and was a member of the U.S. Food and Drug Administration's xenotransplantation advisory subcommittee. He is past chair of the EPSCoR Coalition Board and the Council on Research Policy and Graduate Education. He was a member of the National Academies Committee on Policy Implications of International Graduate Students and Postdoctoral Scholars in the United States, and past president of the Council of the Conference of Research Workers in Animal Diseases.

He is a member of the American Veterinary Medical Association, American Association for the Advancement of Science, American College of Veterinary Microbiologists, American Society for Virology, Conference of Research Workers in Animal Diseases, and the American Association of Swine Veterinarians. He was recognized as the 2015 Dedicatee at the 96th CRWAD Meeting.

Dr. Paul and his wife Melissa (Missy) have two children, Neena who resides in New York City and Ryan who lives in Chicago. The Pauls have one granddaughter. Prem died September 2, 2016.

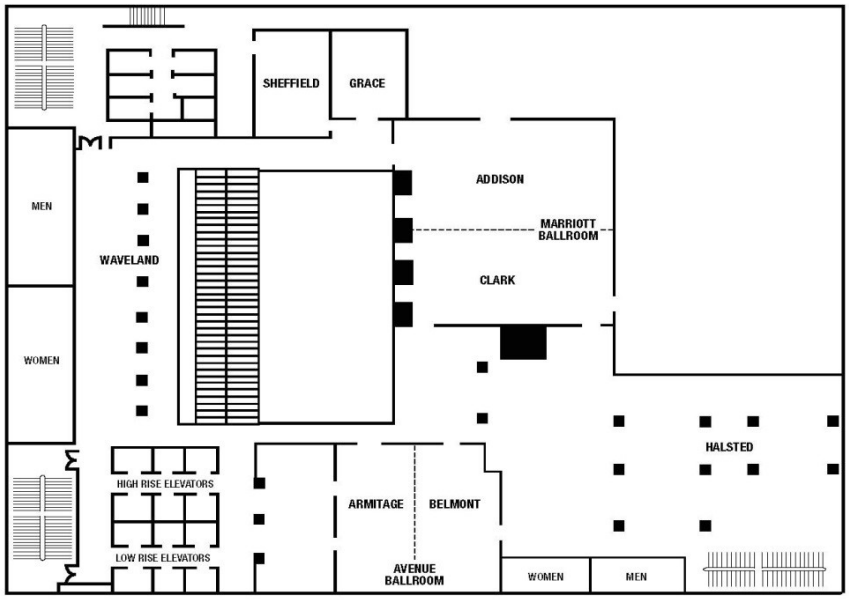
CRWAD At – A – Glance
Friday, Dec. 2 – Sunday, Dec. 4

Meeting Session	Friday AM/PM Room & Floor	Saturday AM Room & Floor	Saturday PM Room & Floor	Sunday AM Room & Floor	Sunday PM Room & Floor
AAVI Business Meeting – by invitation					10am -1 PM Los Angeles – 5th Floor
ACVM Board Of Governors – by invitation				8:00 AM – 12:00 PM Indiana/ Iowa – 5th Floor	
AVEMP Workshop				8:30 AM – 12:00 PM Salon E/F/G/H	
AVEPM Schwabe Symposium – Will Hueston					1:00 PM – 5:00 PM Salon E/F/G/H
CRWAD Council Meeting- Council Members only			6:00 PM – 8:00 PM Great American – 6th Floor		
CRWAD Council Keynote – Randall Prather					5:30 PM -6:30 PM Salon A/B/C/D
NE – 1201 Mycobacterial Diseases of Animals				8:00 AM – 12:00 PM Clark/ Addison – 4th Floor	1:00 PM – 5:00 PM Clark/ Addison – 4th Floor
NC – 1202 Enteric Diseases of Food Animals		8:00 AM – 12:00 PM Denver/ Houston– 5th Floor	1:00 PM – 5:00 PM Denver/ Houston – 5th Floor	8:00 AM – 12:00 PM Denver/Houston 5th Floor	
NC – 229 & NAPRRS Symposium		8:00 AM – 12:00 PM – Intercontinental Hotel	1:00 PM – 5:00 PM Intercontinental Hotel	8:00 AM – 12:00 PM Salon A/B/C/D Marriott	1:00PM – 5:00 PM Salon A/B/C/D Marriott
USDA/NIFA Project Directors Meeting – invitation only	8:00 AM – 5:00 PM Salon A/B/C/D				
Researchers Reception					6:30 PM – 8:00 PM Grand Ballroom – 7th Floor
Poster Session I					6:30 PM – 8:00 PM Salon III – 7th Floor
Speaker Ready Room					7:00 AM – 11:30 PM Streeterville

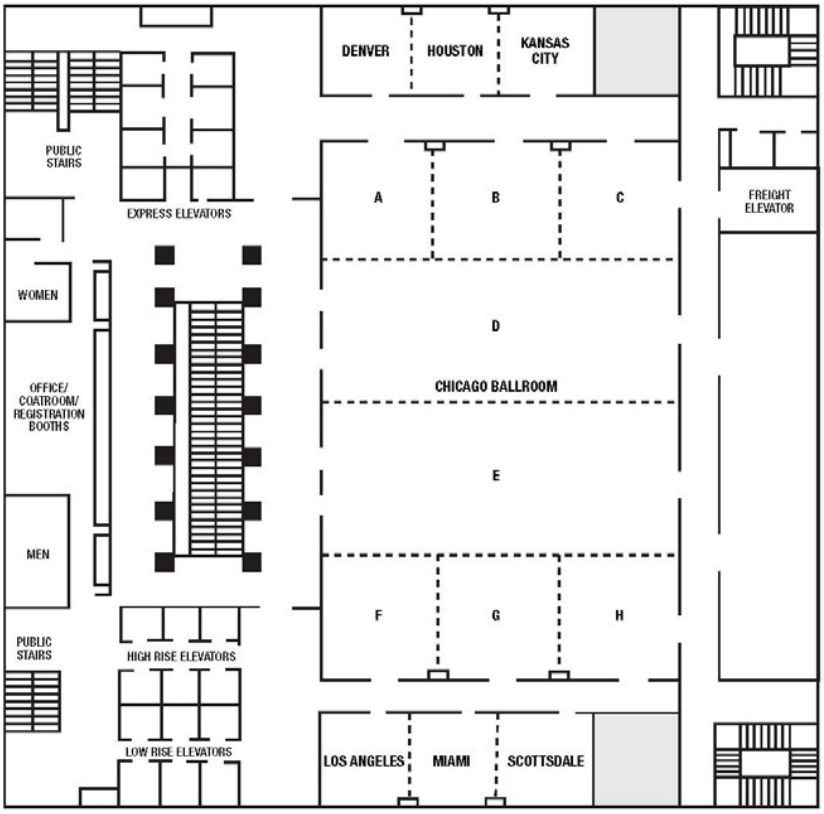
CRWAD At – A – Glance
Monday, Dec 5 – Tuesday, Dec 6

Meeting Session	Monday AM 8:00-11:30 Room & Floor	Monday PM 1:30-4:30 Room & Floor	Tuesday AM 8:00-11:30 Room & Floor	Tuesday PM 1:30 – 5:00 Room & Floor	Wednesday 8:00 – 5:00 Room & Floor
Bacterial Pathogenesis	Avenue Ballroom 4th Floor	Avenue Ballroom 4th Floor			
Biosafety and Biosecurity		Denver/ Houston – 5th Floor			
Companion Animal Epidemiology	Northwestern/ Ohio – 6th Floor	Joining Salon A/B/C/D for Keynote speaker / finish oral presentations in Northwestern/ Ohio			
Ecology and Management of Foodborne Agents	Salon E 5th Floor	Joining Salon A/B/C/D for Keynote speaker/ finish oral presentation in Salon E – 5th Floor			
Epidemiology and Animal Health Economics	Salons A/B/C/D 5th Floor	Salons A/B/C/D 5th Floor	Salons A/B/C/D 5th Floor		
Immunology	Salons F/G/H 5th Floor	Salons F/G/H 5th Floor – Mini Symposium	Salons F/G/H 5th Floor		
Pathobiology of Enteric and Foodborne Pathogens	Michigan/Michigan State 6th Floor	Michigan/Michigan State 6th Floor – Mini Symposium	Michigan/Michigan State 6th Floor		
Respiratory Diseases	Indiana/Iowa 6th Floor	Indiana/Iowa 6th Floor			
Vector-Borne and Parasitic Diseases	Denver/Houston 5th Floor				
Viral Pathogenesis	Los Angeles/Miami 5th Floor	Los Angeles/Miami 5th Floor	Los Angeles/Miami 5th Floor – Mini Symposium		
Posters in Grand Ballroom		Salon III – 7th Floor Monday 5-6:30 PM			
AHRR			11:30 AM – 12:30 PM Indiana – 6th Floor		
Business Meeting			11:45 AM – 12:30 PM Salon A/B/C/D – 5th Floor		
BVDV Symposium				1:30 PM – 5:00 PM Clark/Addison– 4th Floor	8:00 AM – 5:00 PM Clark/ Addison – 4th Floor

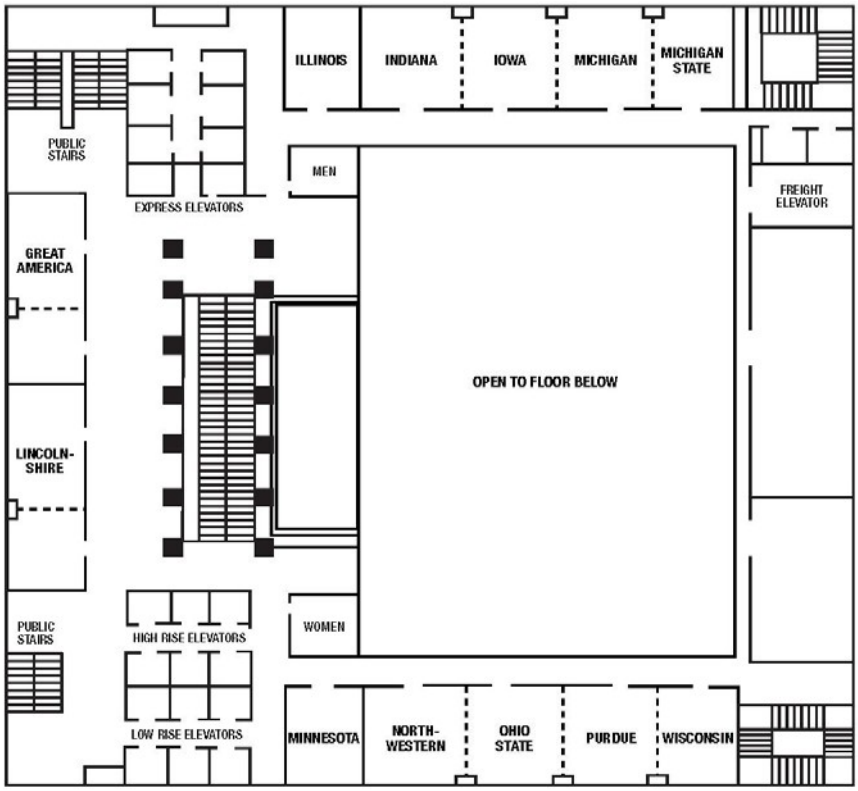
Chicago Marriott Floor Plan 4th Floor



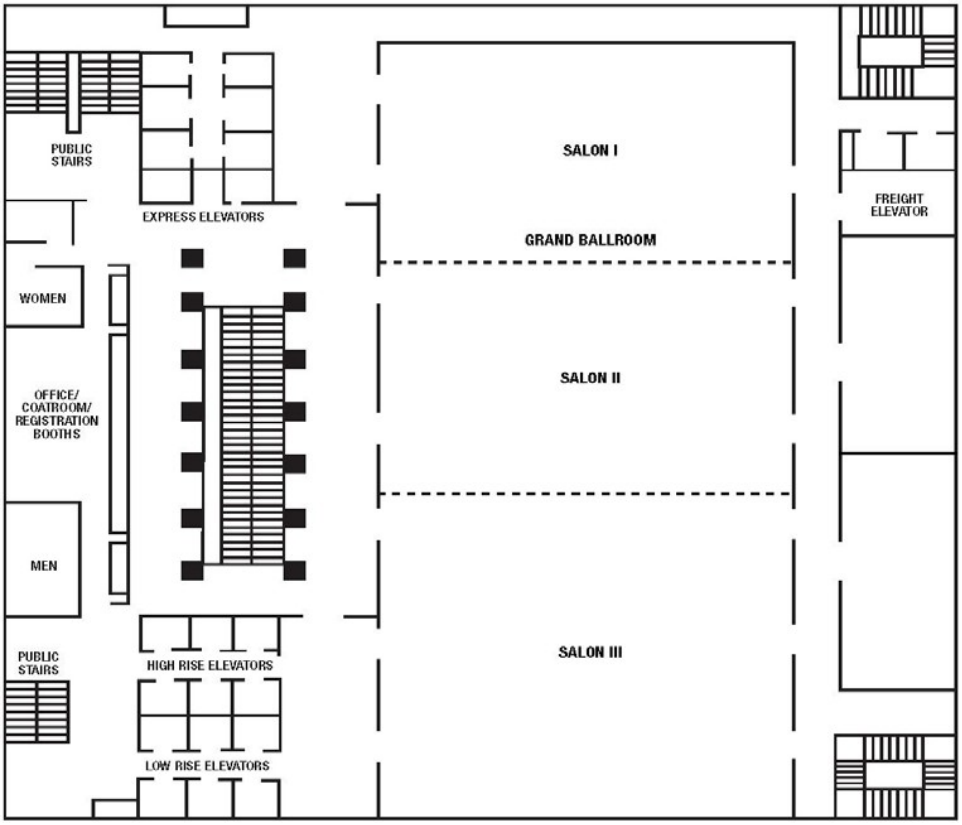
Chicago Marriott Floor Plan 5th Floor



Chicago Marriott Floor Plan 6th Floor



Chicago Marriott Floor Plan 7th Floor



2016 Schwabe Symposium:

"Building public-private partnerships to deliver One Health',"

The Association for Veterinary Epidemiology and Preventive Medicine (AVEPM) is pleased to announce the program for the 2016 Schwabe Symposium honoring the lifetime professional achievements of Dr. Will Hueston.
Dr. Hueston will be honored at The Schwabe Symposium hosted by AVEPM on Sunday the 4th of December, 2016 at the Chicago Marriott Hotel, Downtown Magnificent Mile, Chicago, Illinois.

The theme for the program is:

"Building public-private partnerships to deliver One Health',"
The program will provide a unique opportunity for current and future researchers to hear the insights of leading experts in One Health and successful models of public-private partnerships to delive one health outcomes.
The Calvin W. Schwabe Award recognizes lifetime achievement in veterinary epidemiology and preventive medicine. The Calvin W. Schwabe Award is presented annually by the AVEPM. Previous recipients include Drs. Calvin Schwabe, Robert Anderson, James Steele, S. Wayne Martin, Clive Gay, David W. Hird, Hollis Erb, Preben Willeberg, Dale Hancock, Ian Dohoo, Yrjo Grohn and Roger Morris.
Will Hueston, DVM, PhD, (University of Minnesota, retired) last directed global leadership programs for the Center for Animal Health and Food Safety at the University of Minnesota, a World Organization for Animal Health (OIE) Collaborating Center in Veterinary Services Capacity Building. Professor Hueston held faculty appointments in the College of Veterinary Medicine, School of Public Health and Humphrey School of Public Affairs.
Dr. Hueston's work focused on capacity-building, public policy and risk cmmunication with particular emphasis on global food systems. He was instrumental in expanding public health graduate education for veterinarians at UMN through a combined DVM-MPH program, an executive MPH program for working health professionals and a post-graduate residency program in veterinary public health and preventive medicine. He also has a long history of designing and delivering capacity-building programs for early and mid-career government, industry and academic professionals in collaboration with universities, government agencies, intergovernmental organizations and the private sector. His work has spanned North America, Latin America, Europe, Africa and Asia.
Dr. Hueston began his veterinary career in dairy practice and has since worked in the public, private and academic sectors including a 6 month detail to the United Kingdom in 1991 in support of the BSE epidemiology investigations. His government experience solidified a life-long interest in public policy-making and a passionate commitment to equip veterinarians and other science-trained professionals with the skills necessary to work effectively in the policy arena where science, politics and beliefs often collide.

Sun, Dec 4, 2016

1:00-5:00 PM

Chicago Ballroom, E/F/G/H 5th Floor

Presented by the Association for Veterinary Epidemiology and Preventive Medicine

Recent Past Presidents CRWAD

Roman Ganta	2015	Linda J Saif	2001
David A Benfield	2014	Leon ND Potgieter	2000
Rodney Moxley	2013	MD Salman	1999
Donald L Reynolds	2012	Donald G Simmons	1998
Laura L Hungerford	2011	Bert E Stromberg	1997
Eileen L Thacker	2010	Patricia E Shewen	1996
Bill Stich	2009	Bradford B Smith	1995
Richard E Isaacson	2008	Ronald D Schultz	1994
Lynn A Joens	2007	Lawrence H Arp	1993
Prem S Paul	2006	Richard F Ross	1992
Ian Gardner	2005	Robert M Corwin	1991
Janet MacInnes	2004	Lynette B Corbeil	1990
Katherine M Kocan	2003	William C Wagner	1989
Franklin A Ahrens	2002		

The Dedicatee Tradition

Annually, CRWAD selects a Life Member who has made outstanding contributions to CRWAD and to animal disease research to be honored as the Dedicatee for the CRWAD meeting. The tradition started in 1974 and continues to the present. The Dedicatee is honored with a plaque and an hororarium at the annual business meeting. All recognized Dedicatees are listed below.

WR Hinshaw	1974	SH McNutt	1975	HCH Kernkamp	1976
RW Doughtery	1977	CH Bradley	1978	SF Scheidy	1979
AG Karlson	1980	IA Merchant	1981	LC Ferguson	1982
F Maurer	1983	C Olson, Jr	1984	C Cunningham	1985
BS Pomeroy	1986	N Levine	1987	E Splitter	1988
MJ Twiehaus	1989	RA Packer	1990	DA Barnum	1991
AF Weber	1992	EO Halterman	1993	EM Kohler	1994
EH Bohl	1995	LE Hanson	1996	GR Carter	1997
JB Derbyshire	1998	BC Easterday	1999	L Coggins	2000
DP Anderson	2001	J Storz	2002	AJ Winter	2003
HW Moon	2004	WJ Mengeling	2005	LE Carmichael	2006
RF Ross	2007	SA Ewing	2008	NF Cheville	2009
SK Maheswaran	2010	DO Simmons	2011	WC Wagner	2012
FW Scott	2013	DC Robertson	2014	PS Paul	2015
Yeshia Mohammed Saif	2016				

CRWAD ORAL PRESENTATIONS BY DAY

TIME	ORAL #	SECTION	TITLE
MON 8:00:00 AM	1	Bacterial Pathogenisis	Methods to detect and quantify invasion of eukaryotic cells by obligate intracellular bacteria Lawsonia intracellularis
MON 8:00:00 AM	32	Companion Animals Epidemiology	Patterns and predictors of antimicrobial resistance among Staphylococcus spp. from canine clinical cases presented at a veterinary academic hospital in South Africa.
MON 8:00:00 AM	48	Ecology and Management of Foodborne Agents	Whole-genome sequencing of Salmonella derived from feedlot cattle treated with antibiotics
MON 8:00:00 AM	70	Epidemiology & Animal Health Economics	Salmonella enterica and extended spectrum cephalosporin resistant Escherichia coli recovered from Holstein dairy calves in New Brunswick, Canada
MON 8:00:00 AM	91	Immunology	Characterizing intestinal epithelial and immunological gene expression in healthy calves
MON 8:00:00 AM	110	Pathobiology of Enteric and Foodborne Pathogens	Use of a new in situ platform to co-detect Lawsonia intracellularis and proliferation markers in enterocytes of infected pigs
MON 8:00:00 AM	150	Viral Pathogenesis	Serum and mammary secretion antibody responses in PEDV-exposed gilts following PEDV vaccination
MON 8:15:00 AM	2	Bacterial Pathogenisis	Role of Glutamate Racemase in Mycobacteria
MON 8:15:00 AM	33	Companion Animals Epidemiology	Spatial and antimicrobial susceptibility patterns of Staphylococcus from horses presented at a teaching hospital in South Africa
MON 8:15:00 AM	49	Ecology and Management of Foodborne Agents	Shotgun metagenomic detection of Salmonella enterica in feedlot cattle compared to aerobic culture and PCR techniques.
MON 8:15:00 AM	71	Epidemiology & Animal Health Economics	Evidence for persistent, spatially-explicit reservoirs of antibiotic-resistant Escherichia coli in food-animal production environments
MON 8:15:00 AM	92	Immunology	Induction of antiviral response against avian influenza virus infection using toll like receptor (TLR) 3 ligand, double stranded
MON 8:15:00 AM	111	Pathobiology of Enteric and Foodborne Pathogens	Identifying immuno-dominant epitopes from F18 fimbriae FedF adhesins using reverse epitope vaccinology approach
MON 8:15:00 AM	144	Vector-Borne & Parasitic Diseases	LSDV100 and LSDV101 Lumpy skin disease virus-specific PCR for rapid diagnosis and vaccine quality control.
MON 8:15:00 AM	151	Viral Pathogenesis	Porcine deltacoronavirus induces caspase-dependent programmed cell death

CRWAD ORAL PRESENTATIONS BY DAY

MON 8:30:00 AM	3	Bacterial Pathogenisis	Mutual antagonism between Mannheimia haemolytica and Pasteurella multocida when forming a biofilm on bovine bronchial epithelial cells in vitro.
MON 8:30:00 AM	34	Companion Animals Epidemiology	Extended-spectrum cephalosporin, carbapenem, and fluoroquinolone resistant coliform bacteria from a large equine teaching hospital and a referral equine specialty hospital
MON 8:30:00 AM	50	Ecology and Management of Foodborne Agents	Transmission of Salmonella from farm to food: The impact of clinical outbreaks of salmonellosis in calves on recovery of Salmonella from lymph nodes at harvest.
MON 8:30:00 AM	72	Epidemiology & Animal Health Economics	Annual variation in susceptibility of generic Escherichia coli isolates to ceftiofur from retail chicken meat surveillance in Canada
MON 8:30:00 AM	93	Immunology	Efforts towards developing a universal vaccine against emerging influenza viruses.
MON 8:30:00 AM	112	Pathobiology of Enteric and Foodborne Pathogens	Screening immunodominant epitopes of enterotoxigenic Escherichia coli (ETEC) heat-labile toxin (LT) A subunit
MON 8:30:00 AM	127	Respiratory Diseases	Pathogenicity of a new Russian genotype 1 subtype 2 PRRSV isolate
MON 8:30:00 AM	145	Vector-Borne & Parasitic Diseases	Glycosylated Ehrlichia ruminantium major antigenic protein1 subunit vaccine induces strong antibody and T cell responses in sheep
MON 8:30:00 AM	152	Viral Pathogenesis	Comparison of porcine epidemic diarrhea virus (PEDV) and porcine deltacoronavirus (PDCoV) for pathogenicity in nursery pigs
MON 8:45:00 AM	4	Bacterial Pathogenisis	Comparative genomics of archived pyrazinamide resistant mycobacterium tuberculosis complex isolates from Uganda.
MON 8:45:00 AM	35	Companion Animals Epidemiology	Antimicrobial resistance to extended-spectrum cephalosporins in Enterobacteriaceae from dogs in Southern Ontario, Canada
MON 8:45:00 AM	73	Epidemiology & Animal Health Economics	Characterizing antimicrobial drug use in Canadian beef cattle: Comparison of actual use to Population Corrected Unit methodology
MON 8:45:00 AM	94	Immunology	Development of a recombinant parapoxvirus expressing the spike protein of porcine epidemic diarrhea virus.
MON 8:45:00 AM	113	Pathobiology of Enteric and Foodborne Pathogens - Rodney Moxley - KEYNOTE SPEAKER	Shiga toxin-producing Escherichia coli: key scientific discoveries and challenges that remain
MON 8:45:00 AM	128	Respiratory Diseases	Contribution of PRRSV minor glycoproteins to a protective immune response in swine

CRWAD ORAL PRESENTATIONS BY DAY

MON 8:45:00 AM	146	Vector-Borne & Parasitic Diseases	The distribution of invertebrate reservoir host for Lyme disease in Kyiv, Ukraine
MON 8:45:00 AM	153	Viral Pathogenesis	Development of a new molecular method to discriminate Porcine epidemic diarrhea virus infectious particles, from non-infectious ones, that are contaminating food additives
MON 8:45:00 AM	188	Immunology	Dietary resistant starch modulates intestinal immune status in pigs.
MON 9:00:00 AM	5	Bacterial Pathogenisis	Influence of maternal microbial communities on the intestinal mucosal microbiome of the neonatal pig.
MON 9:00:00 AM	36	Companion Animals Epidemiology	Impact of collateral resistance in methicillin-resistant Staphylococcus pseudintermedius in canine patients
MON 9:00:00 AM	51	Ecology and Management of Foodborne Agents	Analyzing 20 years of Salmonella serotype using NARMS and veterinary diagnostic laboratory data
MON 9:00:00 AM	74	Epidemiology & Animal Health Economics	Serotype diversity and antimicrobial resistance among Salmonella enterica isolated from patients at an equine referral hospital
MON 9:00:00 AM	95	Immunology	Cross-reactivity of immune responses against porcine reproductive and respiratory syndrome virus
MON 9:00:00 AM	129	Respiratory Diseases	Comparison of morbidity and mortality after challenge with two North American PRRS virus isolates shows marked variation in clinical disease between isolates
MON 9:00:00 AM	147	Vector-Borne & Parasitic Diseases	Next generation sequencing and genomic analysis of Tritrichomonas foetus species of bovine and feline origin
MON 9:00:00 AM	154	Viral Pathogenesis	Development of porcine epidemic diarrhea virus vaccines derived from a virulent Korean strain
MON 9:15:00 AM	6	Bacterial Pathogenisis	Construction and evaluation of Edwardsiella piscicida T3SS in-frame deletion mutants
MON 9:15:00 AM	37	Companion Animals Epidemiology	Impact of antimicrobial therapy on the resistance profile of enteric flora of dogs
MON 9:15:00 AM	52	Ecology and Management of Foodborne Agents	Prevalence, quantity and antimicrobial resistance of Salmonella enterica in response to antibiotic use early in the cattle feeding period
MON 9:15:00 AM	75	Epidemiology & Animal Health Economics	Epidemiology of Staphylococcus species and their antimicrobial resistance patterns in livestock-related settings of central Oromia, Ethiopia
MON 9:15:00 AM	96	Immunology	Identification of an epitope from adenine nucleotide translocator that induces inflammation in heart in A/J mice

CRWAD ORAL PRESENTATIONS BY DAY

MON 9:15:00 AM	130	Respiratory Diseases	Differential susceptibility of bighorn sheep and domestic sheep neutrophils to Mannheimia haemolytica leukotoxin is not due to differential expression of cell surface CD18
MON 9:15:00 AM	148	Vector-Borne & Parasitic Diseases	Seroprevalence of bovine anaplasmosis in Kentucky, 2003-2011
MON 9:15:00 AM	155	Viral Pathogenesis	efficacy test and safety test of new genetically variant ped virus vaccine strain
MON 9:30:00 AM		Break and Table Top Exhibits - Foyer	Break and Table Top Exhibits - Foyer
MON 10:00:00 AM	7	Bacterial Pathogenisis	Successful protection against heterologous strains of Haemophilus parasuis: the quest for cross protective factors
MON 10:00:00 AM	38	Companion Animals Epidemiology	Is it possible to diagnose canine brucellosis? - a deterministic model
MON 10:00:00 AM	53	Ecology and Management of Foodborne Agents	Salmonella enterica resistance phenotypes and genotypes of concern isolated from hogs at slaughter
MON 10:00:00 AM	76	Epidemiology & Animal Health Economics	Accounting for data architecture on structural-equation-based modeling of feedlot performance outcomes
MON 10:00:00 AM	97	Immunology	Genome wide association study identifies loci associated with intramammary infection (IMI) phenotypes following experimental challenge with Streptococcus uberis
MON 10:00:00 AM	114	Pathobiology of Enteric and Foodborne Pathogens	Differences in virulence and antimicrobial resistance gene profiles of bovine and human enterohemorrhagic Escherichia coli O157 and O103: A comparative genomics approach
MON 10:00:00 AM	131	Respiratory Diseases	Disparity in nasopharyngeal microbiome between healthy cattle on feed, at entry processing and with respiratory disease
MON 10:00:00 AM	149	Vector-Borne & Parasitic Diseases - Kelly Brayton - KEYNOTE SPEAKER	How genomicshas facilitated vaccine development for Anaplasmamarginale
MON 10:00:00 AM	156	Viral Pathogenesis	Comparison of experimental and commercial PEDV vaccines to protect against PEDV genogroup 2 challenge using the conventional growing pig model
MON 10:15:00 AM	8	Bacterial Pathogenisis	Comparative analysis of plasmid pathogenicity loci and phylogenetic relationship in NetF-producing Clostridium perfringens
MON 10:15:00 AM	39	Companion Animals Epidemiology	The Golden Retriever Lifetime Study: assessing factors affecting owner compliance after the first year of enrollment

CRWAD ORAL PRESENTATIONS BY DAY

MON 10:15:00 AM	54	Ecology and Management of Foodborne Agents	Predictors of selective antimicrobial use practices among dairy calf producers
MON 10:15:00 AM	77	Epidemiology & Animal Health Economics	System dynamics model of broiler production as a tool for studying disease and intervention
MON 10:15:00 AM	98	Immunology	Dairy cows naturally infected with bovine leukemia virus demonstrate abnormal B and T cell responses to routine vaccination
MON 10:15:00 AM	115	Pathobiology of Enteric and Foodborne Pathogens	Frequency of enterohemorrhagic Escherichia coli on cattle hides and quantification of E. coli on matched cattle hides and carcasses in commercial slaughter operations
MON 10:15:00 AM	132	Respiratory Diseases	Microenvironmental sampling techniques of the nasal cavity of cattle and experimental colonization of Mannheimia haemolytica
MON 10:15:00 AM	157	Viral Pathogenesis	Development of murine monoclonal antibodies (mABs) for porcine rotavirus (PoRV) group A, B, and C and their use in a comparative pathogenicity study
MON 10:30:00 AM	9	Bacterial Pathogenisis	Microparticles from Histophilus somni stimulated bovine monocyte-derived macrophages increase fibrin clot formation in vitro
MON 10:30:00 AM	40	Companion Animals Epidemiology	Can animal poison control centre data provide early warning of outbreaks associated with contaminated pet food: using the 2007 melamine poisoning outbreak as a case study
MON 10:30:00 AM	55	Ecology and Management of Foodborne Agents	Effects of feeding Saccharomyces cerevisiae fermentation products on liver abscess rate, foodborne pathogens and the microbiome in natural beef steers.
MON 10:30:00 AM	78	Epidemiology & Animal Health Economics	A model of Foot-and-Mouth Disease transmission within a U.S. beef feedlot
MON 10:30:00 AM	99	Immunology	An improved method for the detection of viral infections using multiplex molecular diagnostic technology. M. M. Hossain*, and R. R. R. Rowland. Department of Diagnostic Medicine/Pathobiology, College of Veterinary Medicine, Kansas State University, Manhattan, Kansas 66506
MON 10:30:00 AM	116	Pathobiology of Enteric and Foodborne Pathogens	Dimethyl adenosine transferase (KsgA) contributes to structural and functional integrity of the cell envelope in Salmonella Enteritidis

CRWAD ORAL PRESENTATIONS BY DAY

MON 10:30:00 AM	133	Respiratory Diseases	Prevalence of multi drug antimicrobial resistance in Mannheimia haemolytica isolated from high risk stocker cattle prior to and following metaphylaxis
MON 10:30:00 AM	158	Viral Pathogenesis	Infectious bronchitis corona virus tropism for macrophages in vitro and in vivo
MON 10:45:00 AM	10	Bacterial Pathogenisis - Michael Federle - KEYNOTE SPEAKER	Microbial Wikileaks: Intercepting PathogenConversations To Understand (and Disrupt) Interactions with the Host
MON 10:45:00 AM	41	Companion Animals Epidemiology	Description of a census of canine intake into Mississippi animal shelters and the relationship to human demographics
MON 10:45:00 AM	56	Ecology and Management of Foodborne Agents	Does the fiber component of distillers grains explain increased fecal shedding of enterohemorrhagic Escherichia coli in feedlot steers?
MON 10:45:00 AM	79	Epidemiology & Animal Health Economics	Adaptation of a simulation model for Foot-and-Mouth Disease (FMD) spread in endemic countries/regions
MON 10:45:00 AM	100	Immunology	Measuring bovine γδ t cell function at the site of Mycobacterium bovis infection
MON 10:45:00 AM	117	Pathobiology of Enteric and Foodborne Pathogens	Lawsonia intracellularis vaccination decreases Salmonella enterica serovar Typhimurium shedding in co-infected pigs
MON 10:45:00 AM	134	Respiratory Diseases	Host gene expression response to experimental BRSV infection
MON 10:45:00 AM	159	Viral Pathogenesis	Specific pathogen-free (SPF) turkey model for emerging reoviral arthritis
MON 10:45:00 AM	194	Immunology	Development of intrauterine vaccination for use in livestock
MON 11:00:00 AM	42	Companion Animals Epidemiology	Recent trends in cat admissions and the effect of the capacity for care program at the Guelph humane society, 2011-2015
MON 11:00:00 AM	57	Ecology and Management of Foodborne Agents	Mapping collateral resistance in four nontyphoidal Salmonella serotypes isolated from chicken carcasses and commercial chicken products
MON 11:00:00 AM	80	Epidemiology & Animal Health Economics	Bioinformatics tools for effective genotypic characterization of carbapenemase-producing Klebsiella pneumoniae
MON 11:00:00 AM	101	Immunology	Cytokine driven monocyte differentiation influences the vitamin D pathway-induced antimicrobial response
MON 11:00:00 AM	118	Pathobiology of Enteric and Foodborne Pathogens	Over-expressed linoleate isomerase gene in Lactobacillus casei and its role against enteric pathogens

CRWAD ORAL PRESENTATIONS BY DAY

MON 11:00:00 AM	135	Respiratory Diseases	Haptoglobin concentrations in cattle either mass-medicated with gamithromycin or sham-treated -- from shipping through sickness and recovery.
MON 11:00:00 AM	160	Viral Pathogenesis	Chicken Anemia Virus CAV in Egyptian broilerSerological survey, clinical signs, pathological parameters, and molecular characterization of the virus.
MON 11:15:00 AM	43	Companion Animals Epidemiology	Pedicle tie as a safe and effective means of ovarian vessel hemostasis in feline ovariohysterectomy
MON 11:15:00 AM	81	Epidemiology & Animal Health Economics	Quantification of vector and host competence and abundance for Japanese Encephalitis Virus: a systematic review of the literature.
MON 11:15:00 AM	119	Pathobiology of Enteric and Foodborne Pathogens	Modulation of poultry gut microbiome with phenolics from berry byproducts
MON 11:15:00 AM	136	Respiratory Diseases	Comparison of leukocyte profile determined by point of care analyzer and manual evaluation in calves inoculated with Mannheimia haemolytica and Bovine Viral Diarrhea Virus.
MON 11:15:00 AM	161	Viral Pathogenesis	Toll-like receptor 3 (TLR3) and influenza pathogenesis in quail
MON 11:30:00 AM	120	Pathobiology of Enteric and Foodborne Pathogens	Characterization of the fecal microbiome from EHEC positive and digital dermatitis negative beef cattle.
MON 11:30:00 AM		Lunch	Lunch
MON 1:00:00 PM	11	Bacterial Pathogenisis	Experimental Staphylococcus aureus mastitis teat dip challenge model
MON 1:15:00 PM	12	Bacterial Pathogenisis	Surface display of Clostridium perfringens alpha toxin on the enterotoxigenic Escherichia coli k88ab vaccine strain
MON 1:15:00 PM	44	Companion Animals Epidemiology - Dan O'Neill - KEYNOTE SPEAKER	Primary-care vet data:the final frontier.
MON 1:15:00 PM	82	Epidemiology & Animal Health Economics - Dan O'Neill - KEYNOTE SPEAKER	Primary-care vet data:the final frontier.
MON 1:15:00 PM	58	Ecology and Management of Foodborne Agents - Dan O'Neill - KEYNOTE SPEAKER	Primary-care vet data:the final frontier.
MON 1:15:00 PM	102	Immunology - Subramaniam Srikumaran - KEYNOTE SPEAKER	Genetic engineering of Disease-Resistant Animals: A Fantasy or Reality?
MON 1:15:00 PM	121	Pathobiology of Enteric and Foodborne Pathogens	Sources and consequences of antibiotic resistance
MON 1:30:00 PM	13	Bacterial Pathogenisis	Dynamics of antibody responses to Lyme disease spirochetes in the context of VlsE-mediated immune evasion

CRWAD ORAL PRESENTATIONS BY DAY

MON 1:30:00 PM	23	Biosafety & Biosecurity	Estimating potential disease spread at an equestrian show in Ontario, Canada using an agent-based network model
MON 1:30:00 PM	162	Viral Pathogenesis	Attenuation of recombinant influenza virus expressing the naturally truncated NS gene from an H3N8 equine influenza virus in mice
MON 1:45:00 PM	14	Bacterial Pathogenisis	Gene expression differences between mastitis-causing Escherichia coli strains grown in planktonic, swimming, and swarming culture conditions
MON 1:45:00 PM	24	Biosafety & Biosecurity	Patient medical records as a reservoir for potential pathogens in a Veterinary Teaching Hospital
MON 1:45:00 PM	163	Viral Pathogenesis	Application of NS1-truncated variant as live attenuated influenza vaccine for early protection and its complementary use with inactivated vaccine in chickens
MON 1:55:00 PM	122	Pathobiology of Enteric and Foodborne Pathogens	Reservoirs of antibiotic-resistant Escherichia coli in production environments: an opportunity for intervention?
MON 2:00:00 PM	15	Bacterial Pathogenisis	Interaction between AI-2 and AI-3 quorum sensing systems in Salmonella Typhimurium
MON 2:00:00 PM	25	Biosafety & Biosecurity	Using microbiome data to calibrate a microbial clock for estimating the postmortem interval in mammals
MON 2:00:00 PM	45	Companion Animals Epidemiology	The case-control design inveterinary sciences: a survey
MON 2:00:00 PM	59	Ecology and Management of Foodborne Agents	The case-control design inveterinary sciences: a survey
MON 2:00:00 PM	83	Epidemiology & Animal Health Economics	The case-control design inveterinary sciences: a survey
MON 2:00:00 PM	103	Immunology	Cross-protective vaccine technology to mitigate respiratory viral diseases in pigs
MON 2:00:00 PM	164	Viral Pathogenesis	Bovine adenoviral vector system for developing effective vaccines against emerging avian influenza viruses
MON 2:15:00 PM	16	Bacterial Pathogenisis	The effect of Mycobacterium avium subsp. paratuberculosis in the development of bovine mastitis caused by Escherichia coli under experimental conditions
MON 2:15:00 PM	26	Biosafety & Biosecurity	Five years of foreign animal disease preparedness training for zoos and aquariums - lessons learned and areas for improvement
MON 2:15:00 PM	46	Companion Animals Epidemiology	Spatial & antimicrobial susceptibility patterns of Staphylococcus from horses presented at a teaching hospital in South Africa

CRWAD ORAL PRESENTATIONS BY DAY

MON 2:15:00 PM	60	Ecology and Management of Foodborne Agents	Carbapenemase-producing Enterobacteriaceae recovered from the environment of a swine farrow-to-finish operation in the United States.
MON 2:15:00 PM	84	Epidemiology & Animal Health Economics	Distribution and diversity of Salmonella in shipments of hatchling poultry, United States, 2013-2015
MON 2:15:00 PM	137	Respiratory Diseases	The upper respiratory tract microbiome and its potential role in canine respiratory infections
MON 2:15:00 PM	165	Viral Pathogenesis	Markers of Apoptosis in different cell lines by Equine Arteritis Virus
MON 2:20:00 PM	123	Pathobiology of Enteric and Foodborne Pathogens	Antibiotics and the search for alternatives: pursuit and paradox
MON 2:30:00 PM	17	Bacterial Pathogenisis	Stress hormones deferentially alter gut microbes over time and affect Salmonella counts in weaned pigs
MON 2:30:00 PM	27	Biosafety & Biosecurity	Development of an interactive online avian influenza preparedness exercise for zoos and aquariums using GIS tools for qualitative risk assessment
MON 2:30:00 PM	47	Companion Animals Epidemiology	An estimate of the number of dogs in US shelters
MON 2:30:00 PM	61	Ecology and Management of Foodborne Agents	Effects of ractopamine and zinc supplementation on antimicrobial resistance of fecal Escherichia coli in finishing cattle
MON 2:30:00 PM	85	Epidemiology & Animal Health Economics	Beef producer survey of the cost to prevent and treat bovine respiratory disease in calves prior to weaning
MON 2:30:00 PM	104	Immunology	PLGA nanoparticle delivery of inactivated swine influenza virus vaccine provides heterologous protection through cell-mediated immunity in pigs
MON 2:30:00 PM	138	Respiratory Diseases	Demonstration of protection against Canine Influenza Virus H3N2 infection following vaccination with an inactivated CIV H3N2 / H3N8 bivalent vaccine
MON 2:30:00 PM	166	Viral Pathogenesis	Porcine reproductive & respiratory syndrome virus takes advantage of host intercellular mitochondria transferring pathway for cell to cell spreading of infection
MON 2:45:00 PM		Break and Table Top Exhibits - Foyer	
MON 3:00:00 PM	18	Bacterial Pathogenisis	20-Hydroxyeicosatetraenoic acid alters vascular endothelial barrier integrity by an oxidative stress-dependent mechanism.
MON 3:00:00 PM	28	Biosafety & Biosecurity - Kathy Havas - KEYNOTE SPEAKER	A biosecurity assessment of U.S. animal production systems

CRWAD ORAL PRESENTATIONS BY DAY

MON 3:00:00 PM	62	Ecology and Management of Foodborne Agents	Zinc and menthol as alternatives to antibiotics: impacts on bacterial resistance in feeder cattle
MON 3:00:00 PM	86	Epidemiology & Animal Health Economics	Analysis of risk factors for an outbreak of bovine respiratory disease in stocker cattle
MON 3:00:00 PM	105	Immunology	Adjuvants and their Mechanisms of Action
MON 3:00:00 PM	124	Pathobiology of Enteric and Foodborne Pathogens	Potential broad spectrum antivirals targeting 3C or 3C-like proteases of picornaviruses, coronaviruses and caliciviruses
MON 3:00:00 PM	139	Respiratory Diseases	The B. bronchiseptica type III secretion system does not negatively affect the protective immunity induced by influenza A virus vaccines
MON 3:00:00 PM	167	Viral Pathogenesis	SAP domain in nsp1-beta of PRRSV correlates with interferon suppression in cells and virulence in pigs
MON 3:15:00 PM	19	Bacterial Pathogenisis	Lactation stage influence on the oxylipid profile of healthy dairy cattle in plasma and milk.
MON 3:15:00 PM	63	Ecology and Management of Foodborne Agents	Dissemination and antibiotic susceptibility patterns of carbapenem resistant Enterobacteriaceae from a municipal wastewater treatment plant
MON 3:15:00 PM	87	Epidemiology & Animal Health Economics	Epidemiology of bovine respiratory disease in pre-weaned dairy calves
MON 3:15:00 PM	140	Respiratory Diseases	Serological prevalence of three H1 phylogenetic clades and two H3 antigenic clusters of influenza A virus in breeding age swine in the United States
MON 3:15:00 PM	168	Viral Pathogenesis	Novel arterivirus proteins and expression mechanism: implication in PRRSV vaccine development
MON 3:25:00 PM	125	Pathobiology of Enteric and Foodborne Pathogens	Emerging antibiotic resistance mechanisms in foodbornepathogen Campylobacter
MON 3:30:00 PM	20	Bacterial Pathogenisis	Serological survey of leptospirosis in pigs from slaughterhouses in Vietnam
MON 3:30:00 PM	64	Ecology and Management of Foodborne Agents	Megarich: a pre-sequencing capture system for enriching and counting resistance genes within metagenomic samples
MON 3:30:00 PM	88	Epidemiology & Animal Health Economics	Impact of bovine leukemia virus on herd level production indicators on US dairy farms
MON 3:30:00 PM	106	Immunology	Intradermal administration of adjuvant PCEP induces innate immune responses at the site of injection in pigs
MON 3:30:00 PM	141	Respiratory Diseases	Evaluation of candidate chimeric influenza hemagglutinin vaccines for induction of broad immunity within the influenza virus H1N1 subtype

CRWAD ORAL PRESENTATIONS BY DAY

MON 3:30:00 PM	169	Viral Pathogenesis	Comparative pathogenesis and genome sequence of recent 1-7-4 PRRSV isolates in weanling age piglets
MON 3:45:00 PM	21	Bacterial Pathogenisis	Chlamydia gallinacea in poultry and cattle of China
MON 3:45:00 PM	29	Biosafety & Biosecurity	Ten years of progress in agrosecurity for concentrated livestock operations and related businesses
MON 3:45:00 PM	65	Ecology and Management of Foodborne Agents	MEGaRES and AmrPlusPlus - A comprehensive database of antimicrobial resistance genes and user-friendly pipeline for analysis of high-throughput sequencing data
MON 3:45:00 PM	89	Epidemiology & Animal Health Economics	Efficacy of bovine herpesvirus 1 vaccination to prevent abortion in cattle: a meta-analysis
MON 3:45:00 PM	107	Immunology	Chemistry and immunobiology of aluminum-containing adjuvants
MON 3:45:00 PM	142	Respiratory Diseases - Suresh Mittal - KEYNOTE SPEAKER	EmergingAvian Influenza Viruses: Their Implications and Control Strategies
MON 3:45:00 PM	170	Viral Pathogenesis	IFN-1 pathway signaling in bovine cells concurrently infected with BVDV and BRSV
MON 3:50:00 PM	126	Pathobiology of Enteric and Foodborne Pathogens	Regulatory mechanisms of beta-lactamase expression in Campylobacter jejuni
MON 4:00:00 PM	22	Bacterial Pathogenisis	Adherence patterns of LA-MRSA ST5 isolates and MRSA ST5 isolates from humans with no swine contact
MON 4:00:00 PM	30	Biosafety & Biosecurity	A field-deployable nucleid acid extraction/PCR system detected bovine leukemia virus proviral DNA in blood with a performance equivalent to a laboratory real-time PCR system
MON 4:00:00 PM	66	Ecology and Management of Foodborne Agents	A proposed analytic framework for determining the impact of an antimicrobial resistance intervention
MON 4:00:00 PM	90	Epidemiology & Animal Health Economics	Lactoferrin reduces mortality in Preweaned Calves with Diarrhea
MON 4:00:00 PM	171	Viral Pathogenesis	Duration of positive viral PCR results following intranasal and injectable multivalent MLV vaccination in naïve calves
MON 4:15:00 PM	31	Biosafety & Biosecurity	Dissemination of antimicrobial resistant enteric bacteria in a zoo environment
MON 4:15:00 PM	67	Ecology and Management of Foodborne Agents	Comparison of the microbiological quality of fresh produce from seasonal farmer's markets and retail grocery stores in Ohio
MON 4:15:00 PM	108	Immunology	Efficacy and safety profile of an alpha-D-glucan nanoparticle based vaccine adjuvant.
MON 4:15:00 PM	143	Respiratory Diseases	Influenza A virus herd-level prevalence and seasonality in Midwestern U.S. pig breeding herds

CRWAD ORAL PRESENTATIONS BY DAY

MON 4:15:00 PM	172	Viral Pathogenesis	Geno typematched NDV vaccines against currently circulating viruses in Indonesia
MON 4:30:00 PM	68	Ecology and Management of Foodborne Agents	Waterfowl and the introduction of foodborne pathogens to agricultural and recreational environments in southern Ontario
MON 4:30:00 PM	109	Immunology	A novel combination adjuvant platform for human and animal vaccines.
MON 4:45:00 PM	69	Ecology and Management of Foodborne Agents	Prevalence and antibiotic resistance profiles of E. coli and Enterococcus species from a sample of wild birds captured on intensive dairy and beef cattle operations
MON 5:00:00 PM		Poster Session II - Grand Ballroom III - 7th Floor	Poster Session II - Grand Ballroom III - 7th Floor
TUES 8:00:00 AM	173	Epidemiology & Animal Health Economics	Spatial autocorrelation and implications for oral fluid-based PRRSV surveillance
TUES 8:00:00 AM	185	Immunology	Johne's Disease-positive and -negative cows exhibit diverse T cell phenotypes in response to in vitro MAP stimulation
TUES 8:00:00 AM	203	Viral Pathogenesis	A novel porcine circovirus distantly related to known circoviruses is associated with porcine dermatitis and nephropathy syndrome and reproductive failure
TUES 8:15:00 AM	174	Epidemiology & Animal Health Economics	An investigation into distribution of Streptococcus suis serotypes in clinical cases & healthy-carrier pigs.
TUES 8:15:00 AM	186	Immunology	Deciphering the cellular immune response in pigs
TUES 8:15:00 AM	204	Viral Pathogenesis	Pathogenesis and infection dynamics of Senecavirus A in pigs
TUES 8:30:00 AM	175	Epidemiology & Animal Health Economics	An investigation of the factors contributing to mortality during an outbreak of Streptococcus suis infection in nursery pigs.
TUES 8:30:00 AM	187	Immunology	Pig leukocyte metabolism - changes associated with stimulation and PRRSV infection.
TUES 8:30:00 AM	197	Pathobiology of Enteric and Foodborne Pathogens	Characterization of A subunit epitopes in enterotoxicity of enterotoxigenic Escherichia coli (ETEC) heat-labile toxin
TUES 8:30:00 AM	205	Viral Pathogenesis	Senecavirus A infection in sows, neonates, and market weight gilts with subsequent protective immunity
TUES 8:45:00 AM	176	Epidemiology & Animal Health Economics	Effect of influenza prevalence in pigs at weaning on transmission, clinical signs and performance after weaning

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TUES 8:45:00 AM	198	Pathobiology of Enteric and Foodborne Pathogens	Escherichia coli from poultry : understanding their zoonotic-risk and development of a vaccine for the control of their infections and carriage in poultry
TUES 8:45:00 AM	206	Viral Pathogenesis	Construction and characterization of a full-length cDNA infectious clone of emerging porcine Senecavirus A
TUES 9:00:00 AM	177	Epidemiology & Animal Health Economics	Knowledge, attitudes and behavioral practices of individuals regarding neglected zoonotic diseases in Addis Ababa, Ethiopia.
TUES 9:00:00 AM	189	Immunology	Campylobacter jejuni strains from Guillain Barre Syndrome patients induce autoimmune peripheral neuropathy via Siglec-1 and IL-4 axes in a mouse model
TUES 9:00:00 AM	199	Pathobiology of Enteric and Foodborne Pathogens	Genetic diversity and antimicrobial resistance of Campylobacter jejuni & Campylobacter coli isolates from chickens
TUES 9:00:00 AM	207	Viral Pathogenesis	Experimental teschovirus encephalomyelitis induced either by Teschovirus A serotype 2 or serotype 11.
TUES 9:15:00 AM	178	Epidemiology & Animal Health Economics	Neglected tropical diseases in Uganda-Impact on food security and public health
TUES 9:15:00 AM	190	Immunology	Immune responses to senecavirus A in pigs
TUES 9:15:00 AM	200	Pathobiology of Enteric and Foodborne Pathogens	Prevalence and antimicrobial resistance patterns of Escherichia coli in raw meat and milk samples in central Oromia, Ethiopia
TUES 9:15:00 AM	208	Viral Pathogenesis	Identification of a divergent strain of Sapelovirus associated with a severe polioencephalomyelitis outbreak in the US
TUES 9:30:00 AM		Break and Table Top Exhibits - Foyer	Break and Table Top Exhibits - Foyer
TUES 10:00:00 AM	179	Epidemiology & Animal Health Economics	Distinguishing case series from cohort studies: do we agree?
TUES 10:00 AM	209	Viral Pathogenesis - Dan Rock KEYNOTE SPEAKER	Challenges for African Swine FeverVaccine Development - " perhaps the end of thebeginning."
TUES 10:00:00 AM	191	Immunology	Non-esterified fatty acids induce proinflammatory macrophage phenotype
TUES 10:00:00 AM	201	Pathobiology of Enteric and Foodborne Pathogens	Extended-spectrum cephalosporin resistance in Escherichia coli from Alberta beef cattle
TUES 10:15:00 AM	180	Epidemiology & Animal Health Economics	Assessing causal interrelationships between health and performance outcomes in feedlot cattle
TUES 10:15:00 AM	192	Immunology	The link between the microbiome and immunological health in the intestines of healthy calves

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TUES 10:15:00 AM	202	Pathobiology of Enteric and Foodborne Pathogens	Antimicrobial resistance patterns of Staphylococcus aureus isolates from cases of bovine mastitis
TUES 10:30:00 AM	181	Epidemiology & Animal Health Economics	Mental wellness in Canadian agricultural producers
TUES 10:30:00 AM	193	Immunology	Neonatal γδ T cell responses to mucosal TB vaccination
TUES 10:45:00 AM	182	Epidemiology & Animal Health Economics	Salmonella monitoring programs in Australian feed mills: A Retrospective analysis
TUES 11:00:00 AM	183	Epidemiology & Animal Health Economics	Prevalence of multi-drug resistant Gram negative bacteria in the backyard poultry flock environment in Washington State
TUES 11:15:00 AM	184	Epidemiology & Animal Health Economics	The effect of dietary flaxseed supplementation on the epidemiology of oviduct leiomyomas in laying hens - a model for uterine fibroids in women
TUES 11:45:00 AM		Business Meeting : Dedication and Graduate Student Competition Award Presentation	Business Meeting : Dedication and Graduate Student Competition Award Presentation

Poster Session I - Sunday 6:30 PM - 8:00 PM - Grandballroom Salon III - 7th Floor Poster Assembly begins at 4 PM Sunday. Please remove your poster by 10:00 AM Monday. Poster Presenters muct be with their competition entry posters for possible judge interviews. Name badges are required.

Bacterial Pathogenesis - Gireesh Rajashekara

P01	Characterization of Salmonella survival in Bedding Sand and Ability to infect Bovine Macrophages	H.E. Pilch; Pathobiological Sciences, University of Wisconsin-Madison, Madison, WI, USA.
P0 2	Alternate vaccination strategies for Johne's disease	E.P. Brenner, S. Sreevatsan; Veterinary Science, University of Minnesota, St. Paul, MN, USA.
P03	Pharmacologic effects of the macrolide antibiotic tulathromycin on Brucella melitensis infection in open and pregnant goats.	S. Olsen [1] , P. Boggiatto [1] , T. Rowan [2] ; [1] National Animal Disease Center, Ames, IA, USA, [2] Global Alliance for Livestock Veterinary Medicine, Edinburgh, UK.
P04	Norepinephrine and cortisol influence Lactobacillus populations in weaned piglets	E. Petrosus [1] , E. Silva [2] , D. Lay, Jr [2] , M. Rostagno [3], S. Eicher [2]; [1] Animal Sciences, Purdue University, West Lafayette, IN, USA, [2] Livestock Behavior Research Unit, USDA-ARS, West Lafayette, IN, USA, [3] Ely Lilly & Co., Indianapolis, IN, USA.
P05	New data about Francisella tularensis disturbance in wild boars and domestic pigs in Ukraine	O. Zlenko, Ms., O. Solodiankin, B. Stegniy, A. Buzun, V. Bolotin, A. Gerilovych; NSC IECVM, Kharkiv, Ukraine.
P06	Medico-veterinary control of Leptospirosis in Ukraine	O. Solodiankin [1] , N. Gopko [2] , S. Protas [3] , B. Stegniy [1] , V. Bolotin [1] , O. Dynaeva [4], A. Gerilovych [1] ; [1] NSC IECVM, Kharkiv, Ukraine, [2] SSESU, Chernivtsi, Ukraine, [3] SSESU, Kiev, Ukraine, KNMU, Kharkiv, Ukraine.
P07	Evaluation of leptospiral protein, LenA as a serological marker for the diagnosis of leptospirosis	B. Beigel [1] , J. Fowler [2] , M. Steinman [3] , E. Erol [3] , A. Verma [1] ; [1] College of Veterinary Medicine, Lincoln Memorial University, Harrogate, TN, USA, [2] School of Mathematics and Science, Lincoln Memorial University, Harrogate, TN, USA, [3]Veterinary Diagnostic Laboratory, University of Kentucky, Lexington, KY, USA.

Poster Session I - Sunday 6:30 PM - 8:00 PM - Grandballroom Salon III - 7th Floor Poster Assembly begins at 4 PM Sunday. Please remove your poster by 10:00 AM Monday. Poster Presenters muct be with their competition entry posters for possible judge interviews. Name badges are required.		
P08	Characterizing the development of the pig tonsillar microbiome from birth to market weight	L.C. Pena Cortes [1] , R.M. LeVeque [2] , J. Funk [3] , T. Marsh [2] , M.H. Mulks [2] ; [1] Facultad de Ciencias Agrarias, Universidad de Pamplona, Pamplona, Colombia, [2] Microbiology and Molecular Genetics, Michigan State University, East Lansing, MI, USA, [3] Large Animal Clinical Science, Michigan State University, East Lansing, MI, USA.
P09	A view into the early development of the pig tonsillar microbiome, the relationship with sow microbiomes and the effect of weaning	L.C. Pena Cortes [1] , R.M. LeVeque[2] , J. Funk [3] , T.L. Marsh [2] , M.H. Mulks [2]; [1] Facultad de Ciencias Agrarias, Universidad de Pamplona, Pamplona, Colombia, [2] Microbiology and Molecular Genetics, Michigan State University, East Lansing, MI, USA, [3] Large Animal Clinical Science, Michigan State University, East Lansing, MI, USA.
Biosafety & Biosecurity - Brandy Burguss		
P10	The use of biological soil amendments of animal origin in organic agriculture and food safety risks	A. Pires [1], M. Jay-Russell [2] ; [1] Population Health and Reproduction, School of Veterinary Medicine, University of California Davis, Davis, CA, USA, [2] Western Center for Food Safety, University of California Davis, Davis, CA, USA.
P11	Evaluation of the ImmunoCard STAT! rapid immunoassay for detecting Cryptosporidium Parvum in calf feces.	C.W. Stilwell, B.A. Burgess, S. Guynn; Virginia-Maryland College of Veterinary Medicine, Blacksburg, VA, USA.
P1 2	A PCR method for rapid and specific detection of toxigenic Microcystis spp. in freshwater based on microcystin synthetase C (mcyC) gene	J. Yuan [1] , H.-J. Kim [2], S. Ensley[1], B. Guo [1] , P. Imerman[1] , C. Filstrup [3] , K.-J. Yoon [1] ; [1] Department of Veterinary Diagnostic and Production Animal Medicine, College of Veterinary Medicine, Iowa State University, Ames, IA, USA, [2] Department of Food Science and Human Nutrition, College of Agriculture and Life Sciences, Iowa State University, Ames, IA, USA, [3] Department of Ecology, Evolution and Organismal Biology, College of Agriculture and Life Sciences, Iowa State University, Ames, IA, USA.
P13	Simultaneous detection of SARS-CoV and MERS-CoV using primers and probes targeting conserved spike S 2 region of the related coronaviruses with human and bat origin	J. Noh, D. Jeong, S.-W. Yoon, D.-J. Kim, M.-S. Lee, J.-H. Kim, S.-K. Park, H. Kim; Korea Research Institute of Bioscience and Biotechnology, Daejeon, Korea, Republic of.

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Companion Animal - Audrey Ruple & Laura Hungerford		
P14	Current status of brucella infection among livestock in Egypt	H.I. Hosein [1], A. Mahrous [2] ; [1] Infectious Diseases, Beni Suef University, Egypt, Beni Suef, Egypt, [2] Zoonoses, GOVS, Giza, Egypt, cairo, Egypt.
P15	Prevalence estimate of periodontal disease (PD) in a population of dogs in commercial breeding facilities in Indiana	A.E. Bauer [1] , J. Stella [2] , M. Hurt [1] , C.C. Croney[1] ; [1] Comparative Pathobiology, Purdue University, West Lafayette, IN, USA, [2] USDA-APHIS, West Lafayette, IN, USA.
P16	Sensitivity and specificity of some serological tests used for diagnosis of bovine brucellosis in Egypt on bacteriological and molecular basis	H.I. Hosein [1] , A.S. Menshawy [1] , H.A. Hussein[2] ; [1] Infectious Diseases, Beni Suef University, Egypt, Beni Suef, Egypt, [2] Department of Animal Reproduction and Artificial Insemination, National Research centre, Dokki, Giza, cairo, Egypt.
P17	Comparison of non-β-lactam resistances in Staphylococcus pseudintermedius isolates with and without the mecA gene in canine patients	A. Trey, W.J. Love, M. Jacob, C. Lanzas; Population Health and Pathobiology, North Carolina State University College of Veterinary Medicine, Raleigh, NC, USA.
Epidemiology & Animal Health Economics - Ashley Hill		
P18	Extended-spectrum cephalosporin resistant Escherichia coli in Canadian New Brunswick dairy colostrum harbors blaCMY- 2 and blaTEM genetic resistant determinants	B.B. AWOSILE, M. Saab, G. Keefe, J. Rodriguez-Lecompte, J. McClure, L. Heider; HEALTH MANAGEMENT, ATLANTIC VETERINARY COLLEGE, UNIVERSITY OF PRINCE EDWARD ISLAND, CHARLOTTETOWN, PE, Canada.
P19	Sentinel turkey farm antimicrobial resistance surveillance in Canada for 2013 and 2014	S. Gow [1] , A. Agunos [2] , D. Leger [2] , A. Deckert [2] , F. Pollari [2] , L. Flockhart [2] , D. Daignault [3] , R. Irwin [2] , R. Reid Smith [2] ; [1]Public Health Agency of Canada, Saskatoon, SK, Canada, [2] Public Health Agency of Canada, Guelph, ON, Canada, [3] Public Health Agency of Canada, St-Hyacinthe, QC, Canada.
P 20	The diversity and abundance of bacterial taxa and antimicrobial resistance factors in cecum shotgun metagenomes of chicken treated with anticoccidia and growth promoters	E. Amene [1], R. Singer [2] , D. Döpfer [1] ; [1]Medical Sciences, University of Wisconsin-Madison, Madison, WI, USA, [2] College of Veterinary Medicine, University of Minnesota, St Paul, MN, USA.

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P 21	A descriptive epidemiologic study of antimicrobial resistance of Staphylococcus isolated from equine samples submitted to a diagnostic laboratory	R. Adams [1], J. Smith [2], C. Carter [2], A. Odoi [1]; [1]Biomedical and Diagnostic Sciences, University of Tennessee, Knoxville, TN, USA, [2] Veterinary Diagnostic Laboratory, University of Kentucky, Lexington, KY, USA.
P 2 2	Extended-spectrum cephalosporin, carbapenem, and fluoroquinolone resistant coliform bacteria present on companion animal, equine, and livestock environmental surfaces	R.J. Adams [1], S. Kim [1], D. Mollenkopf [1], D. Mathys[1], J. Daniels[2], T. Wittum [1]; [1]Dept. of Veterinary Preventive Medicine, The Ohio State University, Columbus, OH, USA, [2] Dept. of Veterinary Clinical Sciences, The Ohio State University, Columbus, OH, USA.
P 23	Whole-genome sequencing of drug-resistant Salmonella enterica isolated from dairy cattle and humans in ny and wa states reveals source and geographic associations	L. Carroll [1], M. Wiedmann [1], H. Bakker [2], J. Siler [3], M. Davis , W. Sischo , T. Besser , L. Warnick[5], R. Pereira [6]; [1] Department of Food Science, Cornell University, Ithaca, NY, USA, [2] Department of Animal and Food Sciences, Texas Tech University, Lubbock, TX, USA, [3] Cornell University, Ithaca, NY, USA, [4]Paul G. Allen School for Global Animal Health, Washington State University, Pullman, WA, USA, [5] Cornell University COllege of Veterinary Medicine, Ithaca, NY, USA, [6] University of California Davis, College of Veterinary Medicine, Davis, CA, USA.
P 24	Animal welfare surveillance on the prevalence of slaughtered pigs with abnormal tail biting in Korea	Y. Lee, K. Min, E. Cho, J. Han; Kangwon National University, Chuncheon, Korea, Republic of.
P 25	Identification of Helicobacter suis from porcine pyloric mucosa by PCR assay and histological examination in Korea	J. Lee, S. Lee, J. Han; Kangwon National University, Chuncheon, Korea, Republic of.
P 26	Preliminary study on factors associated with transmissible of PRRSV in Eastern Thailand	W. Saenglub [1], C. Lekcharoensuk [2], P. Lekcharoensuk [1]; [1] Veterinary Microbiology, Kasetsart University, Bangkok, Thailand, [2] Companion Animal Clinical Sciences, Kasetsart University, Bangkok, Thailand.
P 27	The current knowledge on the pathogenesis, transmission, and prevention of porcine epidemic diarrhea virus (PEDv): A scoping review	A.M. Perri, Z. Poljak, T.L. O'Sullivan; Population Medicine, University of Guelph, Guelph, ON, Canada.

Poster Session I - Sunday 6:30 PM - 8:00 PM - Grandballroom Salon III - 7th Floor Poster Assembly begins at 4 PM Sunday. Please remove your poster by 10:00 AM Monday. Poster Presenters muct be with their competition entry posters for possible judge interviews. Name badges are required.		
P 28	Evaluating the direct, indirect, and total efficacy of a Streptococcus suis autogenous vaccine in nursery piglets &lt!--EndFragment--&gt	D.C. Hopkins, Z. Poljak, V. Farzan, R. Friendship; Population Medicine, University of Guelph, Guelph, ON, Canada.
P 29	Proof of concept: PRRSV IgM/IgA ELISA detects infection in the face of circulating maternal IgG antibody	M. Rotolo [1], J. Ji [2], L. Gimenez-Lirola [3], R. Magtoto [3], C. Wang [2], D. Baum [3], M. Hoogland , R. Main[3], J. Zimmerman [1]; [1] Veterinary Diagnostic and Production Animal Medicine, Iowa State University, Ames, IA, USA, [2] Statistics Department, Iowa State University, Ames, IA, USA, [3] Veterinary Diagnostic Laboratory, Iowa State University, Ames, IA, USA, [4] Iowa State University, Ames, IA, USA.
P30	Identification of epidemiologically relevant SNPs in the Mycobacterium avium ssp. paratuberculosis genome	N.M. Herman [1], F. Shoyama[2], S. Wells [2], S. Sreevatsan [2]; [1] Bioinformatics and Computational Biology, University of Minnesota, Rochester, MN, USA, [2] Veterinary Population Medicine, University of Minnesota, Saint Paul, MN, USA.
P31	Histological evaluation of biopsies of Digital Dermatitis lesions from beef cattle	M.J. Kulow, K. Anklam, D. Döpfer; University of Wisconsin School of Veterinary Medicine, Madison, WI, USA.
P32	Factors affecting the national market price of beef feeder cattle in the United States	M. Wang, L.G. Schneider, D.R. Smith; College of Veterinary Medicine, Mississippi State University, Starkville, MS, USA.
P33	Modelling the dynamics of carcass condemnation in cattle slaughter plants in California using climate data	S. Amirpour Haredasht, B. Martínez-López; Medicine and Epidemiology, UC Davis, Davis, CA, USA.
P34	Leptospirosis in the tri-state area of Tennessee, Virginia, and Kentucky	C.C. Smola, K. Murphy, B. Ervin, R. Goss, V. Shamblen, E. Sears, J. Roberson, P. Nadar, A. Verma; College of Veterinary Medicine, Lincoln Memorial University, Harrogate, TN, USA.
P35	Salmonella enterica prevalence in the Ohio State University veterinary medical center environment	A. Albers [1], D. Mathys [1], D. Mollenkopf [1], J. Daniels [2], T. Wittum [1]; [1] Department of Veterinary Preventative Medicine, The Ohio State University, Columbus, OH, USA, [2] Department of Veterinary Clinical Sciences, The Ohio State University, Columbus, OH, USA.

Poster Session I - Sunday 6:30 PM - 8:00 PM - Grandballroom Salon III - 7th Floor Poster Assembly begins at 4 PM Sunday. Please remove your poster by 10:00 AM Monday. Poster Presenters muct be with their competition entry posters for possible judge interviews. Name badges are required.		
P36	An assessment of potential factors promoting the spread of peste des petits ruminants in East Africa	K.S. Spiegel [1], K. Havas [2], C. Brown [1], F. Torres [1]; [1]University of Georgia, Athens, GA, USA, [1] Foreign Animal Disease Diagnostics Lab, Orient Point, NY, USA.
P37	Evaluation of smectite as medicine against porcine colibacillosis caused by ETEC K88 through rat model	E. Cho, K. Min, Y. Lee, J. Han; Kangwon National University, Chuncheon, Korea, Republic of.
Pathobiology of Enteric and Foodborne Pathogens - Weiping Zhang		
P38	Evaluation of bile salt hydrolase inhibitor as novel alternative to antibiotic growth promoters in chickens	W. GENG [1], S.A. Joyce [2], C.G. Gahan [3], J. Lin[1]; [1] Animal Science, The University of Tennessee, Knoxville, TN, USA, [2] Alimentary Pharmabiotic Centre and Schools of Medicine, University College Cork, Cork, Ireland, [3]Department of Microbiology; School of Pharmacy, University College Cork, Cork, Ireland.
P39	Structural and functional analysis of the bile salt hydrolase from Lactobacillus salivarius	W. GENG [1], F. Xu [2], X. Hu [3], J. Lin [1]; [1] Animal Science, The University of Tennessee, Knoxville, TN, USA, [2] Institute of Animal Science and Veterinary Medicine, Beijing Academy of Agriculture and Forestry Sciences, Beijing, China, [3] Physiology and Biophysics, School of Life Sciences, Fudan University, Shanghai, China.
P40	Genotypic and phenotypic characterization of clinical isolates of Salmonella Typhimurium isolated from systemic and non-systemic sites from human patients in Brazil	P.N. Panzenhagen [1], C.A. Conte Junior [2], D.P. Rodrigues [3], D.H. Shah [1]; [1] Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA, USA, [2] Department of Food Technology, Federal Fluminense University, Niterói, RJ, Brazil, [3] National Reference Laboratory for Diagnosis of Enteric Bacteria, Oswaldo Cruz Institute, Niterói, RJ, Brazil.
P41	Extended-spectrum ß-lactamases producing Salmonella Kentucky and Salmonella Typhimurium isolated from the US poultry	N.C. Paul, D.H. Shah; Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA, USA.

Poster Session I - Sunday 6:30 PM - 8:00 PM - Grandballroom Salon III - 7th Floor Poster Assembly begins at 4 PM Sunday. Please remove your poster by 10:00 AM Monday. Poster Presenters muct be with their competition entry posters for possible judge interviews. Name badges are required.		
P42	Escherichia coli isolates from healthy poultry feces: their potential risk to poultry and human health	A. Van Goor [1], Z.R. Stromberg [1] , J.R. Johnson[2] , J.M. Fairbrother [3] , R. Curtiss,[4] M. Mellata [1] ; [1] Food Science and Human Nutrition, Iowa State University, Ames, IA, USA, [2] Veterans Affairs Medical Center and University of Minnesota, Minneapolis, MN, USA, [3] [3] OIE Reference Laboratory for Escherichia coli (EcL), Faculty of Veterinary Medicine, Université de Montréal, Montreal, QC, Canada, [4]Infectious Diseases and Pathology, University of Florida, Gainesville, FL, USA
P43	Quantification of the porcine epidemic diarrhea virus with a colorimetric assay	P. Singh [1] , J. Karsky [1], E. Nelson [2] , S. Ramamoorthy [1] ; [1]Vet. Microbiological Sciences, N. Dakota State Univversity, Fargo, ND, USA, [2] Department of Veterinary and Biomedical Sciences, S. Dakota State Univversity, Brookings, SD, USA.
P44	Discovery of novel narrow spectrum small molecule growth inhibitors for avian pathogenic E. coli	D. Kathayat; The Ohio State University, Wooster, OH, USA.
P45	BALB/c and C57BL/6 mice given Campylobacter jejuni displayed evidence of Guillain-Barré syndrome autoimmunity, with varied immune responses and disease outcomes	J.M. Brudvig, M.M. Cluett, J.A. Bell, L.S. Mansfield; Large Animal Clinical Sciences, Michigan State University, East Lansing, MI, USA.

Poster Session II - Monday 5:00 PM - 6:30 PM - Grandballroom Salon III - 7th Floor Poster Assembly begins at 12:00 PM Monday. Please remove your poster by 6:30 PM Monday. Poster Presenters muct be with their competition entry posters for possible judge interviews. Name badge are required.		
Ecology and Management of Foodborne Agents		
P46	Changes in the prevalence of antimicrobial resistance through a vertically integrated veal calf production system	H. Hutchinson, S. Finney, L. Muñoz-Vargas, S. Feicht, M. Masterson, G. Habing; The Ohio State University, Columbus, OH, USA.
P47	Distribution of the pco operon among swine Escherichia coli from a controlled feeding trial	G. Chalmers[1], H.M. Scott[2], K.N. Norman[2], K. Rozas[2], J. Vinasco[2], R. Pugh[2], R. Amachawadi[3], T.G. Nagaraja[3], M.D. Tokach[4], J. Feldpausch[4], P. Boerlin[1]; [1]Department of Pathobiology, Ontario Veterinary College, University of Guelph, Guelph, ON, Canada, [2]Department of Veterinary Pathobiology, College of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, TX, USA, [3]Department of Diagnostic Medicine/Pathobiology, Kansas State University, Manhattan, KS, USA, [4]Department of Animal Sciences & Industry, Kansas State University, Manhattan, KS, USA.
P48	Antimicrobial resistance relationships in Escherichia coli modeled with Markov random fields	W.J. Love[1], K.A. Zawack[2], J.G. Booth[2], Y.T. Gröhn[3], C. Lanzas[1]; [1]Population Health & Pathobiology, North Carolina State University, Raleigh, NC, USA, [2]Biological Statistics & Computational Biology, Cornell University, Ithaca, NY, USA, [3]Population Medicine and Diagnostic Sciences, Cornell University, Ithaca, NY, USA.
P49	Viability of bacteria harboring antimicrobial resistance genes in feedyard dust	S. Gonzalez[1], K.N. Norman[1], H.M. Scott[1], B.W. Auvermann[2], J. Jennings[2], B. Pinchak[3], K.D. Casey[2]; [1]Texas A&M University, College Station, TX, USA, [2]Texas A&M AgriLife Research, Amarillo, TX, USA, [3]Texas A&M AgriLife Research, Vernon, TX, USA.

P50	Molecular characterization of staphylococci isolated from retail mushrooms	M.H. Alharpi, M.K. Fakhr; Dept of Biological Science, The University of Tulsa, Tulsa, OK, USA.
P51	Isolation of antibiotic resistant bacteria from the inside and outside of broiler-breeder eggs	J. LeJeune[1], J. Schrock[1], E. Parker[1], G. Ozbey[2], Z. Su[3], S.V. Grooters4; [1]The Ohio State University, Wooster, OH, USA, [2]Firat University, Elazig, Turkey, [3]Xinjiang Agricultural University, Urumqi, China, 4The Ohio State University, Columbus, OH, USA.
P52	Salmonella and Extended-spectrum cephalosporin resistant Enterobacteriaceae from broiler transport cages and fresh retail chicken	S. Feicht, B. De Wolf, D.F. Mollenkopf, J. Cenera, C. King, T.E. Wittum; Veterinary Preventive Medicine, Ohio State University College of Veterinary Medicine, Columbus, OH, USA.
Immunology - Renukaradhya Gourapura		
P53	Evaluation of immunodominant B- and T-cell epitopes as inducers of protective immunity against porcine reproductive and respiratory syndrome virus	M.H.V. Fernandes[1], F. Okda[1], L.R. Joshi[1], K.S. Hain[1], E.A. Nelson[1], J. Christopher-Hennings[1], F.A. Osorio[2], H. Vu[2], D.G. Diel[1]; 1Veterinary and Biomedical Sciences, South Dakota State University, Brookings, SD, USA, [2]School of Veterinary and Biomedical Sciences, University of Nebraska-Lincoln, Lincoln, NE, USA.
P54	Leptospirosis vaccination in cattle induces IL-17	J. Wilson-Welder, D. Alt; Infectious Bacterial Disease of Livestock, National Animal Disease Center, ARS-USDA, Ames, IA, USA.
P55	Polyanhydride nanoparticle based vaccine against swine influenza virus in pigs	S. Dhakal[1], J. Goodman[2], K. Bondra[1], Y. Shaan Lakshmanappa[1], J. Hiremath1, D.L. Shyu[1], K. Ouyang[1], K.I. Kang[1], B. Binjawadagi[1], S. Krakowka[3], C.W. Lee[1], B. Narasimhan[2], R.J. Gourapura[1]; [1]Food Animal Health Research Program, Department of Veterinary Preventive Medicine, The Ohio State University, Wooster, OH, USA,[2]Department of Chemical and Biological Engineering, Iowa State University, Ames, IA, USA,[3]Department of Veterinary Biosciences, The Ohio State University, Columbus, OH, USA.

P56	Development of new immune reagents for swine health, vaccine and disease studies.	J. Lunney[1], M. Bailey[2], J. Manirarora1, G. Renukaradhya[3], S. Kenney[3], J. LaBresh[4], Y. Sang[5], O. Francis[2], L. Wooldridge[2]; [1]USDA ARS BARC APDL, Beltsville, MD, USA, [2]University of Bristol, Bristol, UK, [3]The Ohio State University, Wooster, OH, USA, [4]Kingfisher Biotech, Inc., St. Paul, MN, USA, [5]Tennessee State University,
P57	Recombinant attenuated Salmonella vaccine strains with broad protection of colibacillosis in chickens	Z. Stromberg[1], A. Van Goor[1], R. Curtiss, 3rd[2], M. Mellata[1]; [1]Food Sciences and Human Nutrition, Iowa State University, Ames, IA, USA, [2]Infectious Diseases and Pathology, University of Florida, Gainesville, FL, USA.
P58	Identification of branched chain α-ketoacid dehydrogenase kinase as a novel autoantigen in the induction of autoimmune myocarditis through the generation of autoreactive T cells in A/J mice	B. Krishnan[1], C. Massilamany[1], R.H. Basavalingappa[1], G. Kang[2], Q. Li[2], D. Steffen[1], J. Reddy[1] 1School of Veterinary Medicine and Biomedical Sciences, University of Nebraska-Lincoln, Lincoln, NE, USA, [2]Nebraska Center for Virology, University of Nebraska-Lincoln, Lincoln, NE, USA.
P59	Association of Serum Vitamin D (25(OH)D levels with PPD status in cattle naturally exposed to Mycobacterium bovis	S. López Constantino, Á. García Barragán, E. Alfonseca Silva, J.A. Gutiérrez Pabello; Laboratorio de Investigación en Tuberculosis Bovina, Departamento de Microbiología e Inmunología, Facultad de Medicina Veterinaría y Zootecnia, Universidad Nacional Autónoma de México, Ciudad de México, Mexico.
P60	Cell-mediated immune response to MLV BRD vaccination in Holstein heifers fed an immunomodulatory supplement	D.J. Hurley[1], M. Adkins[1], C. Barber[1], N.A. Norton[2], S.C. Nickerson[3], L.O. Ely[3], F.M. Kautz[3], D.J. McLean[4] J.D. Chapman[4], A.D. Rowson[4]; [1]Food Animal Health and Management, Pop Health, University of Georgia, Athens, GA, USA, [2]Large Animal Medicine, University of Georgia, Athens, GA, USA, [3]Department of Animal and Dairy Sciences, University of Georgia, Athens, GA, USA, [4]Phibro Animal Health Corporation, Quincy, IL, USA.

P61	The use of IgG(t) as a diagnostic tool in foals with naturally acquired r hodococcus equi pneumonia. f. cesar1, s. paudel1*, p. marsh2, p. morresey3, b. barr3, d. horohov1. 1dept. of veterinary sciences, maxwell h. gluck equine research center, university of kentucky, lexington, ky. 2equine medical associates, lexington, ky. 3rood and riddle equine hospital, lexington, ky.	S. Paudel; Veterinary Science, University of Kentucky, Lexington, KY, USA.
P62	The effect of dietary neonicotinoid supplementation on innate and adaptive immune responses to PRRSV infection	J.K. Hernandez[1], B. Leyshon[2], E.E. Ryder[3], R.W. Johnson[1], A.J. Steelman[1]; [1]Animal Sciences, University of Illinois Urbana-Champaign, Urbana, IL, USA, [2]Division of Nutritional Sciences, University of Illinois Urbana-Champaign, Urbana, IL, USA,[3]Neuroscience Program, University of Illinois Urbana-Champaign, Urbana, IL, USA.
P63	CpG oligodeoxynucleotide motifs from Salmonella genome stimulate Interleukin 1-β and nitric oxide production in avian macrophages	A. Sanjaya, J.R. Elder, D.H. Shah; Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA, USA.
P64	Will Eurasian avian-like H1N1 swine influenza jump to humans and should we be worried?	M. Parrillo; Institute for Immunology and Informatics at the University of Rhode Island, Providence, RI, USA.
P65	Potential use of G-CSF for protection against Streptococcus suis infection in swine	S.L. Brockmeier, C.L. Loving, M.E. Kehrli, K.C. Eberle, S.J. Hau, K.T. Mou; Virus and Prion Research Unit, National Animal Disease Center, Ames, IA, USA.
P66	Expression of toll-like receptors and inflammatory cytokines in gut-associated lymphoid tissues in pigs subjected to cross-fostering.	N. Maradiaga, M. Zeineldin, J. Lowe, B. Aldridge; Veterinary Clinical Medicine, University of Illinois art Urbana-Champaign, Champaign, IL, USA.

P67	Macrophage apoptosis induction by proteins and lipids of Mycobacterium bovis.	I.N. Jiménez Vázquez[1], A. Maciel Rivera[1], E. Alfonseca Silva[1], A. Benítez Guzmán[2], H. Esquivel Solís[3], C.I. Espitia Pinzón[4], C. Parada Colín4, L.A. Arriaga Pizano[5], J.A. Gutiérrez Pabello[1]; [1]Laboratorio de Investigación en Brucelosis y Tuberculosis Bovina, Universidad Nacional Autonoma de Mexico, Mexico, Mexico, [2]Laboratorio de Inmunofisiología y Proteómica, Universidad Nacional Autonoma de Mexico, Mexico, Mexico, [3]Centro de Investigación y Asistencia en Tecnología y Diseño del Estado de Jalisco, Jalisco, Mexico, [4]Instituto de investigaciones Biomédicas, Universidad Nacional Autonoma de Mexico, Mexico, Mexico, [5]Unidad de Investigación Médica en Inmunoquímica, Instituto Mexicano del Seguro Social, Mexico, Mexico.
P68	Novel adjuvant for Porcine Epidemic Diarrhea virus vaccine utilizing poly amino Acid/Squalene nanocomplex	M. Yeom[1], W. Na[1], A. Kang[1], H. Yuk[1], J.-W. Lim[2], H.-O. Kim[2], S. Haam[2], D. Song1; [1]pharmacy, Korea university, Sejong, Korea, Republic of, [2]Yonsei university, Seoul, Korea, Republic of.
P69	Transcriptomic analysis of the stress response to weaning at housing in bovine leukocytes using RNA-seq technology	B. Earley[1], A. O'Loughlin[2], M. McGee[3]; [1]Animal and Bioscience, Teagasc, Dunsany, Ireland, [2]Animal and Bioscience, Teagasc, Grange, Dunsany, Co. Meath, Ireland, [3]Livestock Systems, Teagasc, Grange, Dunsany, Co. Meath, Ireland.
P70	Immune related transcriptional responses to colostrum feeding in neonatal dairy calves	A. Dunn[1], K. Keogh[2], S. Waters[2], M. McGee[3], M. Welsh[4], S. Morrison[1], B. Earley[2]; [1]Sustainable Livestock Systems, AFBI, Belfast, UK, [2]Animal and Bioscience, Teagasc, Grange, Dunsany, Co. Meath, Ireland, [3]Livestock Systems, Teagasc, Grange, Dunsany, Co. Meath, Ireland, [4]SiSaf, Belfast, UK.
P71	Serum antibody response to inactivated EU-typed PRRS vaccination in Korea by IFA	K. Min, Y. Lee, E. Cho, J. Han; Kangwon National University, Chuncheon, Korea, Republic of.
Respiratory - Amelia Woolums		
P72	Establishment of marc-145 cell lines expressing nonstructural protein (nsp) 1, nsp1-alpha, and nsp1-beta of porcine reproductive and respiratory syndrome virus	W. Liang, H. Ke, J. Ma, Q. Zhang; University of Illionis at Urbana-Champaign, Urbana, IL, USA.

P73	Genetic diversity of porcine reproductive and respiratory syndrome virus field isolates in Korea during 2015-2016	J. Yu, I.-O. Ouh, H. Kang, S.-M. Song, I.-S. Cho, S.-H. Cha; Viral Disease Division, Animal and Plant Quarantine Agency, Gimcheon, Korea, Republic of.
P74	Seroprevalence of porcine reproductive and respiratory syndrome virus (PRSSV) in an industrial pig production in Ukraine in 2013-2015	D. Masiuk[1], S. Koliada[1], A. Kokarev[1], N. Syityuk[2], P. Gavrilin[1]; [1]Research Center for Biosafety and environmental control resources AIC, Dnepropetrovsk State Agrarian and Economic University, Dnepropetrovsk, Ukraine, [2]Institute of Veterinary Medicine of Ukraine NAAS, Kiev, Ukraine.
P75	Characterization of porcine respiratory primary epithelial cells: differential replication of influenza virus types	C. Sreenivasan[1], M. Thomas[2], L. Antony[3], D. Francis[2], F. Li[4], R.S. Kaushik[5]; [1]Dept. of Biology & Microbiology/BioSNTR, South Dakota State University, Brookings, SD, USA, [2]Dept. of Veterinary and Biomedical Sciences, South Dakota State University, Brookings, SD, USA, [3]Dept. of Biology & Microbiology, South Dakota State University, Brookings, SD, USA, [4]Depts. of Biology and Microbiology/Veterinary and Biomedical Science/BioSNTR, South Dakota State University, Brookings, SD, USA, [5]Depts. of Biology and Microbiology/Veterinary and Biomedical Science, South Dakota State University, Brookings, SD,
P76	Demonstration of protection against Canine Influenza Virus H3N8 infection following vaccination with an inactivated CIV H3N2 / H3N8 bivalent vaccine	T. Davis; Merck Animal Health, Elkhorn, NE, USA.
P77	Identification of bovine respiratory disease causative bacteria using a novel 16S rRNA gene amplicon sequencing assay	D. Johnston[1], M. McCabe[1], P. Cormican[1], S. Waters[1], D. Kenny[1], A.P. Kelly[2], M. McGee[3], B. Earley[1]; [1]Animal and Bioscience, Teagasc, Grange, Dunsany, Co. Meath, Ireland, [2]UCD, Dublin, Ireland, [3]Livestock Systems, Teagasc, Grange, Dunsany, Co. Meath, Ireland.
Vector - Borne and Parasitic Diseases - Roman Ganta/ Jodi McGill		

P78	Genetic characterization of Theileria orientalis from cattle in the Republic of Korea	K.-S. Choi[1], J.-S. Chae[2], J. Park[3], B.-K. Park[4], H.-C. Kim[5]; [1]Horse/Companion and Wild Animal, Kyungpook National University, Sangju, Korea, Republic of, [2]Seoul National University, Seoul, Korea, Republic of, [3]Chonbuk National University, Iksan, Korea, Republic of, [4]Chungnam National University, Daejeon, Korea, Republic of, [5]Kangwon National University, Chuncheon, Korea, Republic of Korea
Viral Pathogenesis - Kyoung-Jin Yoon		
P79	Pathogenic and genomic characteristics involved in porcine alveolar macrophage passages of an attenuated PRRSV nsp2 DEL strain CA-2-P100	S.-C. Lee[1], S. Lee[2], H.-W. Choi[1], I.-J. Yoon[1], S.-Y. Kang3, C. Lee[2]; [1]Choongang Vaccine Laboratory, Daejeon, Korea, Republic of, [2]Kyungpook National University, Daegu, Korea, Republic of, [3]Chungbuk National University, Cheongju, Korea, Republic of.
P80	Development of antibody reagents and assays for Senecavirus A serodiagnosis	S. Lawson, A. Singrey, L. Joshi, J. Leat, J. Nelson, D.G. Diel, J. Christopher-Hennings, E.A. Nelson; Veterinary & Biomedical Sciences, South Dakota State University, Brookings, SD, USA.
P81	Optimization of a double immunofluorescent assay for the detection of infectious bronchitis (IBV) viral nuclear antigen within avian macrophages	S. Nazir[1], A. Amarasinghe[2], M. Abdul-Cader[2], G.M. Keil[3], J.P. Teifke[3], M. Abdul-Careem[2]; [1]University of Calgary, Calgary, AB, Canada, [2]Faculty of Veterinary Medicine, University of Calgary, Calgary, AB, Canada, [3]Federal Research Institute for Animal Health, Greifswald-Insel Riems, Germany.
P82	Evaluation of in vitro biological role of ectodomain of the influenza virus matrix protein 2 (M2e) specific antibodies	M. Elaish, J.M. Ngunjiri, H. Jang, C.-W. Lee; Food Animal Health Research Program, Ohio Agricultural Research and Development Center., The Ohio State University, Wooster, OH, USA.
P83	Isolation of hepatitis E virus genotype 4 from patients with acute cryptogenic hepatitis in Korea	B. Park, H.-S. Ahn, S.-H. Han, Y.-H. Kim, J.-B. Lee, S.-Y. Park, C.-S. Song, S.-W. Lee, I.-S. Choi*; Department of Infectious Disease, College of Veterinary Medicine, Konkuk University, Seoul, Korea, Republic of.
P84	Detection of hepatitis E virus from guanaco (Lama guanicoe) in Korea	B. Park, H.-S. Ahn, S.-H. Han, Y.-H. Kim, J.-B. Lee, S.-Y. Park, C.-S. Song, S.-W. Lee, I.-S. Choi*; Department of Infectious Disease, College of Veterinary Medicine, Konkuk University, Seoul, Korea, Republic of.
P85	Expression of GP5 and M protein from Equine Arteritis Virus in mammalian cells and its relation with apoptosis	G.E. Metz, M.M. Abeya, M.S. Serena, C.J. Panei, M.L. Susevich, M.G. Echeverria; Virologia, Universidad Nacional de La Plata, La Plata, Argentina.

P86	Modulation of NF-kB activity for innate immune evasion by nsp1 of PEDV	Q. Zhang, J. Ma, D. Yoo; Department of Pathobiology, University of Illinois at Urbana-Champaign, Urbana, IL, USA.
P87	PRRSV nsp5 downregulates expression of antiviral genes by suppressing phosphorylation of STAT2	J. Ma, Q. Zhang, H. Ke, W. Liang, C. Kim, D. Yoo; Department of Pathobiology, University of Illinois at Urbana-Champaign, Urbana, IL, USA.
P88	Protective efficacy of NS-1 truncated live attenuated influenza vaccine combined with or without M2e subunit vaccine against heterologous and heterosubtypic challenges	A. Ghorbani, J.M. Ngunjiri, H. Jang, M. Elaish, C.-W. Lee; Food Animal Health Research Program, Ohio Agricultural Research and Development Center, The Ohio State University, Wooster, OH, USA.
P89	Modulation of programmed cell death pathway in cats with feline infectious peritonitis (FIP)	E.A. Anis[1], S. Kania[2], M. Ilha[1], I. Hawkins[1], M.W. Woldemeskel[1], M. Kennedy[2], R. Wilkes[1]; [1]University of Georgia, Tifton, GA, USA, [2]University of Tennessee, Knoxville, TN, USA.
P90	Nationwide Serological surveillance of FMDV antibodies in South Korea during 2014~2016	M.-Y. PARK, S. Park, C. Kim, D. Chae, S. Im, H. Pyo, D. Tark, S. Wee; Foot and mouth disease division, Animal and Plant Quarantine Agency, Gimcheon, Korea, Republic of.
P91	Dissection of complex molecular interactions between important animal nidoviruses and the host	L.J. Sánchez Mendoza[1], C.A. Valle Tejadav, C. Provost1, C.A. Gagnon[1], F. Beaudry[2], L.G. Abrahamyan[1]; [1]Swine and Poultry Infectious Diseases Research Centre (CRIPA), Faculty of Veterinary Medicine, Université de Montréal, Saint-Hyacinthe, QC, Canada, [2]Department of Veterinary Biomedicine, Faculty of Veterinary Medicine, Université de Montréal, Saint-Hyacinthe, QC, Canada.
P92	Humoral immune ontogeny in weaned pigs following experimental porcine epidemic diarrhea virus (PEDV) infection-reinfection	M. Bhandari[1], H. Hoang[1], D. Sun[1], K. Shi[2], L. Bower[1], D. Madson[1], D. Magstadt[1], P. Arruda[1], D. Yoo[2], K. Yoon[1]; [1]Vet Micro and Prventiv Med, Iowa State University, Ames, IA, USA, [2]Dept. of Pathobiology, University of Illinois at Urbana-Champaign, Urbana, IL, USA.

Bacterial Pathogenesis
Avenue Ballroom - 4th Floor
Section Leader : Gireesh Rajashekara

TIME	NO	TITLE	Author Block
MONDAY 8:00	1	Methods to detect and quantify invasion of eukaryotic cells by obligate intracellular bacteria Lawsonia intracellularis	H.L. Wilson, M. Obradovic, J. Pasternak, S. Ng; VIDO-InterVac, University of Saskatchewan, Saskatoon, SK, Canada.
8:15	2	Role of Glutate Racemase in Mycobacteria	G. Rathnaiah, F. Barnawi, D.K. Zinniel, R.G. Barletta; University of Nebraska, Lincoln, NE, USA.
8:30	3	Mutual antagonism between Mannheimia haemolytica and Pasteurella multocida when forming a biofilm on bovine bronchial epithelial cells in vitro.	I. Boukahil, C. Czuprynski; University of Wisconsin-Madison, Madison, WI, USA.
8:45	4	Comparative genomics of archived pyrazinide resistant mycobacterium tuberculosis complex isolates from Uganda	S.I. Wanzala[1], J. Nakavuma[2], D. Travis[1], P. Kia[2], S. Ogwang[3], W. Waters[4], T. Thacker[4], T. Johnson[5], S. Sreevatsan[1]; [1]Veterinary Population Medicine, University of Minnesota, Saint Paul, MN, USA, [2]College of Veterinary Medicine, Animal Resources and Biosecurity, Makerere University, Kampala, Uganda, [3]Joint Clinical Research Center (JCRC), Mengo, Kampala, Uganda, [4]National Animal Disease Center, USDA, Ames, IA, USA, [5]Department of Veterinary Biomedical Sciences, University of Minnesota, Saint Paul, MN, USA.
9:00	5	Influence of maternal microbial communities on the intestinal mucosal microbiome of the neonatal pig.	N. Maradiaga, M. Zieneldin, J. Lowe, B. Aldridge; Veterinary Clinical Medicine, University of Illinois at Urbana-Champaign, Champaign, IL, USA.
9:15	6	Construction and evaluation of Edwardsiella piscicida T3SS in-fre deletion mutants	A.M. Mohamed[1], S.-W. Nho[1], H. Abdelhamed[1], M. Essa[2], A. Karsi[1], M. Lawrence[1]; [1]College of Veterinary Medicine, Starkville, MS, USA, [2]College of Veterinary Medicine, Beni-Suef, Egypt.
9:30		Break and Table Top Exhibitors - Foyer	
10:00	7	Successful protection against heterologous strains of Haemophilus parasuis: the quest for cross protective factors	K.C. Eberle, J.E. Nally, C.L. Loving, S.J. Hau, T.L. Nicholson, S.L. Brockmeier; National Animal Disease Center, Ames, IA, USA.
10:15	8	Comparative analysis of plasmid pathogenicity loci and phylogenetic relationship in NetF-producing Clostridium perfringens	I. Mehdizadeh Gohari[1], A.M. Kropinski[1], S.J. Weese[1], A.E. Whitehead[2], V.R. Parreira[1], P. Boerlin[1], J.F. Prescott[1]; [1]Pathobiology, University of Guelph, Guelph, ON, Canada, [2]Department of Veterinary Clinical and Diagnostic Sciences, University of Calgary, Calgary, AB, Canada.

Bacterial Pathogenesis
Avenue Ballroom - 4th Floor
Section Leader : Gireesh Rajashekara

TIME	NO	TITLE	Author Block
10:30	9	Microparticles from Histophilus somni stimulated bovine monocyte-derived macrophages increase fibrin clot formation in vitro	J.J. Rivera Rivas, C.J. Czuprynski; Pathobiological Sciences, UW-Madison, Madison, WI, USA.
Keynonte Speaker 10:45	10	Microbial Wikileaks: Intercepting PathogenConversations To Understand (and Disrupt) Interactions with the Host	M. Federle; Medicinal Chemistry and Pharmacognosy, University of Illinois at Chicago, Chicago, IL, USA.
11:30		LUNCH	
1:00	11	Experimental Staphylococcus aureus mastitis teat dip challenge model	O. Kerro Dego, B.E. Gillespie, R.A. Almeida, M.J. Lewis, C. Young; Animal Science, The University of Tennessee, Knoxville, TN, USA.
1:15	12	Surface display of Clostridium perfringens alpha toxin on the enterotoxigenic Escherichia coli k88ab vaccine strain	G. Wi, S. Lee, H. Kim, H. Jang; vaccine business division, WOOGENE B&G CO.,LTD, Seoul, Korea, Republic of.
1:30	13	Dynics of antibody responses to Lyme disease spirochetes in the context of VlsE-mediated immune evasion	A. Rogovskyy[1], D.C. Gillis[1], Y. Ionov[2], E. Gerasimov[3], A. Zelikovksy[3]; [1]Texas A&M University, College Station, TX, USA, [2]Rosewell Park Cancer Institute, Buffalo, NY, USA, [3]Georgia State University, Atlanta, GA, USA.
1:45	14	Gene expression differences between mastitis-causing Escherichia coli strains grown in planktonic, swimming, and swarming culture conditions	J. Lippolis; Ruminant Disease and Immunology, National Animal Disease Center / ARS / USDA, Ames, IA, USA.
2:00	15	Interaction between AI-2 and AI-3 quorum sensing systems in Salmonella Typhimurium	E.V. Gart, S.D. Lawhon; VTPB, Texas A&M, College Station, TX, USA.
2:15	16	the effect of Mycobacterium avium subsp. paratuberculosis in the develoent of bovine mastitis caused by Escherichia coli under experimental conditions	F.M. Shoyama[1], D.G. Schwarz[2], M.A.S. Moreira[2], S. Sreevatsan[1]; [1]University of Minnesota, Minneapolis, MN, USA, [2]University of Vicosa, Vicosa, Brazil.
2:30	17	Stress hormones deferentially alter gut microbes over time and affect Salmonella counts in weaned pigs	S. Eicher[1], E. Petrosus[2], D. Lay, Jr[1], M. Rostagno[3], E. Silva[1]; [1]Livestock Behavior Research Unit, USDA-ARS, West Lafayette, IN, USA, [2]Animal Sciences, Purdue University, West Lafayette, IN, USA, [3]Ely Lilly & Co., Indianapolis, IN, USA.
2:45		Break and Table Top Exhibitors - Foyer	

Bacterial Pathogenesis Avenue Ballroom - 4th Floor Section Leader : Gireesh Rajashekara			
TIME	NO	TITLE	Author Block
3:00	18	20-Hydroxyeicosatetraenoic acid alters vascular endothelial barrier integrity by an oxidative stress-dependent mechanism.	V. Mavangira, L.M. Sordillo; Large Animal Clinical Sciences, Michigan State University, East Lansing, MI, USA.
3:15	19	Lactation stage influence on the oxylipid profile of healthy dairy cattle in plasma and milk.	M. Kuhn[1], V. Mavangira[1], J.C. Gandy[1], C. Zhang[2], A.D. Jones[3], L. Sordillo[1]; [1]Department of Large Animal Clinical Sciences, Michigan State University, East Lansing, MI, USA, [2]Department of Chemistry, Michigan State University, East Lansing, MI, USA, [3]Department of Biochemistry and Molecular Biology, Michigan State University, East Lansing, MI, USA.
3:30	20	Serological survey of leptospirosis in pigs from slaughterhouses in Vietnam	H.S. Lee[1], H.N. Xuan[2], V.B. Nghia[2], H. Nguyen-Viet[1], D. Grace[3]; [1]International Livestock Research Institute, Hanoi, Viet Nam, [2]National Institute of Veterinary Research, Hanoi, Viet Nam, [3]International Livestock Research Institute, Nairobi, Kenya.
3:45	21	Chlydia gallinacea in poultry and cattle of China	C. Wang[1], W. Guo[2], J. Li[2], B. Kaltenboeck[1], K. Sachse[3], S. Pu[2], Y. Wu[2], Y. Yang[2], G. Lu[2], J. Zhang[2], L. Luan[2], J. You[2], K. Huang[2], H. Qiu[2], Y. Wang[2], M. Li[2], Z. Yang[2], J. Gong[4], W. Fan[5]; [1]Pathobiology, Auburn University, Auburn, AL, USA, [2]Yangzhou University, Yangzhou, China, [3]Friedrich-Loeffler-Institut, Jena, Germany, [4]Poultry Institute, Chinese Academy of Agricultural Sciences, Yangzhou, China, [5]Laboratory of Zoonosis, China Animal Health and Epidemiology Center, Qingdao, China.
4:00	22	Adherence patterns of LA-MRSA ST5 isolates and MRSA ST5 isolates from humans with no swine contact	S.J. Hau[1], T. Frana[1], P.R. Davies[2], J. Sun[2], T.L. Nicholson[3]; [1]Iowa State University, Ames, IA, USA, [2]University of Minnesota, St. Paul, MN, USA, [3]National Animal Disease Center, Agricultural Research Service, USDA, Ames, IA, USA.
4:30		Break and Table Top Exhibitors - Foyer	
5:00		Poster Session II - Grandballroom Salon III - 7th Floor	

Biosafety and Biosecurity Denver/ Houston - 5th Floor Section Leader : Brandy Burguss			
TIME	NO	TITLE	Author Block
1:30	23	Estimating potential disease spread at an equestrian show in Ontario, Canada using an agent-based network model	K.L. Spence, T.L. O'Sullivan, Z. Poljak, A.L. Greer; Population Medicine, University of Guelph, Guelph, ON, Canada.
1:45	24	Patient medical records as a reservoir for potential pathogens in a Veterinary Teaching Hospital	L. Fargis, F.W. Pierson, B.A. Burgess; Virginia Tech, Blacksburg, VA, USA.
2:00	25	Using microbiome data to calibrate a microbial clock for estimating the postmortem interval in mmals	J.L. Metcalf[1], D.O. Carter[2], R. Knight[3]; [1]COLORADO STATE UNIVERSITY, FORT COLLINS, CO, USA, [2]Chaminade University of Honolulu, Honolulu, HI, USA, [3]University of San Diego California, San Diego, CA, USA.
2:15	26	Five years of foreign animal disease preparedness training for zoos and aquariums - lessons learned and areas for improvement	Y.J. Johnson-Walker[1], Y. Nadler[2], M.S. Myint[1], G.Y. Miller[3], J.A. Herrmann[1], J. Lin[4]; [1]Center for One Health Illinois, University of Illinois, Urbana-Champaign, Urbana, IL, USA, [2]ZAPH Fusion Center, Association of Zoos and Aquariums, Silver Springs, MD, USA, [3]Pathobiology, University of Illinois, Urbana-Champaign, Urbana, IL, USA, [4]Animal Care, USDA APHIS, Riverdale, MD, USA.
2:30	27	Develoent of an interactive online avian influenza preparedness exercise for zoos and aquariums using GIS tools for qualitative risk assessment	Y.J. Johnson-Walker[1], Y. Nadler[2], N. Oliver[3], W.M. Brown[4], M.O. Ruiz[4], M.S. Myint[1], J. Lin[5]; [1]Center for One Health Illinois, University of Illinois, Urbana-Champaign, Urbana, IL, USA, [2]ZAPH Fusion Center, Association of Zoos and Aquariums, Silver Springs, MD, USA, [3]The Design Group College of Vet Med, University of Illinois, Urbana-Champaign, Urbana, IL, USA, [4]Department of Pathobiology, University of Illinois, Urbana-Champaign, Urbana, IL, USA, [5]USDA APHIS, Riverdale, MD, USA.
2:45		Break and Table Top Exhibitors - Foyer	
Keynote Speaker 3:00:00 AM	28	A biosecurity assessment of U.S. animal production systems	K. Havas; Diagnostic Services Section, USDA Foreign Animal Disease Diagnostic Laboratory, Greenport, NY, USA.
3:45	29	Ten years of progress in agrosecurity for concentrated livestock operations and related businesses	R.E. DeOtte, Jr.[1], L.P. Miller[2], M. Mayes[3]; [1]Engineering and Computer Science, West Texas A&M University, Canyon, TX, USA, [2]USDA Animal and Plant Health Inspection Service, Riverdale, MD, USA, [3]North Carolina Department of Agriculture and Computer Services, Raleigh, NC, USA.

Biosafety and Biosecurity Denver/ Houston - 5th Floor Section Leader : Brandy Burguss			
TIME	NO	TITLE	Author Block
4:00	30	A field-deployable nucleid acid extraction/PCR system detected bovine leukemia virus proviral DNA in blood with a performance equivalent to a laboratory real-time PCR system	V.J. Ruggiero[1], O.J. Benitez[1], Y. Tsai[2], C. Tsai[2], Y. Lin[2], P.A. Lee[2], H.G. Chang[2], H.T. Wang[2], P. Bartlett[3]; [1]Comparative Medicine and Integrative Biology, College of Veterinary Medicine, Michigan State University, East Lansing, MI, USA, [2]GeneReach USA, Lexington, MA, USA, [3]Large Animal Clinical Sciences, College of Veterinary Medicine, Michigan State University, East Lansing, MI, USA.
4:15	31	Dissemination of antimicrobial resistant enteric bacteria in a zoo environment	S. Feicht, D.A. Mathys, D.F. Mollenkopf, T.E. Wittum; Veterinary Preventive Medicine, Ohio State University College of Veterinary Medicine, Columbus, OH, USA.
4:30		Break and Table Top Exhibitors - Foyer	
5:00		Poster Session II - Grandballroom Salon III - 7th Floor	

Companion Animal Epidemiology
Northwestern/ Ohio - 6th Floor
Section Leader : Audrey Rupley & Laura Hungerford

TIME	NO	TITLE	Author Block
8:00	32	Patterns and predictors of antimicrobial resistance ong Staphylococcus spp. from canine clinical cases presented at a veterinary academic hospital in South Africa.	D.N. Qekwana[1], J.W. Oguttu[2], F. Sithole[3], A. Odoi[4]; [1]Section Veterinary Public Health, University of Pretoria, Pretoria, South Africa, [2]Department of Agriculture and Animal Health, University of South Africa, Pretoria, South Africa, [3]Ross University School of Veterinary Medicine, Basseterre, Saint Kitts and Nevis, [4]Biomedical and Diagnostic Sciences, University of Tennessee, Knoxville, TN, USA.
8:15	33	Spatial and antimicrobial susceptibility patterns of Staphylococcus from horses presented at a teaching hospital in South Africa	J.W. Oguttu[1], N.D. Qekwana[2], A. Odoi[3]; [1]College of Agriculture and Environmental Sciences, Department of Agriculture and Animal Health,, University of South Africa, Pretoria, South Africa, [2]Section Veterinary Public Health, Department of Paraclinical Sciences, Faculty of Veterinary Science, University of Pretoria, Pretoria, South Africa, [3]College of Veterinary Medicine, Biomedical and Diagnostic Sciences, University of Tennessee, Knoxville, South Africa.
8:30	34	Extended-spectrum cephalosporin, carbapenem, and fluoroquinolone resistant coliform bacteria from a large equine teaching hospital and a referral equine specialty hospital	R.J. Adams[1], D. Mathys[1], D. Mollenkopf[1], M. Mudge[2], A. Bertone[2], J. Daniels[2], T. Wittum[1]; [1]Dept. of Veterinary Preventive Medicine, The Ohio State University, Columbus, OH, USA, [2]Dept. of Veterinary Clinical Sciences, The Ohio State University, Columbus, OH, USA.
8:45	35	Antimicrobial resistance to extended-spectrum cephalosporins in Enterobacteriaceae from dogs in Southern Ontario, Canada	P. Zhang[1], X. Shen[1], R.J. Reid-Smith[2], D. Slavic[3], H. Dick[4], P. Boerlin[1]; [1]Pathobiology, University of Guelph, Guelph, ON, Canada, [2]Centre for Food-borne, Environmental and Zoonotic Infectious Diseases, Public Health Agency of Canada, Guelph, ON, Canada, [3]Animal Health Laboratory, University of Guelph, Guelph, ON, Canada, [4]IDEXX Laboratories, Markham, ON, Canada.
9:00	36	Impact of collateral resistance in methicillin-resistant Staphylococcus pseudintermedius in canine patients	W.J. Love, A. Trey, M.E. Jacob, C. Lanzas; Population Health & Pathobiology, North Carolina State University, Raleigh, NC, USA.
9:15	37	Impact of antimicrobial therapy on the resistance profile of enteric flora of dogs	D.A. Mathys[1], D.F. Mollenkopf[1], J.B. Daniels[2], T.E. Wittum[1]; [1]Department of Veterinary Preventative Medicine, College of Veterinary Medicine, Ohio State University, Columbus, OH, USA, [2]Department of Veterinary Clinical Sciences, College of Veterinary Medicine, Ohio State University, Columbus, OH, USA.
9:30		Break and Table Top Exhibitors - Foyer	

Companion Animal Epidemiology
Northwestern/ Ohio - 6th Floor
Section Leader : Audrey Rupley & Laura Hungerford

TIME	NO	TITLE	Author Block
10:00	38	Is it possible to diagnose canine brucellosis? - a deterministic model	K.J. Hubbard, D.R. Smith; College of Veterinary Medicine, Mississippi State University, Starkville, MS, USA.
10:15	39	The Golden Retriever Lifetime Study: assessing factors affecting owner compliance after the first year of enrollment	M. Jones[1], A. Ruple[2], M. Simpson[3], R. Page[4]; [1]Department of Veterinary Clinical Sciences, Purdue University College of Veterinary Medicine, West Lafayette, IN, USA, [2]Department of Comparative Pathobiology, Purdue University College of Veterinary Medicine, West Lafayette, IN, USA, [3]Morris Animal Foundation, Denver, CO, USA, [4]Flint Animal Cancer Center, Colorado State University College of Veterinary Medicine and Biomedical Sciences, Fort Collins, CO, USA.
10:30	40	Can animal poison control centre data provide early warning of outbreaks associated with continated pet food: using the 2007 meline poisoning outbreak as a case study	A.L. Swirski[1], D.L. Pearl[1], O. Berke[1], T. O'Sullivan[1], D. Stacey[2]; [1]Department of Population Medicine, University of Guelph, Guelph, ON, Canada, [2]School of Computer Science, University of Guelph, Guelph, ON, Canada.
10:45	41	Description of a census of canine intake into Mississippi animal shelters and the relationship to human demographics	U. Donnett, K. Hubbard, C. Loftin, K. Woodruff, D.R. Smith; Mississippi State University College of Veterinary Medicine, Mississippi State, MS, USA.
11:00	42	Recent trends in cat admissions and the effect of the capacity for care progr at the Guelph humane society, 2011-2015	N. Janke; Population Medicine, University of Guelph, Guelph, ON, Canada.
11:15	43	Pedicle tie as a safe and effective means of ovarian vessel hemostasis in feline ovariohysterectomy	J. Shivley[1], U.B. Donnett[1], C. Brookshire[1], K.A. Woodruff[1], D.R. Smith[2]; [1]Clinical Sciences, Mississippi State University College of Veterinary Medicine, Mississippi State, MS, USA, [2]Pathobiology and Population Medicine, Mississippi State University College of Veterinary Medicine, Mississippi State, MS, USA.
11:30		LUNCH	
Keynote Speaker 1:30	44	Primary-care vet data:the final frontier.	D. O'Neill; Royal Veterinary College, University of London, Hertfordshire, UK.

Companion Animal Epidemiology Northwestern/ Ohio - 6th Floor Section Leader : Audrey Rupley & Laura Hungerford			
TIME	NO	TITLE	Author Block
Mark Gearhart Award 2:00:00 AM	45	The case-control design inveterinary sciences: a survey	J.N. Cullen[1], J.M. Sargeant[2], K.M. Makielski[3], A.M. O'Connor[4]; [1]Department of Veterinary Diagnostic and Production Animal Medicine, Iowa State University, Ames, IA, USA, [2]Centre for Public Health and Zoonoses, University of Guelph, Guelph, ON, Canada, [3]Department of Population Medicine, University of Guelph, Guelph, ON, Canada, [4]Department of Veterinary Clinical Sciences, Iowa State University, Ames, IA, USA.
2:15	46	Spatial & antimicrobial susceptibility patterns of Staphylococcus from horses presented at a teaching hospital in South Africa	J.W. Oguttu[1], D.N. Qekwana[2], A. Odoi[3]; [1]Agriculture & Animal Health, University of South Africa, Johannesburg, South Africa, [2]Paraclinical Sciences, University of Pretoria, Pretoria, South Africa, [3]Biomedical & Diagnostic Sciences & Agriculture & Animal Health, University of South Africa & University of Tennessee, Knoxville, TN, USA.
2:30	47	An estimate of the number of dogs in US shelters	K.A. Woodruff[1], D. Smith[2]; [1]Clinical Sciences, Mississippi State University College of Veterinary Medicine, Mississippi State, MS, USA, [2]Pathobiology and Population Medicine, Mississippi State University College of Veterinary Medicine, Mississippi State, MS, USA.
2:45		Break and Table Top Exhibitors - Foyer	
4:30		Break and Table Top Exhibitors - Foyer	
5:00		Poster Session II - Grandballroom Salon III - 7th Floor	

Ecology and Management of Foodborne Agents Salon E - 5th Floor Section Leader : Tom Wittum			
TIME	NO	TITLE	Author Block
8:00	48	Whole-genome sequencing of Salmonella derived from feedlot cattle treated with antibiotics	N. Ohta[1], K.N. Norman[2], H. den Bakker[3], G.H. Loneragan[3], S.D. Lawhon[1], H.M. Scott[1]; [1]Department of Veterinary Pathobiology, Texas A&M University, College Station, TX, USA, [2]Department of Veterinary Integrative Biosciences, Texas A&M University, College Station, TX, USA, [3]Department of Animal and Food Sciences, Texas Tech University, Lubbock, TX, USA.
8:15	49	Shotgun metagenomic detection of Salmonella enterica in feedlot cattle compared to aerobic culture and PCR techniques.	E. Doster[1], P. Rovira[1], N.R. Noyes[1], B.A. Burgess[2], X. Yang[1], M. Weinroth[1], L. Linke[1], R. Magnuson[1], K. Jones[3], C. Boucher[4], J. Ruiz[4], P.S. Morley[1], K.E. Belk[1]; [1]Colorado State University, Fort Collins, CO, USA, [2]Virginia Tech, Blacksburg, VA, USA, [3]University of Colorado Denver, Denver, CO, USA, [4]University of Florida, Gainesville, FL, USA.
8:30	50	Transmission of Salmonella from farm to food: The impact of clinical outbreaks of salmonellosis in calves on recovery of Salmonella from lymph nodes at harvest.	L.M. Munoz-Vargas[1], S. Finney[1], H. Hutchinson[2], M. Masterson[1], G. Habing[1]; [1]Dpt. of Veterinary Preventive Medicine, The Ohio State University, Columbus, OH, USA, [2]Dpt. of Animal Sciences, The Ohio State University, Columbus, OH, USA.
9:00	51	Analyzing 20 years of Salmonella serotype using NARMS and veterinary diagnostic laboratory data	A. O'Connor[1], M.M. Erdman[2], P.J. Fedorka-Cray[3], C.M. Logue[4], C. Yuan[5]; [1]VDPAM, Iowa State University, Ames, IA, USA, [2]USDA-APHIS-VS-STAS National Veterinary Services Laboratories, Ames, IA, USA, [3]College of Veterinary Medicine, NC State University, Raleigh, NC, USA, [4]VMPM, Iowa State University, Ames, IA, USA, [5]Dept. of Statistics, Iowa State University, Ames, IA, USA.
9:15	52	Prevalence, quantity and antimicrobial resistance of Salmonella enterica in response to antibiotic use early in the cattle feeding period	G. Levent[1], A. Schlochtermeier[2], S.E. Ives[2], K.N. Norman[1], S.D. Lawhon[1], G.H. Loneragan[3], R.C. Anderson[4], H.M. Scott[1]; [1]Department of Veterinary Pathobiology, Texas A&M University, College Station, TX, USA, [2]Department of Agricultural Sciences, West Texas A&M University, Canyon, TX, USA, [3]Department of Animal and Food Sciences, Texas Tech University, Lubbock, TX, USA, [4]Agricultural Research Service, United States Department of Agriculture, College Station, TX, USA.
9:30		Break and Table Top Exhibitors - Foyer	
10:00	53	phenotypes and genotypes of concern isolated from hogs at	K.N. Norman[1], R.B. Harvey[2], T.S. Edrington[2], K. Andrews[2], R.E. Droleskey[2], H.M. Scott[3]; [1]Department of Veterinary Integrative

Ecology and Management of Foodborne Agents Salon E - 5th Floor Section Leader : Tom Wittum			
TIME	NO	TITLE	Author Block
10:15	54	Predictors of selective antimicrobial use practices ong dairy calf producers	G. Habing[1], G. Schuenemann[1], C. Djordjevic[1], J. Lakritz[2]; [1]Veterinary Preventive Medicine, The Ohio State University, Columbus, OH, USA, [2]Veterinary Clinical Sciences, The Ohio State University, Columbus, OH, USA.
10:30	55	Effects of feeding Saccharomyces cerevisiae fermentation products on liver abscess rate, foodborne pathogens and the microbiome in natural beef steers.	K.L. Huebner[1], C.J. Weissend[2], K.L. Holzer[2], Z. Abdo[3], J.L. Metcalf[2], G. Georgnaras[2], J.K. Parker[1], P.S. Morley[1], K.E. Belk[2], J.N. Martin[2]; [1]Clinical Sciences, Colorado State University, Fort Collins, CO, USA, [2]Animal Sciences, Colorado State University, Fort Collins, CO, USA, [3]Microbiology, Immunology, and Pathology, Colorado State University, Fort Collins, CO, USA.
10:45	56	Does the fiber component of distillers grains explain increased fecal shedding of enterohemorrhagic Escherichia coli in feedlot steers?	L.G. Schneider[1], G.E. Erickson[2], T.J. Klopfenstein[2], R.A. Moxley[3], G.L. Lewis[3], Z.R. Stromberg[3], D.R. Smith[1]; [1]College of Veterinary Medicine, Mississippi State University, Mississippi State, MS, USA, [2]Animal Science, University of Nebraska-Lincoln, Lincoln, NE, USA, [3]School of Veterinary Medicine and Biomedical Sciences, University of Nebraska-Lincoln, Lincoln, NE, USA.
11:00	57	Mapping collateral resistance in four nontyphoidal Salmonella serotypes isolated from chicken carcasses and commercial chicken products	W.J. Love, C. Lanzas; Population Health & Pathobiology, North Carolina State University, Raleigh, NC, USA.
11:30		LUNCH	
Keynote Speaker 1:30	58	Primary-care vet data:the final frontier.	D. O'Neill; Royal Veterinary College, University of London, Hertfordshire, UK.
Mark Gearhart Award 2:00	59	The case-control design inveterinary sciences: a survey	J.N. Cullen[1], J.M. Sargeant[2], K.M. Makielski[3], A.M. O'Connor[4]; [1]Department of Veterinary Diagnostic and Production Animal Medicine, Iowa State University, Ames, IA, USA, [2]Centre for Public Health and Zoonoses, University of Guelph, Guelph, ON, Canada, [3]Department of Population Medicine, University of Guelph, Guelph, ON, Canada, [4]Department of Veterinary Clinical Sciences, Iowa State University, Ames, IA, USA.
2:15	60	Carbapenemase-producing Enterobacteriaceae recovered from the environment of a swine farrow-to-finish operation in the United States.	D.F. Mollenkopf[1], J.W. Stull[1], D.A. Mathys[1], A.S. Bowman[1], S.M. Feicht[1], J.B. Daniels[2], T.E. Wittum[1]; [1]Veterinary Preventive Medicine, Ohio State University, Columbus, OH, USA, [2]Veterinary Clinical Sciences, Ohio State University, Columbus, OH, USA.

Ecology and Management of Foodborne Agents Salon E - 5th Floor Section Leader : Tom Wittum			
TIME	NO	TITLE	Author Block
2:30	61	Effects of ractopine and zinc supplementation on antimicrobial resistance of fecal Escherichia coli in finishing cattle	A.C. Holbert[1], K.N. Norman[1], R.G. Amachawadi[2], J. Vinasco[1], R.A. Pugh[1], J.S. Drouillard[3], C.L. Van Bibber-Krueger[3], T.G. Nagaraja[2], H.M. Scott[1]; [1]Department of Veterinary Pathobiology, Texas A&M University, College Station, TX, USA, [2]Department of Diagnostic Medicine/Pathobiology, Kansas State University, Manhattan, KS, USA, [3]Department of Animal Sciences & Industry, Kansas State University, Manhattan, KS, USA.
2:45		Break and Table Top Exhibitors - Foyer	
3:00	62	Zinc and menthol as alternatives to antibiotics: impacts on bacterial resistance in feeder cattle	S.A. Murray[1], K.N. Norman[2], S.D. Lawhon[1], R.G. Amachawadi[3], J. Vinasco[1], R.A. Pugh[1], J.S. Drouillard[4], C.L. Van Bibber-Krueger[4], T.G. Nagaraja[3], H.M. Scott[1]; [1]Department of Veterinary Pathobiology, Texas A&M University, College Station, TX, USA, [2]Department of Veterinary Integrative Biosciences, Texas A&M University, College Station, TX, USA, [3]Department of Diagnostic Medicine/Pathobiology, Kansas State University, Manhattan, KS, USA, [4]Department of Animal Sciences & Industry, Kansas State University, Manhattan, KS, USA.
3:15	63	Dissemination and antibiotic susceptibility patterns of carbapenem resistant Enterobacteriaceae from a municipal wastewater treatment plant	D. Stuever, C. King, D. Mollenkopf, D. Mathys, S. Feicht, J. Daniels, T. Wittum; Ohio State University, Columbus, OH, USA.
3:30	64	Megarich: a pre-sequencing capture system for enriching and counting resistance genes within metagenomic sples	N.R. Noyes[1], J.K. Parker[2], J.K. Parker[2], C.J. Dean[1], R.A. Raymond[3], M.E. Weinroth[4], P. Rovira[4], E. Doster[2], Z. Abdo[1], J. Martin[1], K.L. Jones[5], J. Ruiz[6], C.A. Boucher[6], K.E. Belk[4], P.S. Morley[2]; [1]Microbiology, Immunology, and Pathology, Colorado State University, Fort Collins, CO, USA, [2]Clinical Sciences, Colorado State University, Fort Collins, CO, USA, [3]Computer Sciences, Colorado State University, Fort Collins, CO, USA, [4]Animal Sciences, Colorado State University, Fort Collins, CO, USA, [5]School of Medicine, University of Colorado-Denver, Denver, CO, USA, [6]Computer and Information Science and Engineering, University of Florida, Gainesville, FL, USA.

Ecology and Management of Foodborne Agents
Salon E - 5th Floor
Section Leader : Tom Wittum

TIME	NO	TITLE	Author Block
3:45	65	MEGaRES and rPlusPlus - A comprehensive database of antimicrobial resistance genes and user-friendly pipeline for analysis of high-throughput sequencing data	S.M. Lakin[1], C.J. Dean[2], A. Dettenwanger[3], A. Ross[3], E. Doster[1], P. Rovira[1], Z. Abdo[2], K.L. Jones[4], K.E. Belk[5], P.S. Morley[1], C. Boucher[6]; [1]Clinical Sciences, Colorado State University, Fort Collins, CO, USA, [2]Microbiology, Immunology, and Pathology, Colorado State University, Fort Collins, CO, USA, [3]Computer Sciences, Colorado State University, Fort Collins, CO, USA, [4]Biochemistry and Molecular Genetics, University of Colorado-Denver, Denver, CO, USA, [5]Animal Sciences, Colorado State University, Fort Collins, CO, USA, [6]Computer and Information Science and Engineering, University of Florida, Gainesville, FL, USA.
4:00	66	Calibri; a proposed analytic frework for determining the impact of an antimicrobial resistance intervention	Y.T. Grohn[1], C. Carson[2], C. Lanzas[3], L. Pullum[4], M. Stanhope[1], V. Volkova[5]; [1]Pop Med & Diagn Sci, Cornell University, Ithaca, NY, USA, [2]Centre for Foodborne, Environmental and Zoonotic Infectious Diseases, Public Health Agency of Canada, Guelph, ON, Canada, [3]Population Health and Pathobiology, North Carolina State University, Raleigh, NC, USA, [4]Health Data Sciences Institute, Oak Ridge National Laboratory, Oak Ridge, TN, USA, [5]Diagnostic Medicine/Pathobiology, Institute of Computational Comparative Medicine, Kansas State University, Ithaca, KS, USA.
4:15	67	Comparison of the microbiological quality of fresh produce from seasonal farmer's markets and retail grocery stores in Ohio	A. Albers, S. Feicht, D. Mathys, D. Mollenkopf, T. Wittum; Department of Veterinary Preventative Medicine, The Ohio State University, Columbus, OH, USA.
4:30	68	Waterfowl and the introduction of foodborne pathogens to agricultural and recreational environments in southern Ontario	N.A. Vogt[1], D.L. Pearl[1], E.N. Taboada[2], N. Janecko[3], R.J. Reid-Smith[3], B. Bloomfield[1], C.M. Jardine[4]; [1]Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, ON, Canada, [2]National Microbiology Laboratory, Public Health Agency of Canada, Lethbridge, AB, Canada, [3]Centre for Food-borne, Environmental and Zoonotic Infectious Diseases, Public Health Agency of Canada, Guelph, ON, Canada, [4]Department of Pathobiology, Ontario Veterinary College, University of Guelph, Guelph, ON, Canada.
4:45	69	Prevalence and antibiotic resistance profiles of E. coli and Enterococcus species from a sple of wild birds captured on intensive dairy and beef cattle operations	K. Tormoehlen[1], Y.J. Johnson[1], E.W. Lankau[2], M.S. Myint[1], J.A. Herrmann[1]; [1]Department of Veterinary Clinical Medicine, University of Illinois, Urbana, IL, USA, [2]LandCow Consulting, Madison, WI, USA.

Ecology and Management of Foodborne Agents Salon E - 5th Floor Section Leader : Tom Wittum			
TIME	NO	TITLE	Author Block
4:30		Break and Table Top Exhibitors - Foyer	
5:00		Poster Session II - Grandballroom Salon III - 7th Floor	

Epidemiology and Animal Health Economics
Salon A/B/C/D - 5th Floor
Section Leader : Ashley Hill

TIME	NO	TITLE	Author Block
MONDAY 8:00	70	Salmonella enterica and extended spectrum cephalosporin resistant Escherichia coli recovered from Holstein dairy calves in New Brunswick, Canada	B.B. AWOSILE, J. Sanchez, M. Saab, J. Rodriguez-Lecompte, G. Keefe, J. McClure, L. Heider; HEALTH MANAGEMENT, ATLANTIC VETERINARY COLLEGE, UNIVERSITY OF PRINCE EDWARD ISLAND, CHARLOTTETOWN, PE, Canada.
8:15	71	Evidence for persistent, spatially-explicit reservoirs of antibiotic-resistant Escherichia coli in food-animal production environments	J. Liu; University of California, Davis, Davis, CA, USA.
8:30	72	Annual variation in susceptibility of generic Escherichia coli isolates to ceftiofur from retail chicken meat surveillance in Canada	M.C. MacKinnon[1], D.L. Pearl[1], C.A. Carson[2], E.J. Parmley[2], S.A. McEwen[1]; [1]Population Medicine, University of Guelph, Guelph, ON, Canada, [2]Canadian Integrated Program for Antimicrobial Resistance Surveillance, Public Health Agency of Canada, Guelph, ON, Canada.
8:45	73	Characterizing antimicrobial drug use in Canadian beef cattle: Comparison of actual use to Population Corrected Unit methodology	S.A. Brault[1], S.J. Hannon[2], S.P. Gow[3], C.W. Booker[2], P.S. Morley[1]; [1]Clinical Sciences, Colorado State University College of Veterinary Medicine and Biomedical Sciences, Fort Collins, CO, USA, [2]Feedlot Health Management Services, Ltd., Okotoks, AB, Canada, [3]Center for Foodborne, Environmental, and Zoonotic Infectious Diseases, Public Health Agency of Canada, University of Saskatchewan, Saskatoon, SK, Canada.
9:00	74	Serotype diversity and antimicrobial resistance ong Salmonella enterica isolated from patients at an equine referral hospital	I.M. Leon[1], K.N. Norman[2], S.D. Lawhon[1], D.S. Threadgill[1], J. Vinasco[1], H.M. Scott[1]; [1]Department of Veterinary Pathobiology, Texas A&M University, College Station, TX, USA, [2]Department of Veterinary Integrative Biosciences, Texas A&M University, College Station, TX, USA.
9:15:00	75	Epidemiology of Staphylococcus species and their antimicrobial resistance patterns in livestock-related settings of central Oromia, Ethiopia	F. Gizew[1], T. Kekeba[2], F. Teshome[2], M. Kebede[2], T. Abreham[2], H. Hayishe[2], O. Merera[1], T. Beyene[2], B. Mamo[2], O. Kerro Dego[3], D. Ayana[2], A.F. Beyi[4], F. Abunna[2], R.D. Abdi[3]; [1]College of veterinary Medicine, Samara University, Samara, Ethiopia, [2]College of Veterinary Medicine and Agriculture, Addis Ababa University, Bishoftu, Ethiopia, [3]Department of Animal Science, University of Tennessee, Knoxville, TN, USA, [4]University of Florida, Gainesville, FL, USA.
9:30		Break and Table Top Exhibitors - Foyer	

Epidemiology and Animal Health Economics Salon A/B/C/D - 5th Floor Section Leader : Ashley Hill			
TIME	NO	TITLE	Author Block
10:00	76	Accounting for data architecture on structural-equation-based modeling of feedlot performance outcomes	K. Chitakasempornkul[1], E. Cha[2], D. Renter[2], M. Sanderson[2], A. Jager[1], T. Schroeder[3], N.M. Bello[1]; [1]Statistics, Kansas State University, Manhattan, KS, USA, [2]Diagnostic Medicine/Pathobiology and Center for Outcomes Research and Education (CORE), Kansas State University, Manhattan, KS, USA, [3]Agricultural Economics and Center for Risk Management Education and Research, Kansas State University, Manhattan, KS, USA.
10:15	77	System dynics model of broiler production as a tool for studying disease and intervention	K.D. Galarneau[1], R.S. Singer[2], R.W. Wills[1]; [1]Pathobiology and Population Medicine, Mississippi State University, Mississippi State, MS, USA, [2]Veterinary and Biomedical Sciences, University of Minnesota, Saint Paul, MN, USA.
10:30	78	A model of Foot-and-Mouth Disease transmission within a U.S. beef feedlot	A.H. Cabezas, M.W. Sanderson, V.V. Volkova; Department of Diagnostic Pathobiology, Kansas State University, Manhattan, KS, USA.
10:45	79	Adaptation of a simulation model for Foot-and-Mouth Disease (FMD) spread in endemic countries/regions	M.U. Zaheer[1], S. Rao[1], S. Case[1], K. Steneroden[1], M. Afzal[2], M.J. Arshed[2], S. Weber[3], M. Hussain[2], E. Khan[4], N. Panhwar[2], A. Ahmad[5], M.D. Salman[1]; [1]Animal Population Health Institute (APHI), Department of Clinical Sciences, College of Veterinary Medicine & Biomedical Sciences (CVMBS), Colorado State University (CSU), Fort Collins, CO, USA, [2]Food and Agriculture Organization of United Nations-Pakistan (FAO-Pakistan), ASI Premises, National Agricultural Research Center (NARC), Islamabad, Pakistan, [3]Department of Clinical Sciences, College of Veterinary Medicine & Biomedical Sciences, Colorado State University, Fort Collins, CO, USA, [4]Livestock and Dairy Development Department, Government of Punjab, Lahore, Pakistan, [5]Livestock and Dairy Development Department, Government of Khyber Pakhtunkhwa, Peshawar, Pakistan.
11:00	80	Bioinformatics tools for effective genotypic characterization of carbapenemase-producing Klebsiella pneumoniae	S.V. Grooters, D.F. Mollenkopf, T.E. Wittum; Veterinary Preventive Medicine, The Ohio State University, Columbus, OH, USA.
11:15	81	Quantification of vector and host competence and abundance for Japanese Encephalitis Virus: a systematic review of the literature.	A.R.S. Oliveira[1], E. Strathe[2], L. Etcheverry[1], L.W. Cohnstaedt[3], D. Scott McVey[3], N. Cernicchiaro[1]; [1]Department of Pathobiology/Diagnostic Medicine, Kansas State University, Manhattan, KS, USA, [2]Department of Clinical Sciences, Kansas State University, Manhattan, KS, USA, [3]USDA-ARS Arthropod-Borne Animal Diseases Research, Manhattan, KS, USA.
11:30		LUNCH	

Epidemiology and Animal Health Economics
Salon A/B/C/D - 5th Floor
Section Leader : Ashley Hill

TIME	NO	TITLE	Author Block
Keynote Speaker 1:15	82	Primary-care vet data:the final frontier.	D. O'Neill; Royal Veterinary College, University of London, Hertfordshire, UK.
Mark Gearhart Award 2:00	83	The case-control design inveterinary sciences: a survey	J.N. Cullen[1], J.M. Sargeant[2], K.M. Makielski[3], A.M. O'Connor[4]; [1]Department of Veterinary Diagnostic and Production Animal Medicine, Iowa State University, Ames, IA, USA, [2]Centre for Public Health and Zoonoses, University of Guelph, Guelph, ON, Canada, [3]Department of Population Medicine, University of Guelph, Guelph, ON, Canada, [4]Department of Veterinary Clinical Sciences, Iowa State University, Ames, IA, USA.
2:15	84	Distribution and diversity of Salmonella in shients of hatchling poultry, United States, 2013-2015	A. Sharma[1], M.M. Erdman[2], L. MuÃ±oz-Vargas[1], T.E. Wittum[1], D.F. Mollenkopf[1], G.G. Habing[1]; [1]Department of Veterinary Preventive Medicine, The Ohio State University, Columbus, OH, USA, [2]National Veterinary Services Laboratory, Ames, IA, USA.
2:30	85	Beef producer survey of the cost to prevent and treat bovine respiratory disease in calves prior to weaning	M. Wang[1], L.G. Schneider[1], K.J. Hubbard[1], D.M. Grotelueschen[2], R. Daly[3], J. Stokka[4], R.W. Wills[1], D.R. Smith[1]; [1]Department of Pathobiology and Population Medicine, College of Veterinary Medicine, Mississippi State University, Starkville, MS, USA, [2]Great Plains Veterinary Educational Center, University of Nebraska, Clay Center, NE, USA, [3]South Dakota State University, Brookings, SD, USA, [4]Department of Animal Sciences, North Dakota State University, Fargo, ND, USA.
2:45		Break and Table Top Exhibitors - Foyer	
3:00	86	Analysis of risk factors for an outbreak of bovine respiratory disease in stocker cattle	K.J. Hubbard[1], A. Woolums[1], B. Karisch[2], J. Blanton, Jr.[2], B. Epperson[1], D.R. Smith[1]; [1]College of Veterinary Medicine, Mississippi State University, Starkville, MS, USA, [2]Animal and Dairy Science, Mississippi State University, Starkville, MS, USA.
3:15	87	Epidemiology of bovine respiratory disease in pre-weaned dairy calves	S. Dubrovsky[1], A. Van Eenennaam[1], B. Karle[2], T.W. Lehenbauer[3], S. Aly[3]; [1]Animal Science, UC Davis, Davis, CA, USA, [2]University of California Cooperative Extension, Orland, CA, USA, [3]Population Health and Reproduction, UC Davis School of Veterinary Medicine, Davis, CA, USA.
3:30	88	Impact of bovine leukemia virus on herd level production indicators on US dairy farms	R.M. LaDronka[1], B. Norby[1], T.M. Byrem[2], R.J. Erskine[1], P.C. Bartlett[1]; [1]Large Animal Clinical Sciences, Michigan State Universtiy, East Lansing, MI, USA, [2]Antel BioSystems, Lansing, MI, USA.

Epidemiology and Animal Health Economics Salon A/B/C/D - 5th Floor Section Leader : Ashley Hill			
TIME	NO	TITLE	Author Block
3:45	89	Efficacy of bovine herpesvirus 1 vaccination to prevent abortion in cattle: a meta-analysis	B. Newcomer, L. Cofield, P.H. Walz, M. Givens; Auburn University, Auburn, AL, USA.
4:00	90	Lactoferrin reduces mortality in Preweaned Calves with Diarrhea	G. Habing[1], K. Harris[1], G. Schuenemann[1], J. PiÃ±eiro[1], J. Lakritz[2], X. Alcaraz Clavijo[3]; [1]Veterinary Preventive Medicine, The Ohio State University, Columbus, OH, USA, [2]Veterinary Clinical Sciences, The Ohio State University, Columbus, OH, USA, [3]Universidad Nacional de Columbia, Bogota, Colombia.
4:30		Break and Table Top Exhibitors - Foyer	
5:00		Poster Session II - Grandballroom Salon III - 7th Floor	
TUESDAY 8:00	173	Spatial autocorrelation and implications for oral fluid-based PRRSV surveillance	M. Rotolo[1], M. Haddad[2], Y. Sun[3], L. Gimenez-Lirola[4], S. Bade[4], D. Baum[4], P. Gauger[4], M. Hoogland[5], R. Main[4], J. Zimmerman[1]; [1]Veterinary Diagnostic and Production Animal Medicine, Iowa State University, Ames, IA, USA, [2]Community and Regional Planning Department, Iowa State University, Ames, IA, USA, [3]Statistics Department, Iowa State University, Ames, IA, USA, [4]Veterinary Diagnostic Laboratory, Iowa State University, Ames, IA, USA, [5]Iowa State University, Ames, IA, USA.
8:15	174	An investigation into distribution of Streptococcus suis serotypes in clinical cases & healthy-carrier pigs.	E.R. Arndt[1], A.V. Farzan[1], J.I. MacInnes[2], R.M. Friendship[1]; [1]Population Medicine, University of Guelph, Guelph, ON, Canada, [2]Pathobiology, University of Guelph, Guelph, ON, Canada.
8:30	175	An investigation of the factors contributing to mortality during an outbreak of Streptococcus suis infection in nursery pigs. &lt!-- EndFragment--&gt	D.C. Hopkins, Z. Poljak, V. Farzan, R. Friendship; Population Medicine, University of Guelph, Guelph, ON, Canada.
8:45	176	Effect of influenza prevalence in pigs at weaning on transmission, clinical signs and performance after weaning	F. Chamba[1], S. Wayne[2], M. Culhane[1], A. Perez[1], M. Torremorell[1]; [1]Veterinary Population Medicine, University of Minnesota, St Paul, MN, USA, [2]Swine Health Management, Pipestone Veterinary Services, Pipestone, MN, USA.
9:00	177	Knowledge, attitudes and behavioral practices of individuals regarding neglected zoonotic diseases in Addis Ababa, Ethiopia.	A. Stringer[1], F. Abunna[2], Z. Dessalegn[2]; [1]Dept. Population Health and Pathobiology, College of Veterinary Medicine, NCSU, Raleigh, NC, USA, [2]Dept. of Clinical Sciences, College of Veterinary Medicine and Agriculture, AAU, Debre Zeit, Ethiopia.

Epidemiology and Animal Health Economics
Salon A/B/C/D - 5th Floor
Section Leader : Ashley Hill

TIME	NO	TITLE	Author Block
9:15	178	Neglected tropical diseases in Uganda-Impact on food security and public health	S.A. Baluka[1], J. Katalaga[1], T. Naligoyi[1], T. Dihn[2], T. Graham[3], E. Okori[4], M.L. Khaitsa[5]; [1]Biosecurity, Ecosystems and Veterinary Public Health, Makerere University, Kampala, Uganda, [2]Annimal and Diary Sciences, Mississippi State University, Mississippi State, MS, USA, [3]Veterinarians Without Borders, Davis, CA, USA, [4]Food and Agricultural Organization, Kampala, Uganda, [5]Pathobiology & Population Medicine, Mississippi State University, Mississippi State, MS, USA.
9:30		Break and Table Top Exhibitors - Foyer	
10:00	179	Distinguishing case series from cohort studies: do we agree?	J.M. Sargeant[1], J. Cullen[2], A. O'Connor[3], K. Makielski[3], A. Jones-Bitton[1]; [1]Population Medicine, Ontario Veterinary College, Guelph, ON, Canada, [2]Iowa State University, Guelph, IA, USA, [3]Iowa State University, Ames, IA, USA.
10:15	180	Assessing causal interrelationships between health and performance outcomes in feedlot cattle	E. Cha[1], M. Sanderson[1], N. Cernicchiaro[1], A. Jager[2], T. Schroeder[3], D. Renter[1], N. Bello[4]; [1]Department of Diagnostic Medicine/Pathobiology and Center for Outcomes Research and Education (CORE), Kansas State University, Manhattan, KS, USA, [2]Department of Statistics, Kansas State University, Manhattan, KS, USA, [3]Department of Agricultural Economics and Center for Risk Management Education and Research, Kansas State University, Manhattan, KS, USA, [4]Department of Statistics and Center for Outcomes Research and Education (CORE), Kansas State University, Manhattan, KS, USA.
10:30	181	Mental wellness in Canadian agricultural producers	A. Jones-Bitton[1], C. Best[1], J. Hewson[2]; [1]Department of Population Medicine, University of Guelph, Guelph, ON, Canada, [2]Department of Clinical Studies, University of Guelph, Guelph, ON, Canada.
10:45	182	Salmonella monitoring programs in Australian feed mills: A Retrospective analysis	E.M. Parker[1], L.J. Edwards[2], J. LeJeune[3]; [1]Animal Sciences, Ohio State University, Wooster, OH, USA, [2]Ridley AgriProducts, Pakenham, Australia, [3]Farm Animal Health Research Program, Ohio State University, Wooster, OH, USA.
11:00	183	Prevalence of multi-drug resistant Gram negative bacteria in the backyard poultry flock environment in Washington State	D.H. Shah[1], N.C. Paul[1], A.M. Clarridge[1], M. Board[1], D. Diaz[1], R. Crespo[1], C. Faux[2]; [1]Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA, USA, [2]Department of Integrated Physiology and Neurology, Washington State University, Pullman, WA, USA.

Epidemiology and Animal Health Economics Salon A/B/C/D - 5th Floor Section Leader : Ashley Hill			
TIME	NO	TITLE	Author Block
11:15	184	The effect of dietary flaxseed supplementation on the epidemiology of oviduct leiomyomas in laying hens - a model for uterine fibroids in women	M.C. Neu[1], R.A. Nowak[2], Y.J. Johnson-walker[3], M.S. Myint[3]; [1]School of Public Health, University of Illinois, Chicago, Chicago, IL, USA, [2]Animal Sciences, University of Illinois, Urbana-Champaign, Urbana, IL, USA, [3]Center for One Health Illinois, University of Illinois, Urbana-Champaign, Urbana, IL, USA.
11:45		Business Meeting, Dedication and Graduate Student Competition Awards Presentation	

Immunology Salon F/G/H - 5th Floor Section Leader : Renukaradhya Gourapura			
TIME	NO	TITLE	Author Block
MONDAY 8:00	91	Characterizing intestinal epithelial and immunological gene expression in healthy calves	K.H. Wade, E. Bichi, J.F. Lowe, B.M. Aldridge; College of Veterinary Medicine, University of Illinois, Urbana, IL, USA.
8:15	92	Induction of antiviral response against avian influenza virus infection using toll like receptor (TLR) 3 ligand, double stranded RNA	H. Ahmed-Hassan[1], M. Mohamed Abdul-Cader[2], E. Hamza[3], M. Sabry[3], M. Abdul Careem[2]; [1]Department of Ecosystem and Public Health, Faculty of Veterinary Medicine, University of Calgary, Calgary, AB, Canada, [2]Department of Ecosystem and Public Health, Faculty of Veterinary Medicine, University of Calgary, Calgary, AB, Canada, [3]Department of Zoonoses, Faculty of Veterinary Medicine, University of Cairo, Cairo, Egypt.
8:30	93	Efforts towards developing a universal vaccine against emerging influenza viruses.	A.O. Hassan[1], O. Amen[1], S. Vemula[1], E. Sayedahmed[1], I. York[2], S. Sambhara[2], S. Mittal[1]; [1]Comparative Pathobiology, Purdue University, WEST LAFAYETTE, IN, USA, [2]Influenza Division, Centers for Disease Control and Prevention, Atlanta, GA, USA.
8:45	94	Develoent of a recombinant parapoxvirus expressing the spike protein of porcine epidemic diarrhea virus.	K. Hain, 57007[1], L.R. Joshi[1], F. Okda[1], J. Nelson[1], A. Singrey[1], S. Lawson[1], M. Martins[2], A. Pillatzki[1], G. Kutish[3], E. Nelson[1], E.F. Flores[2], D.G. Diel, 57007[1]; [1]Veterinary and Biomedical Sciences, South Dakota State University, Brookings, SD, USA, [2]Preventive Veterinary Medicine, Federal University of Santa Maria, Santa Maria, Brazil, [3]University of Connecticut, Storrs, CT, USA.
9:00	95	Cross-reactivity of immune responses against porcine reproductive and respiratory syndrome virus	I. Correas, H.L.X. Vu, A.K. Pattnaik, F.A. Osorio; Nebraska Center for Virology and School of Veterinary Medicine and Biomedical Sciences, University of Nebraska-Lincoln, Lincoln, NE, USA.
9:15	96	Identification of an epitope from adenine nucleotide translocator1 that induces inflmation in heart in A/J mice	R.H. Basavalingappa1, C. Massilany1, B. Krishnan1, A. Gangaplara1, G. Kang2, V. Khalilzad-Sharghi3, Z. Han3, S. Othman3, Q. Li2, J.-J. Riethoven4, R.A. Sobel5, D. Steffen1, J. Reddy1; 1School of Veterinary Medicine and Biomedical Sciences, University of Nebraska-Lincoln, Lincoln, NE, USA, 2Nebraska Center for Virology and School of Biological Sciences, University of Nebraska-Lincoln, Lincoln, NE, USA, 3Department of Biological Systems Engineering, University of Nebraska-Lincoln, Lincoln, NE, USA, 4Center for Biotechnology, University of Nebraska-Lincoln, Lincoln, NE, USA, 5Department of Pathology, Stanford University School of Medicine, Stanford, CA, USA.
9:30		Break and Exhibitor Tables - Foyer	

Immunology Salon F/G/H - 5th Floor Section Leader : Renukaradhya Gourapura			
TIME	NO	TITLE	Author Block
10:00	97	Genome wide association study identifies loci associated with intrmary infection (IMI) phenotypes following experimental challenge with Streptococcus uberis	L.J. Siebert[1], M.E. Staton[2], S.P. Oliver[3], G.M. Pighetti[1]; [1]Animal Science, University of Tennessee, Knoxville, TN, USA, [2]Entomology and Plant Pathology, University of Tennessee, Knoxville, TN, USA, [3]AgResearch, University of Tennessee, Knoxville, TN, USA.
10:15	98	Dairy cows naturally infected with bovine leukemia virus demonstrate abnormal B and T cell responses to routine vaccination	M.C. Frie[1], K.R. Sporer[1], J.C. Wallace[1], R.K. Maes[2], L.M. Sordillo[3], P.C. Bartlett[3], P.M. Coussens[1]; [1]Department of Animal Science, Michigan State University, East Lansing, MI, USA, [2]Virology, Diagnostic Center for Population and Animal Health, East Lansing, MI, USA, [3]Department of Large Animal Clinical Sciences, Michigan State University, East Lansing, MI, USA.
10:30	99	detection of viral infections using multiplex molecular diagnostic technology. M. M. Hossain*, and R. R. R. Rowland. Department of Diagnostic Medicine/Pathobiology, College of Veterinary Medicine, Kansas State University, Manhattan, Kansas 66506	M. Hossain; Diagnostic Medicine/Pathobiology, Kansas State university, Manhattan, KS, USA.
10:45	100	Measuring bovine γδ t cell function at the site of Mycobacterium bovis infection	R.A. Rusk1, M. Palmer2, J. McGill1, R. Waters2; 1Diagnostic Medicine and Pathobiology, Kansas State University, Manhattan, KS, USA, 2National Animal Disease Center, IA, USA.
11:00	101	Cytokine driven monocyte differentiation influences the vitin D pathway-induced antimicrobial response	M.F. Kweh, K.E. Merriman, C.D. Nelson; Animal Science, University of Florida, Gainesville, FL, USA.
11:30		LUNCH	
Keynote Speaker 1:15	102	Genetic engineering of Disease-Resistant Animals: A Fantasy or Reality?	S.D. Srikumaran; Department of Veterinary Micobiology and Pathology, Washington State University, Pullman, WA, USA.
2:00	103	Cross-protective vaccine technology to mitigate respiratory viral diseases in pigs	R.J. Gourapura; Food Animal Health Research Program, OARDC, The Ohio State University, Wooster, OH, USA.

Immunology Salon F/G/H - 5th Floor Section Leader : Renukaradhya Gourapura			
TIME	NO	TITLE	Author Block
2:30	104	PLGA nanoparticle delivery of inactivated swine influenza virus vaccine provides heterologous protection through cell-mediated immunity in pigs	S. Dhakal[1], J. Hiremath[1], K. Bondra[1], Y. Shaan Lakshmanappa[1], D.L. Shyu[1], K. Ouyang[1], B. Binjawadagi[1], K.I. Kang[1], J. Goodman[2], K. Tabynov[3], S. Krakowka[4], B. Narasimhan[2], C.W. Lee[1], R.J. Gourapura[1]; [1]Food Animal Health Research Program, Department of Veterinary Preventive Medicine, The Ohio State University, Wooster, OH, USA, [2]Department of Chemical and Biological Engineering, Iowa State University, Ames, IA, USA, [3]The Research Institute for Biological Safety Problems (RIBSP), Gvardeiskiy, Kazakhstan, [4]Department of Veterinary Biosciences, The Ohio State University, Columbus, OH, USA.
2:45		Break and Exhibitor Tables - Foyer	
3:00	105	Adjuvants and their Mechanisms of Action	G. Mutwiri; University of Saskatchewan, Saskatchewan, SK, Canada.
3:30	106	Intradermal administration of adjuvant PCEP induces innate immune responses at the site of injection in pigs	R.B. Magiri[1], K. Lai[1], A.M. Chaffey[1], Y. Huang[2], H.L. Wilson[1], G.K. Mutwiri[1]; [1]VIDO-InterVac, School of Public Health, University of Saskatchewan, Saskatoon, SK, Canada, [2]Prairie Diagnostic Services Inc, Saskatoon, SK, Canada.
3:45	107	Chemistry and immunobiology of aluminum-containing adjuvants	H. HogenEsch; College of Vet Med, Purdue University, West Lafayette, IN, USA.
4:15	108	Efficacy and safety profile of an alpha-D-glucan nanoparticle based vaccine adjuvant.	F. Lu[1], R. Rodriguez Rosales[2], Y. Yao[2], H. HogenEsch[1]; [1]Comparative Pathobiology, Purdue University, West Lafayette, IN, USA, [2]Food Science, Purdue University, West Lafayette, IN, USA.
4:30	109	A novel combination adjuvant platform for human and animal vaccines.	V. Gerdts[1], S. Halperin[2], M.-N. Kweon[3], R.E. Hancock[4], S. van den Hurk[5], P. Timms[6], G. Mutwiri[7], A.A. Potter[5], L.A. Babiuk[8]; [1]Vaccine and Infectious Disease Organization - InterVac, Saskatoon, SK, Canada, [2]Dalhousin University, Halifax, NS, Canada, [3]International Vaccine Institute, Seoul, Korea, Republic of, [4]Univeristy of British Columbia, Vancouver, BC, Canada, [5]Vaccine and Infectious Disease Organization-InterVac, Saskatoon, SK, Canada, [6]Univeristy of the Sunshine Coast, Australia, Australia, [7]Vaccine and Infectious Organization-InterVac, Saskatoon, SK, Canada, [8]University of the Sunshine Coast, Australia, Australia.
4:30		Break and Exhibitor Tables - Foyer	
5:00		Poster Session II Grandballroom Salon III - 7 Floor	

Immunology
Salon F/G/H - 5th Floor
Section Leader : Renukaradhya Gourapura

TIME	NO	TITLE	Author Block
TUESDAY 8:00	185	Johne's Disease-positive and -negative cows exhibit diverse T cell phenotypes in response to in vitro MAP stimulation	K.R. Sporer, M.C. Frie, P.M. Coussens; Animal Science, Michigan State University, East Lansing, MI, USA.
8:15	186	Deciphering the cellular immune response in pigs	T. Kaeser[1], J.A. Pasternak[2], M. Delgado-Ortega[2], G. Hamonic[2], K. Lai[2], J. Erickson[2], S. Walker[2], J.-A.R. Dillon[2], V. Gerdts[2], F. Meurens[3]; [1]College of Veterinary Medicine, North Carolina State University, Raleigh, NC, USA, [2]Vaccine and Infectious Disease Organization (VIDO), University of Saskatchewan, Saskatoon, SK, Canada, [3]Oniris, LUNAM University, Nantes, France.
8:30	187	Pig leukocyte metabolism - changes associated with stimulation and PRRSV infection.	C.L. Loving[1], W.P. Schweer[2], H.R. Hughes[1], N.K. Gabler[2]; [1]Food Safety and Enteric Pathogens, USDA-ARS-National Animal Disease Center, Ames, IA, USA, [2]Department of Animal Science, Iowa State University, Ames, IA, USA.
8:45	188	Dietary resistant starch modulates intestinal immune status in pigs.	C. Briggs[1], J.M. Trachsel[2], N.K. Gabler[3], H.K. Allen[2], C.L. Loving[2]; [1]College of Veterinary Medicine, Washington School University, Pullman, WA, USA, [2]Food Safety and Enteric Pathogens, USDA-ARS-National Animal Disease Center, IA, USA,[3]Department of Animal Science, Iowa State University, IA, USA.
9:00	189	Cpylobacter jejuni strains from Guillain Barre Syndrome patients induce autoimmune peripheral neuropathy via Siglec-1 and IL-4 axes in a mouse model	L.S. Mansfield, A. Malik, J.M. Brudvig, B.J. Gadsden; Department of Microbiology and Molecular Genetics, Michigan State University, East Lansing, MI, USA.
9:15	190	Immune responses to senecavirus a in pigs	S. Lawson, L. Joshi, M.F. Maggioli, M.H.V. Fernandes, F. Okda, J. Christopher-Hennings, E. Nelson, D.G. Diel; Veterinary and Biomedical Sciences, South Dakota State University, Brookings, SD, USA.
9:30		Break and Exhibitor Tables - Foyer	
10:00	191	Non-esterified fatty acids induce proinflmatory macrophage phenotype	W. Raphael, G. Contreras; Large Animal Clinical Sciences, Michigan State University, East Lansing, MI, USA.
10:15	192	The link between the microbiome and immunological health in the intestines of healthy calves	K.H. Wade[1], E. Bichi[1], S.L. Ishaq[2], C.J. Yeoman[2], J.F. Lowe[1], B.M. Aldridge[1]; [1]College of Veterinary Medicine, University of Illinois, Urbana, IL, USA, [2]Department of Land Resources and Environmental Sciences, Montana State University, Bozeman, MT, USA.

Immunology Salon F/G/H - 5th Floor Section Leader : Renukaradhya Gourapura			
TIME	NO	TITLE	Author Block
10:30	193	Neonatal γδ T cell responses to mucosal TB vaccination	M. Guerra-Maupome[1], J. McGill[1], M. Larsen[2], M. Palmer[3], W. Waters[3]; [1]Diagnostic Medicine/Pathobiology, College of Veterinary Medicine, Kansas State University, Manhattan, KS, USA, [2]Microbiology & Immunology, Albert Einstein College of Medicine, Bronx, NY, USA, [3]Infectious bacterial Diseases Research Unit, National Animal Disease Center, Agricultural Research Service, USDA, Ames, IA, USA.
10:45	194	Develoent of intrauterine vaccination for use in livestock	J.A. Pasternak[1], G. Hamonic[1], N. Forsberg[1], M.K. Dyck[2], H.L. Wilson[1]; [1]VIDO-InterVac, University of Saskatchewan, Saskatoon, SK, Canada, [2]Agricultural, Food & Nutritional Science, University of Alberta, Edmonton, AB, Canada.
11:45		Business Meeting, Dedication and Graduate Student Competition Awards Presentation	

Pathobiology of Enteric and Foodborne Pathogens
Michigan/ Michigan State - 6th Floor
Section Leader : Weiping Zhang

TIME	NO	TITLE	Author Block
8:00	110	Use of a new in situ platform to co-detect Lawsonia intracellularis and proliferation markers in enterocytes of infected pigs	T.P. Resende[1], F.A. Vannucci[2], C.J. Gebhart[2]; [1]Veterinary and Biomedical Sciences, University of Minnesota, Saint Paul, MN, USA, [2]Veterinary Diagnostic Laboratory, University of Minnesota, Saint Paul, MN, USA.
8:15	111	Identifying immuno-dominant epitopes from F18 fimbriae FedF adhesins using reverse epitope vaccinology approach	T. Lu, W. Zhang, Q. Duan, R. Nandre; Diagnostic Medicine/Pathobiology, Kansas State University, Manhattan, KS, USA.
8:30	112	Screening immunodominant epitopes of enterotoxigenic Escherichia coli (ETEC) heat-labile toxin (LT) A subunit	J. Huang, Q. Duan, R. Nandre, W. Zhang; Diagnostic Medicine/Pathobiology, Kansas State University, Manhattan, KS, USA.
Keynote Speaker 8:45	113	Shiga toxin-producing Escherichia coli: key scientific discoveries and challenges that remain	R.A. Moxley; School of Veterinary Medicine & Biomedical Sciences, University of Nebraska-Lincoln, Lincoln, NE, USA.
9:30		Break and Exhibitor Tables - Foyer	
10:00	114	Differences in virulence and antimicrobial resistance gene profiles of bovine and human enterohemorrhagic Escherichia coli O157 and O103: A comparative genomics approach	L.W. Noll[1], J.N. Worley[2], X. Yang[2], X. Shi[1], J. Meng[2], T.G. Nagaraja[1]; [1]Diagnostic Medicine and Pathobiology, Kansas State University, Manhattan, KS, USA, [2]Nutrition and Food Science, University of Maryland, College Park, MD, USA.
10:15	115	Frequency of enterohemorrhagic Escherichia coli on cattle hides and quantification of E. coli on matched cattle hides and carcasses in commercial slaughter operations	A. Hoehn[1], L.W. Noll[1], P.B. Shridhar[1], X. Shi[1], T. Nagaraja[1], S.E. Ives[2], D.G. Renter[1], M.W. Sanderson[1], N. Cernicchiaro[1]; [1]Department of Diagnostic Medicine/Pathobiology, College of Veterinary Medicine, Kansas State University, Manhattan, KS, USA, [2]Department of Agricultural Sciences, College of Agriculture and Natural Sciences, West Texas A&M University, Canyon, TX, USA.
10:30	116	Dimethyl adenosine transferase (KsgA) contributes to structural and functional integrity of the cell envelope in Salmonella Enteritidis	K. Chiok, N.C. Paul, D.H. Shah; Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA, USA.
10:45	117	Lawsonia intracellularis vaccination decreases Salmonella enterica serovar Typhimurium shedding in co-infected pigs	F.L.L. Leite, C. Gebhart, R. Singer, R. Isaacson; University of Minnesota, St Paul, MN, USA.

Pathobiology of Enteric and Foodborne Pathogens
Michigan/ Michigan State - 6th Floor
Section Leader : Weiping Zhang

TIME	NO	TITLE	Author Block
11:00	118	Over-expressed linoleate isomerase gene in Lactobacillus casei and its role against enteric pathogens	M. Peng, D. Biswas; Animal Science, University of Maryland, College Park, MD, USA.
11:15	119	Modulation of poultry gut microbiome with phenolics from berry byproducts	S. Salaheen, D. Biswas; Department of Animal and Avian Sciences, University of Maryland-College Park, College Park, MD, USA.
11:30	120	Characterization of the fecal microbiome from EHEC positive and digital dermatitis negative beef cattle.	T. Turinski[1], M. Kulow[1], K. Anklam[1], E. Amene[1], K. Dill-McFarland[2], G. Suen[2], D. DÃ¶pfer[1]; [1]Department of Medical Sciences, School of Veterinary Medicine, University of Wisconsin-Madison, Madison, WI, USA, [2]Department of Bacteriology, University of Wisconsin-Madison, Madison, WI, USA.
11:30		LUNCH	
1:15	121	Sources and consequences of antibiotic resistance	K. Bush; Indiana University, Bloomington, IN, USA.
1:55	122	Reservoirs of antibiotic-resistant Escherichia coli in production environments: an opportunity for intervention?	D. Call[1], J. Liu[1], Z. Zhao[2], M. Davis[1], W. Sischo[1], T. Besser[1]; [1]Washington State University, Pullman, WA, USA, [2]Hohai University, Nanjing, China.
2:20	123	Antibiotics and the search for alternatives: pursuit and paradox	T. Turinski[1], M. Kulow[1], K. Anklam[1], E. Amene[1], K. Dill-McFarland[2], G. Suen[2], D. DÃ¶pfer[1]; [1]Department of Medical Sciences, School of Veterinary Medicine, University of Wisconsin-Madison, Madison, WI, USA, [2]Department of Bacteriology, University of Wisconsin-Madison, Madison, WI, USA.
2:45		Break and Exhibitor Tables - Foyer	
3:00	124	Potential broad spectrum antivirals targeting 3C or 3C-like proteases of picornaviruses, coronaviruses and caliciviruses	K.-O. Chang; Kansas State University, Manhattan, KS, USA.
3:25	125	Emerging antibiotic resistance mechanisms in foodbornepathogen Cpylobacter	Q. Zhang; Veterinary Microbiology and Precentive Medicine, Iowa State University, es, IA, USA.
3:50	126	Regulatory mechanisms of beta-lactase expression in Cpylobacter jejuni	J. Lin[1], X. Zeng[1], F. van den Akker[2]; [1]Dept. of Animal Science, University of Tennessee, Knoxville, TN, USA, [2]Biochemistry, Case Wester Reserve University, Cleveland, OH, USA.
4:30		Break and Exhibitor Tables - Foyer	

Pathobiology of Enteric and Foodborne Pathogens
Michigan/ Michigan State - 6th Floor
Section Leader : Weiping Zhang

TIME	NO	TITLE	Author Block
5:00		Poster Session II Grandballroom Salon III - 7 Floor	
TUESDAY 8:30	197	Characterization of A subunit epitopes in enterotoxicity of enterotoxigenic Escherichia coli (ETEC) heat-labile toxin	J. Huang, Q. Duan, R. Nandre, W. Zhang; Diagnostic Medicine/Pathobiology, Kansas State University, Manhattan, KS, USA.
8:45	198	Escherichia coli from poultry : understanding their zoonotic-risk and develoent of a vaccine for the control of their infections and carriage in poultry	M. Mellata1, J.R. Johnson2, J.M. Fairbrother3, R. Curtiss, 3rd4; 1Food Science and Human Nutrition, Iowa State University, es, IA, USA, 2Veterans Affairs Medical Center, University of Minnesota, Minneapolis, MN, USA, 3Faculty de medecine vÃ©tÃ©rinaire, University de Montral, St-Hyacinthe, QC, Canada, 4Department of Infectious Diseases and Pathology, University of Florida, Gainesville, FL, USA.
9:00	199	Genetic diversity and antimicrobial resistance of Cpylobacter jejuni & Cpylobacter coli isolates from chickens	M. Nisar[1], G. Rajashekara[2], S.M. Goyal[3], K.V. Nagaraja[1]; [1]Department of Veterinary and Biomedical Sciences, University of Minnesota, Saint Paul, MN, USA, [2]Department of Veterinary Preventive Medicine, The Ohio State University, Wooster, OH, USA, [3]Department of Veterinary Population Medicine, University of Minnesota, Saint Paul, MN, USA.
9:15	200	Prevalence and antimicrobial resistance patterns of Escherichia coli in raw meat and milk sples in central Oromia, Ethiopia	Y. Equar1, S. Tikuye1, D. Tesfaye1, G. Mu1, B. Arega1, R.D. Abdi2; 1National Agricultural Biotechnology Research Center, Ethiopian Institute of Agricultural Research, Holota, Ethiopia, 2Animal Science, University of Tennessee, Knoxville, TN, USA.
9:30		Break and Exhibitor Tables - Foyer	
10:00	201	Extended-spectrum cephalosporin resistance in Escherichia coli from Alberta beef cattle	A.C. Cormier[1], G. Chalmers[1], T.A. McAllister[2], S.R. Cook[2], R. Zaheer[2], S. Hannon[3], C.W. Booker[3], R.R. Read[4], S. Gow[5], P. Boerlin[1]; [1]Pathobiology, University of Guelph, Guelph, ON, Canada, [2]Agriculture and Agrifood Canada, Lethbridge, AB, Canada, [3]Feedlot Health Management Services, Okotoks, AB, Canada, [4]Microbiology, Immunology and Infectious Diseases, University of Calgary, Calgary, AB, Canada, [5]Large Animal Clinical Sciences, University of Saskatchewan, Saskatoon, SK, Canada.
10:15	202	Antimicrobial resistance patterns of Staphylococcus aureus isolates from cases of bovine mastitis	R.D. Abdi, J.M. Vaughn, B.E. Gillespie, C. Merrill, O. Kerro Dego; Animal Science, University of Tennessee, Knoxville, TN, USA.
11:45		Business Meeting, Dedication and Graduate Student Competition Awards Presentation	

Respiratory
Indiana/ Iowa - 6th Floor
Section Leader : Amelia Woolums

TIME	NO	TITLE	Author Block
8:30	127	Pathogenicity of a new Russian genotype 1 subtype 2 PRRSV isolate	S.A. Raev[1], A.G. Yuzhakov[2], A.M. Mishin[3], A.N. Shkrylev[4], T.V. Grebennikova[5], V.V. Stafford[6], O.A. Verkhovskii[7], A.D. Zaberezhny[5], T.I. Aliper[1], H. Nauwynck[8]; [1]Swine diseases, Y.R. Kovalenko All-Russian Research Institute of Experimental Veterinary Medicine (VIEV), Moscow, Russian Federation, [2]Molecular biology, Diagnostics and Prevention Research Institute for Human and Animal Diseases, Moscow, Russian Federation, [3]Virology, Diagnostics and Prevention Research Institute for Human and Animal Diseases, Moscow, Russian Federation, [4]Production, Siberian Agrarian Group, Tomsk, Russian Federation, [5]Molecular biology, Y.R. Kovalenko All-Russian Research Institute of Experimental Veterinary Medicine (VIEV), Moscow, Russian Federation, [6]Pathomorphology, Y.R. Kovalenko All-Russian Research Institute of Experimental Veterinary Medicine (VIEV), Moscow, Russian Federation, [7]Immunology, Diagnostics and Prevention Research Institute for Human and Animal Diseases, Moscow, Russian Federation, [8]Virology, parasitology and immunology, Ghent University, Ghent, Belgium.
8:45	128	Contribution of PRRSV minor glycoproteins to a protective immune response in swine	K. Kimpston-Burkgren[1], H. Vu[1], I. Correas[1], D. Steffen[1], A. Pattnaik[1], Y. Fang[2], F. Osorio[1]; [1]University of Nebraska-Lincoln, Lincoln, NE, USA, [2]Kansas State University, Manhattan, KS, USA.
9:00	129	Comparison of morbidity and mortality after challenge with two North erican PRRS virus isolates shows marked variation in clinical disease between isolates	L. Constance[1], B. Bloomberg[2], J.K. Lunney[3], J.C.M. Dekkers[4], R.R.R. Rowland[1], M.C. Niederwerder[5]; [1]Department of Diagnostic Medicine/Pathology, Kansas State University, Manhattan, KS, USA, [2]Comparative Medicine Group, Kansas State University, Manhattan, KS, USA, [3]Agricultural Research Services, United State Department of Agriculture: Beltsville Agricultural Research Center, Beltsville, MD, USA, [4]Department of Animal Science, Iowa State University, Ames, IA, USA, [5]Department of Diagnostic Medicine/Pathology; Kansas State Veterinary Diagnostic Laboratory, Kansas State University, Manhattan, KS, USA.
9:15	130	Differential susceptibility of bighorn sheep and domestic sheep neutrophils to Mannheimia haemolytica leukotoxin is not due to differential expression of cell surface CD18	R.P. Dassanayake[1], S. Shanthalingam[2], W. Liu[2], D.P. Knowles[3], E. Casas[1], S. Srikumaran[2]; [1]ARS, NADC, USDA, Ames, IA, USA, [2]Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, WA, USA, [3]ADRU, ARS, USDA, Pullman, WA, USA.

Respiratory
Indiana/ Iowa - 6th Floor
Section Leader : Amelia Woolums

TIME	NO	TITLE	Author Block
9:30		Break and Exhibitor Tables - Foyer	
10:00	131	Disparity in nasopharyngeal microbiome between healthy cattle on feed, at entry processing and with respiratory disease	M. Zeineldin[1], J. Lowe[1], N. Maradiaga[1], M. Ghanem[2], Y. Abdelraof[2], B. Aldridge[1]; [1]Veterinary Clinical Medicine, Illinois University, Urbana, IL, USA, [2]College of Veterinary Medicine, Benha University, Toukh, Egypt.
10:15	132	Microenvironmental spling techniques of the nasal cavity of cattle and experimental colonization of Mannheimia haemolytica	S.L. Collins, M. Caldwell, C. Benh; University of Tennessee College of Veterinary Med, Knoxville, TN, USA.
10:30	133	Prevalence of multi drug antimicrobial resistance in Mannheimia haemolytica isolated from high risk stocker cattle prior to and following metaphylaxis	E. Snyder[1], B. Credille[2], R. Berghaus[1], S. GiguÃ¨re[3]; [1]Department of Population Health, University of Georgia, Athens, GA, USA, [2]Depatment of Population Health, University of Georgia, Athens, GA, USA, [3]Department of Large Animal Medicine, University of Georgia, Athens, GA, USA.
10:45	134	Host gene expression response to experimental BRSV infection	L.J. Gershwin[1], A.L. Van Eenennaam[2], H.L. Neibergs[3], J.F. Taylor[4], J. Womack[5]; [1]Pathology, Microbioloby, & Immunology, University of California, Davis, Davis, CA, USA, [2]Animal Science, University of California, Davis, Davis, CA, USA, [3]Animal Sciences, Washington State University, Pullman, WA, USA, [4]Division of Animal Sciences, University of Missouri, Columbia, MO, USA, [5]Veterinary Pathobiology, Texas A & M, College Station, TX, USA.
11:00	135	Haptoglobin concentrations in cattle either mass-medicated with githromycin or sh-treated -- from shipping through sickness and recovery.	C.G. Chitko-McKown[1], A.M. Workman[1], K.D. DeDonder[2], G.L. Bennett[1], M.D. Apley[2], G.P. Harhay[1], D.M. Harhay[3], L.A. Kuehn[1], B.J. White[2], R.L. Larson[2], S.F. Capik[2], B.V. Lubbers[2], M.L. Clawson[1]; [1]Genetics, Breeding, and Animal Health Research Unit, U.S. Meat Animal Research Center, Clay Center, NE, USA, [2]College of Veterinary Medicine, Kansas State University, Manhattan, KS, USA, [3]Meat Safety and Quality Research Unit, U.S. Meat Animal Research Center, Clay Center, NE, USA.
11:15	136	Comparison of leukocyte profile determined by point of care analyzer and manual evaluation in calves inoculated with Mannheimia haemolytica and Bovine Viral Diarrhea Virus.	A.S. Lear, J.M. Caldwell; Large Animal Clinical Sciences, University of Tennessee, Knoxville, TN, USA.
11:30		LUNCH	

Respiratory
Indiana/ Iowa - 6th Floor
Section Leader : Amelia Woolums

TIME	NO	TITLE	Author Block
2:15	137	The upper respiratory tract microbiome and its potential role in canine respiratory infections	G. MORE, M. Dunowska, P.J. Biggs, E. Acke, N. Cave; INSTITUTE OF VETERINARY ANIMAL AND BIOMEDICAL SCIENCES, MASSEY UNIVERSITY, Palmerston North, New Zealand.
2:30	138	Demonstration of protection against Canine Influenza Virus H3N2 infection following vaccination with an inactivated CIV H3N2 / H3N8 bivalent vaccine	T. Davis; Merck Animal Health, Elkhorn, NE, USA.
3:00	139	The B. bronchiseptica type III secretion system does not negatively affect the protective immunity induced by influenza A virus vaccines	T.L. Nicholson1, A.L. Vincent1, S.L. Brockmeier1, D.S. RajÃ£o1, E.J. Abente1, P.C. Gauger2; 1National Animal Disease Center-ARS-USDA, es, IA, USA, 2Department of Veterinary Diagnostic and Production Animal Medicine, Iowa State University, es, IA, USA.
3:15	140	Serological prevalence of three H1 phylogenetic clades and two H3 antigenic clusters of influenza A virus in breeding age swine in the United States	J.S. Carlson, P. Gauger; Iowa State University, es, IA, USA.
3:30	141	Evaluation of candidate chimeric influenza hemagglutinin vaccines for induction of broad immunity within the influenza virus H1N1 subtype	P. Shang[1], Z. Li[2], S. Zaiser[3], P. Katwal[3], Y. Li[1], S. Sunwoo[1], J. Richt[1], Y. Fang[1], B. He[2], V.C. Huber[3]; [1]DMP, Kansas state university, Manhattan, KS, USA, [2]University of Georgia, Athens, GA, USA, [3]University of South Dakota, Vermillion, SD, USA.
Keynote Speaker 3:45	142	EmergingAvian Influenza Viruses: Their Implications and Control Strategies	S.K. Mittal[1], A.O. Hassan[1], O. Amen[1], S.V. Vemula[1], E.E. Sayedahmed[1], I. York[2], S. Gangappa[2], S. Sambhara[2]; [1]Purdue University, College of Veterinary Medicine, West Lafayette, IN, USA, [2]Center for Disease Control and Prevention, Atlanta, GA, USA.
4:15	143	Influenza A virus herd-level prevalence and seasonality in Midwestern U.S. pig breeding herds	F. Chamba[1], A. Alba[1], J. Nerem[2], M. Torremorell[1]; [1]Veterinary Population Medicine, University of Minnesota, St Paul, MN, USA, [2]Swine Health Management, Pipestone Veterinary Services, Pipestone, MN, USA.
4:30		Break and Exhibitor Tables - Foyer	
5:00		Poster Session II Grandballroom Salon III - 7 Floor	

Vector - Borne & Parasitic Disease
Denver/ Houston - 5th Floor
Section Leader : Roman Ganta & Jill McGill

TIME	NO	TITLE	Author Block
8:15	144	LSDV100 and LSDV101 Lumpy skin disease virus-specific PCR for rapid diagnosis and vaccine quality control.	A. Yousif[1], O. Refaei[2], M. Bayoumi[1], H. El-Sheikh[3], M. Elgmal[1], A. EL-sayed[2], A. Fayed[2], M. Shalaby[1]; [1]Virology, Faculty of Veterinary Medicine, Giza, Egypt, [2]Infectious Diseases, Faculty of Veterinary Medicine, Giza, Egypt, [3]Infectious Diseases, Faculty of Veterinary Medicine, Zagazig, Egypt.
8:30	145	Glycosylated Ehrlichia ruminantium major antigenic protein1 subunit vaccine induces strong antibody and T cell responses in sheep	B. Faburay[1], J. McGill[1], F. Jongejan[2]; [1]Diagnostic Medicine/Pathobiology, Kansas State University, Manhattan, KS, USA, [2]Faculty of Veterinary Medicine, Utrecht University, Utrecht Center for Tick-Borne Diseases, Utrecht, Netherlands.
8:45	146	The distribution of invertebrate reservoir host for Lyme disease in Kyiv, Ukraine	A. Rogovskyy[1], I.V. Nebogatkin[2], D.C. Gillis[1]; [1]Texas A&M University, College Station, TX, USA, [2]I.I. Schmalhausen Institute of Zoology of National Academy of Sciences of Ukraine, Kyiv, Ukraine.
9:00	147	Next generation sequencing and genomic analysis of Tritrichomonas foetus species of bovine and feline origin	E. Fleetwood; University of Tennessee, Memphis, TN, USA.
9:15	148	Seroprevalence of bovine anaplasmosis in Kentucky, 2003-2011	S.L. Collins[1], B.K. Whitlock[1], J.A. Daniel[2], J.F. Coetzee[3]; [1]University of Tennessee College of Veterinary Med, Knoxville, TN, USA,[2]Berry College, Mt. Bery, GA, USA, [3]Iowa State University, IA, USA.
9:30		Break and Exhibitor Tables - Foyer	
Keynote Speaker 10:00	149	How genomicshas facilitated vaccine develoent for Anaplasmarginale	K.A. Brayton; Veterinary of Microbiology and Pathology, Washington State University, Pullman, WA, USA.
4:30		Break and Exhibitor Tables - Foyer	
5:00		Poster Session II Grandballroom Salon III - 7 Floor	

Viral Pathogenesis
Los Angeles/Miami - 5th Floor
Section Leader : Kyoung - Jin Yoon

TIME	NO	TITLE	Author Block
MON. 8:15	151	Porcine deltacoronavirus induces caspase-dependent progrmed cell death	Y. Lee, C. Lee; Kyungpook National University, Daegu, Korea, Republic of.
8:30	152	Comparison of porcine epidemic diarrhea virus (PEDV) and porcine deltacoronavirus (PDCoV) for pathogenicity in nursery pigs	K.A. Gibson[1], S.M. Curry[2], E.R. Burrough[1], K.J. Schwartz[1], B. Guo[1], W.P. Schweer[2], M. Bhandari[1], H. Hoang[1], S. Azeem[1], N.K. Gabler[1], K.J. Yoon[1]; [1]Veterinary Diagnostic and Production Animal Medicine, Iowa State University, Ames, IA, USA, [2]Animal Science, Iowa State University, Ames, IA, USA.
8:45	153	Develoent of a new molecular method to discriminate Porcine epidemic diarrhea virus infectious particles, from non-infectious ones, that are contaminating food additives	C. Provost[1], P. Garneau[1], D. Ojkic[2], J. Harel[1], C.A. Gagnon[1]; [1]Swine and Poultry Infectious Diseases Research Center (CRIPA), FacultÃ© de mÃ©decine vÃ©tÃ©rinaire, UniversitÃ© de MontrÃ©al, St-Hyacinthe, QC, Canada, [2]Animal Health Laboratory (AHL), University of Guelph, Guelph, ON, Canada.
9:00	154	Develoent of porcine epidemic diarrhea virus vaccines derived from a virulent Korean strain	S. Lee, C. Lee; Kyungpook National University, Daegu, Korea, Republic of.
9:15	155	Efficacy test and safety test of new genetically variant ped virus vaccine strain	H. Jang; WOOGENE Co., GyeonginRo 775, Yedeungpogu, Seoul, Korea, Republic of.
9:30		Break and Table Top Exhibitors - Foyer	
10:00	156	Comparison of experimental and commercial PEDV vaccines to protect against PEDV genogroup 2 challenge using the conventional growing pig model	T. Opriessnig[1], P. Gerber[1], J. Zhang[2], Q. Chen[2], P. Halbur[2]; [1]The Roslin Insitute, University of Edinburgh, Midlothian, UK, [2]Iowa State University, Ames, IA, USA.
10:15	157	Develoent of murine monoclonal antibodies (mABs) for porcine rotavirus (PoRV) group A, B, and C and their use in a comparative pathogenicity study	H.T. Hoang[1], D. Madson[2], R. Derscheid[2], C. Miller[1], J. Groeltz[2], D. Sun[1], K.-J. Yoon[2]; [1]Veterinary Microbiology and Preventive Medicine, Iowa State University, Ames, IA, USA, [2]Veterinary Diagnostic and Production Animal Medicine, Iowa State University, Ames, IA, USA.
10:30	158	Infectious bronchitis corona virus tropism for macrophages in vitro and in vivo	A. Amarasinghe, S. Nazir, M. Abdul-Cader, A. Kameka, F. van der Meer, M. Abdul-Careem; Faculty of Veterinary Medicine, University of Calgary, Calgary, AB, Canada.
10:45	159	Specific pathogen-free (SPF) turkey model for emerging reoviral arthritis	J.M. Ngunjiri, S. Waliullah, H. Jang, M. Elaish, A. Ghorbani, M. KC, M.C. Abundo, C.-W. Lee; Food Animal Health Research Program, Ohio Agricultural Research and Development Center, The Ohio State University, WOOSTER, OH, USA.

Viral Pathogenesis
Los Angeles/Miami - 5th Floor
Section Leader : Kyoung - Jin Yoon

TIME	NO	TITLE	Author Block
11:00	160	Chicken Anemia Virus CAV in Egyptian broilerSerological survey, clinical signs, pathological pareters, and molecular characterization of the virus.	D.M.H. Ahmed, Jr.; Avian and Rabbit Med., Faculty of Vet. Med., Ismailia, Egypt.
11:15	161	Toll-like receptor 3 (TLR3) and influenza pathogenesis in quail	M. KC[1], J. Lee[2], J.M. Ngunjiri[1], H. Jang[1], Y. Suh[2], K. Lee[2], C.-W. Lee[1]; [1]Food Animal Health Research Program, Ohio Agricultural Research and Development Center, The Ohio State University, Wooster, OH, USA, [2]Department of Animal Sciences, College of Food, Agricultural, and Environmental Sciences, The Ohio State University, Columbus, OH, USA.
11:30		LUNCH	
1:30	162	Attenuation of recombinant influenza virus expressing the naturally truncated NS gene from an H3N8 equine influenza virus in mice	W. Na[1], K.-S. Lyoo[2], S.-W. Yoon[3], M. Yeom[1], H.-O. Kim[4], D. Song[1]; [1]Korea university, Sejong, Korea, Republic of, [2]2Korea Zoonosis Research Institute, Iksan, Korea, Republic of, [3]Korea Research Institute of Bioscience and Biotechnology, Daejeon, Korea, Republic of, [4]Yonsei University, Seoul, Korea, Republic of.
1:45	163	Application of NS1-truncated variant as live attenuated influenza vaccine for early protection and its complementary use with inactivated vaccine in chickens	H. Jang, J.M. Ngunjiri, M. Elaish, C.-W. Lee; The Ohio state university, Wooster, OH, USA.
2:00	164	Bovine adenoviral vector system for developing effective vaccines against emerging avian influenza viruses	E.E. Sayedahmed, A.O. Hassan, R. Kumari, S.K. Mittal; Comparative Pathobiology, Purdue University, West Lafayette, IN, USA.
2:15	165	Markers of Apoptosis in different cell lines by Equine Arteritis Virus	M.M. Abeya, G.E. Metz, M.S. Serena, C.J. Panei, C.G. Aspitia, M.G. Echeverria; Virologia, Universidad Nacional de La Plata, La Plata, Argentina.
2:30	166	Porcine reproductive & respiratory syndrome virus takes advantage of host intercellular mitochondria transferring pathway for cell to cell spreading of infection	R. Guo, Y. Fang; Diagnostic Medicine & Pathobiology, Kansas state University, Manhattan, KS, USA.
2:45		Break and Table Top Exhibitors - Foyer	

Viral Pathogenesis
Los Angeles/Miami - 5th Floor
Section Leader : Kyoung - Jin Yoon

TIME	NO	TITLE	Author Block
3:00	167	SAP domain in nsp1-beta of PRRSV correlates with interferon suppression in cells and virulence in pigs	H. Ke[1], M. Han[1], M. Kerrigan[2], R.R.R. Rowland[2], D. Yoo[1]; [1]Department of Pathobiology, University of Illinois at Urbana-Champaign, Urbana, IL, USA, [2]Department of Diagnostic Medicine & Pathobiology, Kansas State University, Manhattan, KS, USA.
3:15	168	Novel arterivirus proteins and expression mechanism: implication in PRRSV vaccine develoent	Y. Li[1], S. Napthine[2], E. Treffers[3], P. Shang[1], A. Tas[3], A. Firth[2], I. Brierley[2], E. Snijder[3], Y. Fang[1]; [1]Diagnostic Medicine and Pathobiology, Kansas State University, Manhattan, KS, USA, [2]Department of Pathology, University of Cambridge, Cambridge, UK, [3]Leiden University Medical Center, Leiden, Netherlands.
3:30	169	Comparative pathogenesis and genome sequence of recent 1-7-4 PRRSV isolates in weanling age piglets	A.G.M. Van Geelen[1], K.S. Faaberg[2], P. Das[1], N.A. Montiel[1], L.C. Miller[2], V. Kulshreshtha[1], A.C. Buckley[1], K.M. Lager[2]; [1]Oak Ridge Institute for Science and Education, Oak Ridge, TN, USA, [2]Virus and Prion Research Unit, ARS-USDA, Ames, IA, USA.
3:45	170	IFN-1 pathway signaling in bovine cells concurrently infected with BVDV and BRSV	A.A. Alkheraif, C.L. Topliff, J. Reddy, C.L. Kelling; School of Veterinary Medicine and Biomedical Sciences, University of Nebraskaâ€“Lincoln, Lincoln, NE, USA.
4:00	171	Duration of positive viral PCR results following intranasal and injectable multivalent MLV vaccination in naïve calves	B. Newcomer[1], K.P. Riddell[1], D. Scruggs[2], V.S. Cortese[2], P.H. Walz[1]; [1]Auburn University, Auburn, AL, USA, [2]Zoetis, Florham Park, NJ, USA.
4:15	172	Genotypematched NDV vaccines against currently circulating viruses in Indonesia	V. Manoharan[1], S. Kim[1], B. Varghese[1], S. Samal[2]; [1]College of Veterinary Medicine, University of Maryland, College Park, MD, USA, [2]College of Veterinary Medicine, University Of Maryland, College Park, MD, USA.
4:30		Break and Table Top Exhibitors - Foyer	
5:00		Poster Session II - Grandballroom Salon III - 7th Floor	
TUESDAY 8:00	203	A novel porcine circovirus distantly related to known circoviruses is associated with porcine dermatitis and nephropathy syndrome and reproductive failure	R. Palinski[1], P. Pineyro[2], P. Shang[1], F. Yuan[1], R. Guo[1], Y. Fang[1], E. Byers[3], B. Hause[4]; [1]Kansas State University, Manhattan, KS, USA, [2]Iowa State University College of Veterinary Medicine, Ames, IA, USA, [3]Smithfield Hog Production, Warsaw, NC, USA, [4]Kansas State University Veterinary Diagnostic Laboratory, Manhattan, KS, USA.
8:15	204	Pathogenesis and infection dynics of Senecavirus A in pigs	L.R. Joshi[1], M.H.V. Fernandes[1], T. Clement[1], S. Lawson[1], A. Pillatzki[1], T.P. Resende[2], F. Vanucci[2], E. Nelson[1], D.G. Diel[1]; [1]Veterinary and Biomedical Sciences, South Dakota State University, Brookings, SD, USA, [2]Veterinary Diagnostic Laboratory, University of Minnesota, St. Paul, MN, USA.

Viral Pathogenesis
Los Angeles/Miami - 5th Floor
Section Leader : Kyoung - Jin Yoon

TIME	NO	TITLE	Author Block
8:30	205	Senecavirus A infection in sows, neonates, and market weight gilts with subsequent protective immunity	A. Buckley[1], B. Guo[2], N. Montiel[1], V. Kulshreshtha[1], A. van Geelen[1], K. Yoon[2], K. Lager[3]; [1]Oak Ridge Institute for Science and Education, National Animal Disease Center, USDA, Ames, IA, USA, [2]College of Veterinary Medicine, Iowa State University, Ames, IA, USA, [3]National Animal DIsease Center, USDA, Ames, IA, USA.
8:45	206	Construction and characterization of a full-length cDNA infectious clone of emerging porcine Senecavirus A	P. Shang[1], Z. Chen[1], F. Yuan[1], Y. Li[1], R. Schroeder[2], K. Lechtenberg[2], J. Henningson[1], B. Hause[1], J. Bai[1], R.R.R. Rowland[1], A. Clavijo[1], Y. Fang[1]; [1]Kansas state university, Manhattan, KS, USA, [2]Midwest Veterinary Services, Inc, Oakland, NE, USA.
9:00	207	Experimental teschovirus encephalomyelitis induced either by Teschovirus A serotype 2 or serotype 11.	F.S. Matias Ferreyra, P. Arruda, G. Stevenson, B. Arruda, K.J. Schwartz, K.J. Yoon, D. Madson, J. Zhang, Q. Chen; VDPAM, Iowa State University, Ames, IA, USA.
9:15	208	Identification of a divergent strain of Sapelovirus associated with a severe polioencephalomyelitis outbreak in the US	P.H.E. Arruda; Veterinary Diagnostic and Production Animal Medicine, Iowa State University, Ames, IA, USA.
9:30		Break and Table Top Exhibitors - Foyer	
10:15		In Memory of Prem Paul	Don Reynolds, University of Nebraska Lincoln
Keynote Speaker 10:15:00 AM	209	Challenges for African Swine FeverVaccine Development - " perhaps the end of the beginning."	D. Rock, University of Illinois at Urbana
Second Keynote Speaker 11:00:00 AM		"PRRSV Vaccines: Pursuing A Broader, Heterologous Protection"	Fernando Osoiro, Unverisity of Nebraska Lincoln
11:45		Business Meeting, Dedication, and Graduate Competition Award Presentation	

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1
Differential detection, genomic characterization and phylogenetic analysis of Porcine Epidemic Diarrhea Viruses from vaccinated pig herds in Fujian, China 2016

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Porcine epidemic diarrhea virus (PEDV) causes devastating impact on global pig-breeding industry and current vaccines have become not effective against the circulating PEDV variants since 2011. In this study, a multiplex RT-PCR assay for seven swine pathogens were performed on samples collected from pig herds suffering severe diarrhea, which were immunized with commercial bivalent (PEDV and TGEV) attenuated vaccines. PEDV was identified as the major causative agent for the outbreaks. Two complete genomes (XM1-2 and XM2-4) of PEDV isolated from two pig herds in Fujian province were determined. Genomic comparison showed that the two isolates share the highest nucleotide identities (99.09% and 98.77%) with ZMDZY strain isolated in China 2011, but have only 96.65% and 96.49% nucleotide identities with CV777 vaccine strain, respectively. Amino acid alignment of spike proteins indicated that our isolates have the same insertion and deletion pattern as other Chinese PEDV variants. And also the same three substitutions in the neutralizing epitopes generating serines were found, which might change the neutralization activities against the variants. There is only one unique substitution $A_{1100}S$ in the spike protein of 2016 isolates differed themselves. Phylogenetic analysis showed that our isolates belong to the IIa subgroup of genotype II group and form a new branch. To sum up, we detected new PEDV variants in China 2016 by using a multiple RT-PCR assay. Genomic and phylogenetic analysis showed that the new isolates are clustered with PEDV variants, which could not be effectively controlled by current commercial vaccines. Our findings suggest that more effective vaccines are urgently needed for the prevention and control of Chinese PEDV variants.

2

A cost effective method for surveillance of PRRSV and IAV-S in oral fluids using a newly developed multiplex rtRT-PCR

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The objective of this study was to develop a cost effective method for respiratory disease surveillance in swine oral fluid samples, specifically for porcine reproductive and respiratory syndrome (PRRSV) and influenza A virus in swine (IAV-S). Individual real-time reverse transcription polymerase chain reaction (rtRT-PCR) tests for both PRRSV and IAV-S are well established. Here, we have developed a multiplex rtRT-PCR that detects the conserved region of the 3'untranslated region of PRRSV and the matrix region of IAV-S to cut the cost of testing to the producer and promote the continued surveillance for both PRRSV and IAV-S in a single reaction. Recently, the USDA discontinued the funding for IAV-S matrix testing making the cost of the IAV-S surveillance screening by rtRT-PCR the responsibility of the producer. The characterization of circulating IAV-S for vaccine selection remains important to swine and human health. Screening for IAV by rtRT-PCR is a vital step in surveillance. The mechanism by which PRRSV interacts with other pathogens, such as IAV-S, is still being explored but it is believed that these interactions can increase the severity of pathogenicity. The producer will see a 50% cost savings when using the multiplex testing versus the singleplex. In conclusion, having a well validated and rapid diagnostic tool such as this new multiplex rtRT-PCR will be vital for continued swine health and production.

3
ELISAs based on recombinant nsp7 proteins from PRRSV type 1 and 2 as DIVA tests

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Tests for Differentiation between Infected and Vaccinated Animals (DIVA) are of high importance for the establishment of PRRS control programs. The present study aimed to develop ELISAs based on recombinant nsp7 to assess their potential application as DIVA tests. For this purpose, RT-PCR products of nsp7 from Olot91 (type 1) and from VR2332 (type 2) PRRSV isolates were cloned into two baculovirus vectors. Then, the recombinant baculoviruses were propagated in Sf9 cells (CRL1711, ATCC). Nsp7s were purified, quantified and used to develop the ELISAs. The optimal coating conditions were determined by checkerboard titration and the background was minimized by comparing different dilution buffers. ELISAs were set up using sera from experimentally infected and non-infected animals. The positive or negative status of immunization was previously determined by commercial ELISAs based on N protein: PRRS X3 Ab test (IDEXX) and INgezim PRRS Universal (INGENASA). Cut-off of the assays were adjusted to 0.4 by ROC analysis with the MedCalc software. With this value, both the sensitivity and the specificity of the assay was 100%.

Dynamics of antibodies anti nsp7 were evaluated in 35 pigs experimentally infected with six different type 1 strains; detection started at 14-21 days post infection (dpi) and pigs remained as positive until the last dpi tested (35, 49 or 77 dpi). Also, 20 sera from pigs vaccinated under experimental conditions with PRRS type 1 or type 2 attenuated vaccines -Porcilis (MSD) and Ingelvac (Boehringer Ingelheim), respectively- were evaluated. Despite the fact that vaccinated pigs were positive in commercial ELISAs from 7 dpi onwards, antibodies against nsp7 were never noticed. Based on these results, the nsp7 ELISA assays were further analyzed as candidate ELISAs for DIVA tests using sera from infected or vaccinated animals belonging to experimental studies and field. Commercial ELISAs against N protein were used as references. For type 2, the analysis of sera from vaccinated and infected pigs under experimental conditions indicated that the nsp7 type 2 ELISA had a sensitivity of 100% and a specificity of 94.7% as a DIVA test; for PRRSV type 1, low values of sensitivity and specificity were obtained. Under field conditions, there was a clear decrease in these two parameters: sensitivity 83.3%, specificity 83.2 %; however, there were significant statistical differences ($p<0.05$) when infected and vaccinated pigs were compared at population level:

	Parameter	Infected	Vaccinated	p value
PRRSV type 1	**Mean OD nsp7**	1.54	0.27	<0.0001
	n	77	150	
PRRSV type 2	**Mean OD nsp7**	1.66	0.45	<0.0001
	n	178	103	

In conclusion, ELISAs based on nsp7 were able to differentiate between infected and vaccinated animals under experimental conditions. Regarding sera collections from the field, the results indicated that the assays were also useful as DIVA tests but at the population level.

4

Genetic characterization and phylogenetic analysis of Senecavirus A

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Senecavirus A (SVA) is an emerging picornavirus that has been associated with outbreaks of vesicular disease and neonatal mortality in the major swine producing countries of the world. Since November 2014, SVA has also been frequently reported in swine in Brazil and since July 2015 over 200 cases of SVA have been confirmed in the US. The factors that contributed for the emergence of SVA remain unknown. The overall goal of our study was to determine the genetic diversity of SVA strains circulating in the US and Brazil. The complete genome sequence of 21 contemporary SVA isolates circulating in the US or in Brazil were obtained. Complete genome sequences of seventeen SVA isolates obtained in the US and four SVA isolates obtained in Brazil were compared to other SVA sequences available on GenBank. Complete genome sequence comparisons revealed that the US contemporary isolates characterized here share 91-93% nucleotide identity with the prototype US SVA strain SVV001 and an isolate obtained in Canada in 2007 (SVA-11-55910-3), and 98-99% nt identity with other contemporary isolates recently obtained in the US, 95-97% nt identity with contemporary Brazilian isolates and 94-96% nt id with a recent Chinese isolate (CH-1-2015). Comparison of the amino acid sequences of SVA polyprotein (2181 aa) revealed that the US contemporary isolates here share 97-99% aa identity with other SVA strains. A greater genetic divergence (86-88% nt id), however, was observed when the contemporary SVA isolates were compare to historical US isolates obtained prior to 2002. Sequence comparisons between the isolates obtained here and other contemporary or historical strains available on GenBank revealed a high degree of sequence homology between contemporary isolates. Additionally, both US and Brazilian SVA isolates share a high degree of homology with a recent SVA strain obtained in China. Phylogenetic analysis using complete genome sequences of contemporary SVA isolates and historical sequences suggest that SVA is continuously evolving. Results here provide important information on the genetic diversity of contemporary SVA isolates that have been recently associated outbreaks of vesicular disease in swine.

5
Epitope mapping of M protein of PRRS virus

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Porcine reproductive and respiratory syndrome virus (PRRSV) is coding three major structural proteins – the nucleocapsid protein N, the membrane protein M and the envelope glycoprotein GP5, from which N protein is extensively used in serological diagnostics of the disease. The use of additional virus proteins in serological assays requires their detailed antigenic analysis. The goal of this work was to determine immunodominant peptide within the structure of M protein and potential for using of the peptide for serological diagnostics of the disease.

The ORF 6 gene of PRRS virus was first analyzed by software provided on the "Immune epitope database" (IEDB) web site based on previously published algorithms for the prediction of linear epitopes from protein sequence. Following protein properties were analyzed: surface accessibility, antigenicity, hydrophilicity and the presence of linear epitope. Protein sequence of ORF 6 gene was then splitted into six fragments of various length (from 20 to 30 amino acids) to cover all sites with predicted surface accessibility. Peptides of M protein were applied as antigens in indirect ELISA tests. Immunodominant peptides were identified by checking serological reactivity of all tested peptides with a panel of 91 PRRS-positive serum samples. Peptide reacting with highest number of positive sera was considered as immunodominant.

Peptide "D" located at the very N´ terminal part of the M protein (aa residues 1-30) and peptide "E" located in the central part of the protein (aa residues 51-70) reacted with the highest number of PRRS positive sera. The position of these peptides is in agreement with in silico calculated values. These two immunodominant peptides would be convenient candidates for their usage like antigens in indirect ELISA test.

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6
Assessing the value of full genome sequence analyses for genotype 1 PRRS viruses

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The expanding genetic diversity of porcine reproductive and respiratory syndrome virus (PRRSV) is well known and has been previously described. The majority of these studies have relied on data from only small portions of the genome, such as ORF5. As full PRRSV genome sequences have become increasingly obtainable, some studies have been carried out using these, but usually with genotype 2 viruses, for which many more complete sequences are published and available. This study aims to analyse the available genotype 1 sequences, including five from Great Britain , to determine what extra information the full genome sequences are able to provide beyond that already available from analyses of individual gene sequences.

The published full genome sequences of 48 genotype 1 viruses from Europe, Asia and America, including five British viruses were analysed and compared. The sequences were aligned using MUSCLE, and the phylogenies derived using the Neighbor Joining algorithm. Full length virus sequence from the inoculum (Lelystad virus) used in an experimental *in vivo* infection was also compared to that obtained in tissues 3 days post inoculation.

Comparison of all 48 nucleotide sequences revealed that their similarities ranged between 80.1% and 99.9%, while they were only 65.4% to 67.2% similar to the prototype genotype 2 virus VR2332. The genome lengths varied from 14889 to 15120 nucleotides. The phylogenetic analysis displayed geographic clusters, where for example the British viruses all belonged to a single cluster, but, as previously described, Danish viruses are found in two distinct clusters. In comparison to a phylogeny generated using whole genomes, the tree topology differed when using only ORF5 sequence data, with the geographic groupings being more disparate. The most variable area of the genome is clearly the nsp2 region, where multiple patterns of deletions were found. For the development of diagnostic reagents such as oligonucleotide primers and probes, conserved areas beyond ORF7 may also be suggested. When examining micro-evolution during the process of *in vivo* infection, genetic changes after 3 days were found only in some non-structural genes of PRRSV which would have been missed if focusing only on structural genes such as ORF5.

The use of only ORF5 sequence data for molecular epidemiology purposes seems largely satisfactory, except for the potential confounding effects of recombination. For other analyses such as those relating to the evolution of PRRSV including recombination events, for the analysis of potential antigens important for immunity, or for diagnostic test development, full genome data is much more revealing, whereas the use of only partial sequences may lead to inappropriate conclusions.

7

Development of a novel vaccine for Porcine Epidemic Diarrhea Virus

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Infections with Porcine Epidemic Diarrhea Virus (PEDV) have resulted in significant economic losses to the swine industry. Here we describe the development of a novel inactivated vaccine for PEDV that has proven highly effective in newborn piglets. When administered to sows four and two weeks prior to farrowing, high levels of neutralizing antibodies against PEDV were found in colostrum and milk, as well as in the serum of their piglets. Piglets were orally infected at 5 days of life with PEDV isolate CO 025. It was found that 95% of all piglets from vaccinated sows (n = 83) survived the infection and showed significantly reduced clinical symptoms, weight loss and viral shedding. In contrast, all piglets from unvaccinated sows displayed severe clinical symptoms including weight loss and dehydration, and 50% of these piglets died within 6 days post infection. A large field trial was performed in three commercial swine units in Saskatchewan, Canada, to assess the vaccine under conditions with different genetics, health statuses and management systems. The vaccine demonstrated to be completely safe to use; no adverse events including injection site reactions and reproductive complications were observed. Vaccine efficacy was evaluated in 8% of these animals by transporting them back to our high containment facility prior to farrowing, and infecting their piglets orally within the first week of life. Again, protection rates were significantly higher in piglets born to vaccinated sows than those from control sows. These results show that this experimental vaccine is highly effective against the neonatal form of PEDV.

8
Development of a new strategy for detection of classical swine fever virus antibodies in alphavirus based replicon particle derived E2 and E^{rns} vaccinated swine

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Introduction: Classical swine fever virus (CSFV) is a member of the *Pestivirus* genus of the family *Flaviviridae*. It is a causative agent of classical swine fever (CSF), a highly contagious disease that threatens swine production globally. CSFV is closely related to the ruminant *pestiviruses* that cause bovine viral diarrhea (BVD) in cattle and the border disease (BD) in sheep. BVD and BD viruses can naturally infect swine and antibodies generated during infections cross-react with CSFV, thus making a CSF diagnosis problematic. For effective disease surveillance, rapid and sensitive assays are needed. The fluorescent microsphere immunoassay (FMIA) or Luminex is a multiplex serological platform that can be used for the detection of multiple targets including antigenic domains of E2 and Erns with high sensitivity and specificity. Therefore, the objective of this study was to detect changes in the serum antibody response following vaccination against CSFV with an alphavirus based RP expressed E2 and E^{rns} subunit vaccine.
Methods: E2 and E^{rns} play an important role in protective immunity in the natural host. E2 and E^{rns} genes have been fragmented into 7 and 5 small pieces respectively. The recombinant protein fragments were expressed in BL-21 (DE3) *Escherichia coli* and purified proteins were covalently coupled to Luminex MagPlex® polystyrene, carboxylated microsphere beads. The target antigens were assembled into a single multiplex and tested against sera immunized with alphavirus based replicon particles (RP) expressed antigens.
Results: To determine changes in CSFV-specific IgA, IgG, and IgM overtime, animals were vaccinated with alphavirus based RP expressed E2 and E^{rns} antigens and serum samples were collected at 0, 7, 14, 21, 28, 35, 42, 49, and 56 days post-infection (dpi). The IgA, IgG, and IgM response against CSFV antigens were determined by multiplex FMIA. The results were reported as mean fluorescence intensity (MFI) and then converted to positive per sample (S/P) ratio. The results showed that vaccinated animals had CSFV-specific IgA, IgG, and IgM in serum and oral fluids. Peak IgA and IgG antibody responses were detected at 28 dpi and IgM response was found at 7 dpi. Antibody response to CSFV antigens were IgG> IgM> IgA.
Conclusion: A strong antibody response to E2 and E^{rns} suggest that these antigens are suitable targets for diagnostic tests. Therefore, the detection of infection with multiple recombinant antigen targets in FMIA is an alternative diagnostic tool over the traditional ELISA.
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Progress in the development of real-time PCR assays for detection of foot-and-mouth disease

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Mobile real-time reverse transcriptase PCR (rRT-PCR), provides a realistic option for accurate and timely diagnosis of foot-and-mouth disease (FMD) *in situ*. Here we describe the laboratory and field evaluation of both a pan-specific and serotype-specific rRT-PCR assay using the T-COR™ 8 (Tetracore, Inc), a robust field-ready platform. For laboratory evaluation of the pan-specific assay, analytical sensitivity was determined using an FMDV RNA standard and diagnostic sensitivity was determined using RNA extracted from a panel of clinical samples (n=32), with the T-COR 8™ assays consistently showing equivalent sensitivity comparatively to the gold-standard laboratory rRT-PCR and RT-LAMP (Genie® II). The serotype-specific assay was evaluated in the laboratory using a panel of clinical samples from East Africa (serotypes: A, O, SAT1 and SAT2), with reliable detection of all serotypes evident. Robust sample preparation methods for serum, oesophageal-pharyngeal fluid and epithelial suspensions were developed to negate the need for RNA extraction prior to rRT-PCR. The final rRT-PCR protocol and associated lyophilised reagents were field evaluated in three endemic settings (Kenya, Tanzania and Ethiopia), consistently detecting both clinical and subclinical FMD infection. The ability of the T-COR™ 8 rRT-PCR to utilise simple sample preparation, amplification and detection methods offers promise for rapid *in situ* FMD diagnosis and demonstrates an important transition for FMDV-specific molecular assays into formats suitable for field diagnostic use.

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Development of antibody reagents & assays for Senecavirus A serodiagnosis

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Senecavirus A (SVA) is a non-enveloped, positive stranded, RNA virus belonging to the *Picornaviridae* family. Since July 2015, approximately 200 cases of SVA associated with vesicular disease and/or neonatal mortality have been reported in the US. Currently, however, there are minimal diagnostic reagents and serological assays available for herd surveillance and confirmation of disease. To address these industry needs, we developed reagents for immunohistochemistry (IHC), and fluorescent antibody (FA) staining. These reagents were applied to develop serological assays including an indirect ELISA, fluorescent microsphere immunoassay (FMIA) and a fluorescent focus neutralization (FFN) assay. Serological reagent development began with the cloning, expression and purification of SVA capsid proteins including VP1, VP2 and VP3. Recombinant VP1, VP2 and VP3 were used to immunize mice and rabbits for monoclonal and polyclonal antibody production. For the ELISA and FMIA assay development, microtiter plates were coated with 400 ng of each antigen (VP1, VP2 and VP3) while Luminex microspheres were coupled with 15 ug of protein per 3 x 10^6 microspheres. Both assays were optimized using a checkerboard titration using samples of known serostatus. Serum samples were obtained from uninfected pigs (n = 612) and from SVA-infected animals (n=171). Initial testing via FMIA showed that the reactivity of SVA positive samples with VP2 was approximately 10-fold greater than the reactivity to VP1 and VP3, thus providing the rational for further development of a VP2 indirect ELISA and FMIA. Both tests were validated and ROC analysis showed diagnostic sensitivities and specificities of 96.9, 92.0 and 96.2 and 91.9 respectively. Next, inter-rater (kappa) analysis was performed to assess testing agreement between assays. The ELISA and FMIA assays were compared to an indirect immunofluorescence assay (IFA) and kappa values were determined as 0.923 and 0.925, respectively, which demonstrates significant testing agreement. ELISA and FMIA results show the detection of SVA antibodies as soon as one to two weeks post infection. Although the sensitivity of both assays was adequate, the specificity was lower (50/612 false positives). Twenty-five false positive samples were randomly selected and subjected to FFN testing. Notably, all 25 samples were resolved as true negatives via FFN. Monoclonal antibodies against VP1, VP2 & VP3 are being used to develop a blocking ELISA to increase specificity. These new diagnostic reagents and assays should aid in improved surveillance and control strategies for SVA.

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Evaluation of a portable real-time PCR platform (T-COR 8™) for ASF during outbreaks in an endemically infected population in Uganda

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The objective of this study was to evaluate the feasibility and performance of a diagnostic system (including sample preparation and real-time PCR assays on a portable real-time PCR thermocycler, powered by battery) for the detection of ASFV on-site during outbreak investigations or in a simple laboratory setting in remote areas. The study was carried out as part of an OIE twinning project between the OIE Collaborating Centre at the Swedish National Veterinary Institute (SVA), and the Ugandan National Animal Disease Diagnosis and Epidemiology Center (NADDEC).

Blood and/or tissue samples were collected from domestic pigs during outbreak investigations in five districts of Uganda. Sample preparations included either simple dilution in PBS or magnetic bead nucleic acid extraction. A dried-down ASFV PCR kit with internal control (IC) (Tetracore Inc., Rockville, Maryland) was used on a portable real-time PCR thermocycler T-COR 8™ (Tetracore Inc.), performed on-site in the affected villages and in a simple lab setting. As a reference, the OIE recommended UPL assay (Fernández-Pinero et al 2013) was performed on a Stratagene Mx3000P at NADDEC.

Pigs from two of the five suspected outbreak sites investigated were positive for ASFV using the ASF kit on the T-COR 8™ and these results matched those of the reference method in the lab at NADDEC. For blood diluted in PBS, inhibition was prevalent in 20-fold diluted and present in some 40-fold diluted samples. Archived samples were also tested and in total samples for twenty-two pigs were positive for ASFV out of sixty-nine tested. Overall, the portable platform performed on par with the reference method.

This study showed that confirmation of an outbreak can be performed on-site within 1.5-2 hrs, and appropriate actions can be taken. The experience of performing the PCR assays in remote areas highlighted several factors that need to be carefully considered, including biosafety issues, simplicity and effectiveness of sample preparation and turn-around time.

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Molecular phylogenetic diversity of PRRSV Type 2 in Mexico, 2005-2013

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PRRSV Type 2 is globally distributed, and its current diversity is mainly derived from North American prototypes. While the viruses are relatively well tracked in the United States and Canada, it is still unclear where Mexico stands in the global diversity. In this study, we analyzed 445 ORF5 sequences representing samples obtained during the period 2005-2013 from all pig-producing states in Mexico. The phylogenetic analyses showed that the Mexico viruses were found in diverse locations within the tree of global type 2 PRRSV. After removing sporadic introductions, there are at least 10 well-supported monophyletic clusters representing present sustained circulations within Mexico. Among them, three clusters were likely to be the remnants of earliest PRRSV endemic in North America, whose divergence from other North America viruses were all dated back to before 1990. On the other hand, the rest of the clusters were from more recently introductions from the United States or Canada. Compared to the early endemic clusters in Mexico, these later introductions dominated the 2010-2013 sampling, with the two most prominent clusters being (i) introduced from United States and sister to China HP-PRRSV related viruses (i.e. Lineage 8), and (ii) derived (more recently) from a more pathogenic variant of Canadian-like PRRSV (i.e. Lineage 1). Within Mexico, there is frequent virus flow among the states, which resulted in the mixing of diverse viruses and subsequently recombination. Indeed, from this study there are 2.1% of the sequences identified as recombinants, despite of the fact that only ORF5 was investigated. These recombination events were either between two divergent field strains or between a field strain and a vaccine strain. In conclusion, our study reveals that Mexico harbors extensive genetic diversity of PRRSV derived from both earlier endemic viruses as well as later introductions from other North American countries.

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Comparison of five different strategies for high level expression of soluble recombinant PRRSV-nucleocapsid protein for its use in diagnostic

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The PRRSV nucleocapsid is the most immunogenic protein and an ideal target for the detection of infected pigs and currently serological testings are widely based on PRRSV N as the antigen, for the detection of antibodies produced in response to infection with North American type II or European-like type I PRRSV. However, recombinant expression systems are often difficult to develop in procaryotic systems without a high co-expression levels of inclusion bodies.

In this study, four different systems were compared in order to obtain high expression rates of soluble PRRSV-N recombinant protein. The N gene sequence was first optimized for *E. coli* expression. The first system consist of was designed to have a N- or a C-terminal HIS-tag in the pD441 plasmid. The N-PRRSV-Cterm (pNC-term) and N-PRRSV-Nterm (pNN-term) plasmids were transformed into a BL21 *E. coli* (F– *ompT hsdS*B(rB–, mB–) *gal dcm*). In the second system pNC-term was transformed into Shuffle K12 *E. coli* and Shuffle B *E.*coli (New England Biolabs). In the third system is designed for autoinduction with rhamnose. The His-tag optimized N gene was transformed into the pD861 plasmid. The pNC-Rha plasmid, was transformed into a BL21 *E. coli* (F– *ompT hsdS*B(rB–, mB–) *gal dcm*). The fourth system consist of transformation of the pNC-term into BL21 *E. coli* that contain various combinations of the five chaperone plasmids (TaKaRa). Several times and temperatures of induction as well as and concentrations of inducers were compared. Levels of protein expression at diffrent steps were verified and analyzed by SDS-Analysis. Finally, beyond these different systems inclusion bodies were also solubilized in Urea refording solution.

Results showed that different strains (Shuffle), type of induction (rhamnose) or addition of chaperones did not drastically improve or decrease the amount of soluble N_PRRSV. However they revealed that by adding a N-terminal HIS-tag to N_PRRSV and using a strong RBS in BL21 we were able to express soluble protein at good yields (~200 mg/L of culture) and, the proteins in inclusion bodies were able to be solubilized under certain conditions giving yet another option for production. The potential use of these recombinant proteins in diagnostic will be discussed.

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Alternative sampling methods for assessing vertical transmission of PRRSV

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The objective of the present work was to test the efficiency of umbilical cord (UC) sampling and ear vein (EV) blood swabs as alternative samples to cava/jugular vein bleeding (VB) for assessing vertical transmission of PRRS in maternities. With this purpose, 21 batches of newborn were sampled on farms suspected to be unstable for PRRSV. On each batch, weak newborns were targeted and the three type of samples were collected. The final number of examined piglets was 387. The time needed to collect UC, EV and for VB was recorded as well. After collection samples were immediately shipped at 4ºC and were processed in less than 24 h. RNA was extracted with the MagMAX™ and analyzed by a commercial qRT-PCR (Thermo Fisher Scientific). Diagnostic sensitivity was calculated for individual samples and at a batch level. Agreement for batch classification according to each sample results (Cohen's Kappa, k) was calculated as well. Ct in the different samples were compared with a correlation test. 105/387 samples were positive resulting in 14/21 positive batches. By samples, 76 UC were positive compared to 55 VB and 45 EV ($p<0.05$). Apparent differences in sensitivity for batch classification -85.7% for UC, 78.6% for VB and 71.4% for EV- were non-significant. The agreement for the classification of batches were: $k = 0.52$ for UC vs. VB, $k = 0.71$ for VB vs. EV and, $k = 0.62$ for UC vs. EV. Average Ct values were 26.6±8.5 for VB, 30.8±6.4 for EV and 32.1±4.85 for UC ($p<0.01$). Correlation of Ct values between samples (27 animals positive for UC, VB and EV) was $r^2=0.63$ for VB vs. EV, $r^2=0.33$ for VB vs. UC and, $r^2=0.13$ for EV vs. UC. Some VB-negative animals UC or EV resulted positive. Average Ct values for positive UC or EV samples in those animals (34.3 and 35.5, respectively) were higher than those of the equivalent samples in viremic animals (29.7 and 28.9, respectively) ($p<0.05$). It can be hypothesized that some UC or EV samples were contaminated during the delivery, in the uterus or in the birth canal. Collection of UC was faster than any other else sample (on average 24 s vs. 55 s for EV and 72 s for VB; $p<0.05$). As a conclusion, UC testing results in a sensitive alternative that saves time of collection. This study was supported by the European PRRS Research Award 2015 from Boehringer Ingelheim.

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Type of influenza A virus reassortants present in Quebec swine herds from 2011 to 2015 and their antiviral drugs resistance

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Data about molecular diversity of commonly circulating swine influenza A viruses (SIV) in Quebec swine are scarce. Yet, this information is essential for surveillance of animal and public health, vaccine updates and for understanding virus evolution and its large-scale spread. Different clinical samples including lung tissues, saliva and nasal swabs were obtained from 24 outbreaks of swine flu that have occurred in 2011 to 2015. Only, eighteen viruses were isolated in MDCK cells or in embryonated eggs. All eight gene segments of the isolated SIV strains were sequenced and analysed. Antiviral drugs resistance against oseltamivir carboxylate, zanamivir (SIGMA) and amantadine hydrochloride was evaluated by MUNANA (2'2′-(4-Methylumbelliferyl)-α-D-N-acetylneuraminic acid sodium salt hydrate) neuraminidase activity and inhibition assay (NAIs) and plaque reduction assay. Two subtypes of SIV, H3N2 and H1N1, were identified in Quebec pig herds. Twelve SIV strains were genetically related to trH3N2 cluster IV from which at least 6 different reassortment profiles were identified. On the other hand, 6 Quebec SIV strains were found to be genetically related to the pandemic virus A(H1N1)pdm09 from which two reassortment profiles were identified. One H1N1 (1/6 = 16.7%) and one trH3N2 (1/12 = 8.3%) strains were found to be resistant against Oseltamivir. In contrast, two H1N1 (2/6 = 33.3%) and two trH3N2 (2/12 = 16.7%) strains were found to be resistant against Zanamivir. All antiviral resistant strains were from 2014 and 2015. Interestingly, SIV strains resistant against Oseltamivir were different compared to the ones resistant against Zanamivir. Overall, the SIV resistance against antiviral neuraminidase inhibitor drugs was (33.3%). In addition, it was not surprising to find that all SIV tested strains were resistant against amantadine since they were all having the amino acid sequences at the M2 protein which is known to provide resistance against amantadine. The presence of influenza A virus antiviral drug resistance in swine and the possible emergence of new SIV strains are public health concerns supporting the surveillance of influenza A virus in swine.

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Detection of Porcine Reproductive and Respiratory Syndrome (PRRS) in Bhutan

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Bhutan is located between China and India, village backyard pig farming is characterized by small numbers of pigs reared by subsistence farmers (Timsina and Sherpa, 2005). Pig farming plays an integral role in providing nutrients and household income in many low-income countries in Bhutan. In addition, there are three government-owned pig-breeding farms in the country to supply hybridized piglets to the farmers for fattening and cross-breeding purposes. These government breeding farms have been set up to improve local breeds through cross breeding with exotic breeds. Bhutan is always at risk of introduction of exotic diseases in the country through the import of exotic pigs and more so, Bhutan shares a border with India in the south, across which there are imports of fresh pig meat and sometimes illegal live pig imports.

PRRS is a viral disease of swine that emerged in the US in the late 80s. Both genotypes of PRRSV, genotype 1 (EU type) and genotype 2 (NA type) are reported in Asia. The highly virulent strains presently circulating in China and Vietnam pose a serious threat for the pig producing countries in Asia and worldwide.

PRRS status in Bhutan was largely unknown until 2008, when it was first reported officially in Bhutan at National Pig Breeding farm with sudden abortion storm at the later stage of pregnancy. Most sows that aborted were between 3rd to 9th lactation, which indicated that all the above sows have furrowed healthy piglets before. There was also high morality in weaner piglets. Here, we report the first detection of PRRSV in pigs from in Bhutan following the sudden abortion storm.

An outbreak resembling PRRS occurred in 2008 and 2010 in a government pig breeding farms. Detection of antibodies by HerdCheck-PRRS ELISA from the IDEXX Laboratories for specific PRRSV NA type A was performed on serum samples of pigs from these farms. To confirm and determine the PRRSV genotype, RT-PCR was performed on selected sera and tissue samples and the positive samples were sequenced.

All affected sows were positive for PRRSV antibodies during the suspected outbreak. Pigs which were in contact with the affected ones also showed high levels of PRRSV antibodies. One month after the suspected outbreak, most sows and weaned piglets were positive for PRRSV antibodies. By RT-PCR, PRRSV antigen was detected in two PRRSV antibody seropositive and one seronegative sows, and in 3 of 6 tissues tested from pigs and in serum. PCR result also detected specific 90 nt deletion in nsp2 coding fragment, considered the marker of highly pathogenic strains from China and Vietnam. Sequence analysis revealed high identity among them and to that of highly pathogenic strains but low identity to the prototype PRRSV genotype 2 strain, VR2332. Furthermore, the sequences from Bhutan clustered together with those from China and Vietnam.

The disease was controlled by isolation and culling of affected animals followed by decontamination and strict biosecurity measures. Acclimatization of gilts entering the farm were also followed to mainly to develop protective immunity prior to introduction into the herd.

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An indirect enzyme-linked immunosorbent assay for the identification of antibodies to Senecavirus A in swine

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Background: Seneca Valley virus (SVV), a member of the family *Picornaviridae*, genus *Senecavirus*, species *Senecavirus A (SVA)*, is a recently identified single-stranded RNA virus closely related to members of the *Cardiovirus* genus. SVV was originally identified as a cell culture contaminant and was not associated with disease until 2007 when it was first observed in pigs with Idiopathic Vesicular Disease (IVD). Vesicular disease is sporadically observed in swine, is not debilitating, but is significant due to its resemblance to foreign animals diseases, such as foot and mouth disease, whose presence would be economically devastating to the United States. IVD disrupts swine production until foreign animal diseases can be ruled out. Identification and characterization of SVA as a cause of IVD will help to quickly rule out infection by foreign animal diseases.

Results: We have developed and characterized an indirect ELISA assay to identify serum antibodies to SVA. Viral protein 1, 2 and 3 (VP1, VP2, VP3) were expressed, isolated, and purified from *E. coli* and used to coat plates for an indirect ELISA. Sera from pigs with and without IVD symptoms as well as a time course following animals from an infected farm, were analyzed to determine the antibody responses to VP1, VP2, and VP3. Antibody responses to VP2 were higher than VP1 and VP3 and showed high affinity binding on an avidity ELISA. ROC analysis of the SVA VP2 ELISA showed a sensitivity of 94.2% and a specificity of 89.7%. Compared to IFA, the quantitative ELISA showed an 89% agreement in negative samples and positive samples from 4-60 days after appearance of clinical signs.

Conclusions: A simple ELISA based on detection of antibodies to SVA VP2 helps to differentially diagnose IVD due to SVA and rule out the presence of economically devastating foreign animal diseases.

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A novel porcine circovirus distantly related to known circoviruses is associated with porcine dermatitis and nephropathy syndrome and reproductive failure

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Porcine circovirus associated disease (PCVAD) is clinically manifested by postweaning multisystemic wasting syndrome (PMWS), respiratory and enteric disease, reproductive failure, and porcine dermatitis and nephropathy syndrome (PDNS). Porcine circovirus type 2 (PCV2) is an essential component of PCVAD although an etiologic role in PDNS is not well established. Here, a novel circovirus, designated porcine circovirus 3 (PCV3), was identified in sows that died acutely with PDNS-like clinical signs. The capsid and replicase proteins of PCV3 share only 37% and 55% identity to PCV2 and bat circoviruses, respectively. Aborted fetuses from sows with PDNS contained high levels of PCV3 ($7.57x10^7$ genomic copies/ml) and no other viruses were detected by PCR and metagenomic sequencing. Immunohistochemistry (IHC) on sow tissues identified antigen in skin, kidney, lung and lymph nodes localized in typical PDNS lesions including necrotizing vasculitis, glomerulonephritis, granulomatous lymphadenitis and bronchinterstitial pneumonia. Further study of archived PDNS tissues, that were negative for PCV2 by IHC, identified 45 of 48 were PCV3 positive by qPCR with 60% of a subset also testing positive for PCV3 by IHC. Analysis by qPCR of 271 porcine respiratory disease diagnostic submissions identified 34 PCV3 positive cases (12.5%), and ELISA detection of anti-PCV3 capsid antibodies in sera found 46 positive samples of 83 tested (55%). These results suggest PCV3 commonly circulates within U.S. swine and may play an etiologic role in reproductive failure and PDNS. Due to the high economic impact of PCV2, this novel circovirus warrants further studies to elucidate its significance and role in PCVAD.

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Development, characterization and diagnostic application of monoclonal antibodies against ASFV p30

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African swine fever virus (ASFV), the causative agent of African swine fever (ASF), is a large enveloped DNA virus and the only known member of the family *Asfaviridae*. ASFV has a complex organization, containing more than 100 proteins, including those with structural roles and enzymes that are packed in the virus core for use in early infection. Since there are currently no commercial vaccines against ASFV, the detection of ASFV specific antibodies in commercial or feral swine indicates previous infection. Many of the viral proteins are potentially useful for ASFV diagnosis; among them is p30, an early protein that is part of the inner membrane of the viral particle and a very efficient inducer of humoral responses. Although ASFV is not present in the US and no diagnostic tests are available, the current outbreaks in Eastern Europe have prompted interest in developing rapid and specific diagnostic assays for surveillance programs. The overall goal of this study was to develop, characterize and evaluate monoclonal antibodies (mAbs) against ASFV p30 that could be used in diagnostic assays.

Briefly, recombinant p30 protein, based on BA71V strain, was expressed in *E.coli* and purified. Three 6-8 week old female BALB/c mice were immunized with the purified protein (100ug/mouse/inoculation) at 2-week intervals for 4 weeks. Splenocytes from immunized mice were fused with NS-1 myeloma cells and cultured on 24-well plates. Cell culture supernatants from wells containing hybridoma colonies were screened by indirect immunofluorescence (IFA) using Vero cells infected with Alphavirus replicon particles (RP) expressing ASFV p30. Hybridoma cells from positive wells were subcloned by limited dilution and expanded. From three clones, eleven subclones were generated (47- 3, 47- 26, 47- 53, 62- 22, 62- 23, 62- 32, 62- 35, 142- 1, 142- 2, 142- 4, 142- 20) and subjected to further testing.

The reactivity of the mAbs was tested by IFA on Vero cells infected with BA71V strain. In total 8 out of 11 mAbs reacted with the infected cells, and clone 62-35 showed the highest reactivity. Next, we investigated whether the mAbs recognize different ASFV strains. Immunohistochemical (IHC) staining was performed on formalin fixed paraffin embedded (FFPE) tissues (lung, spleen, lymph nodes and tonsil) from pigs challenged with the Georgia/07 strain. Two mAbs showed weak reactivity (142-4 and 62-35) and one (47-3) had high reactivity to antigen in the FFPE tissue sections. To identify the mAbs target epitopes, eight overlapping fragments covering the p30 protein of ASFV BA71V were expressed in *E. coli* in a soluble form and purified by affinity chromatography. ELISA plates were coated with the protein fragments and with the whole protein. All mAbs recognized the whole p30 protein and three (47-3, 47-26, 47-53) reacted with a conserved region between amino acids 130-143. Similar results were obtained by Western blot analysis. Interestingly, sera from pigs immunized with Alphavirus RP-p30 recognized the same conserved region. In a competitive ELISA only one mAb (142-4) could compete off the RP-p30 sera.

In summary, this work describes the generation of p30 mAbs and their potential for use in the development of diagnostic tests.

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Oral fluids diagnostic methods for chronic Classical swine fever virus

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Classical Swine Fever virus (CSFV) is one of the most impactful swine pathogens worldwide, causing significant economic and animal welfare losses. Historically, CSFV strains caused acute disease with high mortality. Current strains cause chronic, moderate disease. This milder disease is hard to differentiate from common swine pathogens (e.g. PRRSV, PCV2, bacterial septicemia), making these newer strains the perfect candidates for infecting and persisting in naïve swine populations. Regions free of CSFV must actively survey their swine so as to avert the massive damages an unchecked outbreak would cause. In the United States the surveillance carried out by the Animal and Plant Health Inspection Service (APHIS) is limited by a lack of mass sampling techniques. Oral fluid sampling can address these limitations, and has already been shown to be effective in detecting other diseases in swine. We performed a pilot study using 10 pigs infected with the moderate CSFV strain, Paderborn. Clinical signs and rectal temperatures were evaluated daily throughout the study. Observed symptoms were typical of chronic, moderate CSFV infection. Serum was collected via jugular venipuncture at regular intervals throughout the study, while oral fluids were collected daily via cotton ropes hung in the pen. Both sets of samples were analyzed by qRT-PCR and the CSFV detection efficiency compared. Our results show that the virus could be detected in oral fluids using a single sample, and using less resources than with traditional serum sampling. This study paves the way for the validation of oral fluids for use in mass population sampling, which will greatly strengthen the surveillance capabilities of APHIS.

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Development of a new molecular method to discriminate Porcine Epidemic Diarrhea Virus infectious viral particles, from non-infectious ones, which are contaminating pig derived food additives

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Porcine epidemic diarrhea (PED) emerged in North America in April 2013. The ethological agent of this infectious disease is a coronavirus specific to swine named porcine epidemic diarrhea virus (PEDV). In affected herds, PEDV can cause significant economic losses, primarily due to a very high mortality (50% to 100%) in young piglets. It is essential to put in place biosecurity measures to assure PEDV negative status of swineherds in order to keep a good financial health of this industry. At the moment, PEDV molecular diagnostic tools do not allow us to establish if virus particles, that are detected in the environment (ex: in transportation trucks) or in food additives, are infectious and thus if they could be a biohazard threat for the swine industry. Thus, the main objective of this study is to develop a new molecular diagnostic tool that can differentiate infectious viral particles from non-infectious ones. Recently, new molecules have been reported to specifically crosslink with DNA/RNA and by doing so; inhibit reverse-transcription (RT) and PCR amplification of the viral genome. In addition, those molecules are nearly completely cell membrane-impermeable, and thus cannot pass through an intact lipid membrane. Our research hypothesis is that infectious virus particles (with an intact lipid membrane) will not allow the crossover of those new compounds to bind their inner viral genome. Consequently, only samples containing infectious viral particles will be expected to give a PEDV positive RT-qPCR reaction when pre-treated with those new molecules. Results show that pre-treatment with the molecules of spiked PEDV samples allows the distinction between infectious viral particles and non-infectious ones by using RT-qPCR reactions. Moreover, the efficiency of the new molecules combined with RT-qPCR has been also demonstrated on PEDV positive food additives. In conclusion, this molecular test will ensure the biosafety of food additives derived from swine that may be carrying some PEDV viral genome.

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Proof of concept: PRRSV IgM/IgA ELISA detects infection in the face of circulating maternal IgG antibody

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INTRODUCTION

Detection of PRRSV antibody in oral fluids (OF) is a convenient approach for PRRSV surveillance. However, in weaned pig populations originating from PRRSV-infected or vaccinated sow herds, maternal antibody (IgG) cannot be differentiated from IgG antibody produced by pigs in response to infection. Therefore, we developed and evaluated IgM- and/or IgA-specific oral fluid ELISAs as a means to detect active infection in weaned pig populations with circulating maternal IgG.

MATERIALS AND METHODS

OF samples were collected from 3 wean-to-finish (WTF) sites (A, B, C) beginning within 2 weeks of placement. Pigs originated from PRRSV vaccinated and/or exposed sow herds, but the pigs themselves were not vaccinated for PRRSV. Each site had 3 WTF barns and each barn had 36 occupied pens (~25 pigs per pen).

A total of ~2,916 OF samples were collected: 3 sites x 108 pens per site x 9 samplings. To establish the PRRSV status of each pen, all OF samples were randomized and then tested by PRRSV rRT-PCR. OF samples were subsequently tested for PRRSV IgG, IgA, IgM, and the combination of IgM/IgA using ELISAs developed in our laboratory. ELISA cutoffs, diagnostic sensitivity and specificity were determined by ROC analyses.

RESULTS

PRRSV qRT-PCR: On Site A, 3.7% of pens were positive at the 1st sampling, with all pens in all 3 barns positive ≥ 1 times by the 9th sampling. All Site B samples were negative, except for one positive pen at the 9th sampling. All Site C samples were negative.

PRRSV Antibody: Among the 3 sites, 90.6% (278/307) of the OF samples collected on the 1st sampling were IgG positive, but 273 of these were from rRT-PCR-negative pens. In samples collected over time, rising IgA, IgM, and IgM/IgA S/P values were associated with spread of PRRSV (rising rRT-PCR positivity). An ROC analysis estimated the sensitivity and specificity of the three ELISAs, at ≥ 63% and ≥ 99%, respectively.

DISCUSSION

Practitioners need both nucleic acid- and antibody-based tests to track PRRSV. This study suggested that the pigs' IgM/IgA response could be used to detect a pig's response to infection in the presence of maternal antibody.

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Spatial autocorrelation and implications for oral fluid-based PRRSV surveillance

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INTRODUCTION

Tobler's 1st Law of Geography says, "*Everything is related to everything else, but near things are more related than distant things*." "Spatial autocorrelation" can be positive (near pens have similar PRRSV status) or negative (near pens have dissimilar PRRSV status). Two questions were addressed in this study: 1) Does PRRSV infection exhibit spatial autocorrelation? 2) Is random or "fixed spatial" sampling better for PRRSV surveillance? (Fixed spatial sampling = sampling pens spaced evenly over the length of the barn.)

MATERIALS AND METHODS

In 3 wean-to-finish barns on one site, oral fluid (OF) samples were collected weekly (9 samplings) from every occupied pen (108 pens; ~25 pigs per pen) for a total of 972 OF samples. OF samples were randomized prior to PRRSV RT-PCR testing.

1. RT-PCR results were used to test for PRRSV spatial autocorrelation on the site, both globally and locally, using threshold distance as the spatial weight matrix. Moran's *I*, an indicator of global spatial autocorrelation, was used to test for clustering within barns. LISA (Local Indicators of Spatial Association) analysis, an indicator of local spatial autocorrelation, was used to identify clusters of PRRSV concentration within barns.
2. Statistical analyses were used to compare detection using random vs "fixed" spatial sampling.

RESULTS

1. Moran's *I* analysis revealed positive global spatial autocorrelation in the distribution of PRRSV virus in the swine barns. LISA analysis revealed clusters at the local level, indicating the presence of local spatial autocorrelation.
2. Analyses comparing the probability of detection showed that "fixed" spatial sampling was as good as, or better than, random sampling for the detection of PRRSV.

DISCUSSION

PRRSV (and probably most infectious diseases of swine) exhibits spatial autocorrelation. This is obvious to most swine vets, but spatial autocorrelation has not previously been tested at the barn level. This concept is important because it implies that pens' disease status exhibits spatial dependence; which helps explain why fixed spatial sampling is as good as random sampling. Overall, the results suggested that a simple, reliable, oral fluid-based surveillance strategy can be based on fixed spatial sampling.

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Construction and characterization of a full-length cDNA infectious clone of emerging porcine Senecavirus A

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A full-length cDNA infectious clone, pKS15-01-Clone, was constructed from an emerging Senecavirus A (SVA; strain KS15-01). To explore the potential use as a viral backbone for expressing marker genes, the enhanced green fluorescent protein (EGFP)-tagged reporter virus (vKS15-01-EGFP) was generated using reverse genetics. Compared to the parental virus, the pKS15-01-Clone derived virus (vKS15-01-Clone) replicated efficiently in vitro and in vivo, and induced similar levels of neutralizing antibody and cytokine responses in infected animals. In contrast, the vKS15-01-EGFP virus showed impaired growth ability and induced lower level of immune response in infected animals. Lesions on the dorsal snout and coronary bands were observed in all pigs infected by parental virus KS15-01, but not in pigs infected with vKS15- 01-Clone or vKS15-01-EGFP viruses. These results demonstrated that the infectious clone and EGFP reporter virus will be important tools in further elucidating the SVA pathogenesis and development of control measures.

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Assessment of Porcine Reproductive and Respiratory Syndrome (PRRS) impact in US sow farms

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Background: Porcine reproductive respiratory syndrome (PRRS) is an endemic swine disease causing large industry impact. The complex epidemiology of the disease, coupled with a lack of complete information and the diverse clinical outcomes observed in infected farms, have hampered efforts to quantify PRRS' impact on production over time.
Objective: To measure the impact of PRRS outbreaks in routinely vaccinated sow farms.
Methods: Longitudinal production data, regularly collected on 16 sow farms from a single system that had been affected with PRRS, were used to build a fixed-effects model to evaluate the post-outbreak production of weaned pigs. Seven indicators of farm performance (litter size, number of stillbirths, number of pre-wean piglets and sows dead, number of sows with abortions, number of sows with repetition of services, and sows farrowing) were also assessed. Pre-outbreak data were used to establish a baseline that was used to estimate the decrease in weaned pigs produced, and losses were translated into a revenue decrease assuming the average market price of $45.40 / weaned pig.
Results: Production declined one week before the outbreak was reported, and the decline was greatest between 5 and 6 weeks after. Recovery was not monotonic, and a new decay was observed between the 11th and 18th week post-outbreak. By the end of the study (35 weeks post-outbreak) a trend towards recovery was observed in all performance indicators, although baseline levels were never reached. Abortions increased significantly the week before the outbreak was reported, and stillbirths remained significantly higher than baseline even in the 35th week after the outbreak. Through the 36 weeks following an outbreak, PRRS caused a decrease of 1.9 weaned pigs per sow, leading to decrease revenue in a standard farm of this system of approximately $350,000 through the same period.
Conclusions: PRRS caused a significant decrease in weaned pig production and the negative effect lingered. Around 25% of total losses occurred within the first six weeks of the outbreak, 50% of losses by the 12th week post-outbreak. We were only able to measure production losses and not the full economic impact of PRRS. Still, our estimates indicate a larger loss than previously estimated, i.e., a decrease of 1.90 weaned pigs over 36 weeks compared with the 1.44 per sow year reported elsewhere (Holtkamp *et al.* 2013), even though farms here were performing routine PRRS vaccination.
Relevance: Metrics of PRRS-associated losses here demonstrate, in quantitative terms, the impact of the disease, and would be useful for informing cost-benefit analyses and bio-economic models of interventions. The methods presented here may also be applied to measure impacts in other type of farms, such as farms without vaccination protocols, for comparative purposes.
Acknowledgement: We thank the system, which participates in the SHMP, for sharing the information used for these analyses.

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Detection of PCV2 DNA in serum, feces and in oral fluid of pigs vaccinated against PCV2

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The aim of the study was to compare the presence of PCV2 DNA in serum, feces and oral fluid of pigs from 7 Polish farms vaccinated against PCV2.

Materials and methods

Serum, feces and oral fluid samples from piglets, weaners and fatteners, were obtained from farms with different vaccination protocols (Table 1) and analyzed with in house Real Time PCR for PCV2.

Results

PCV2 was detected in serum from 3 out of 7 farms. In farms 4 and 5 viremia was detected in fatteners and in farm 2 in weaners and fatteners. PCV2 DNA was detected in feces from all farms except from farm 1. PCV2 DNA was detected in oral fluid of weaners and fatteners from most of the farms. In farm 1 it was detected only in 12 weeks old pigs and in farm 6 only in 4 and 19 weeks old pigs.

Farm	Vaccine (age of application in weeks)	Serum			Feces			Oral fluid		
		Total no.	No. of pos.	% pos.	Total no.	No. of pos.	% pos.	Total no.	No. of pos.	% pos.
1	CircoFlex (3)	56	0	0	56	0	0	14	1	7.1
2	CircoFlex (3)	60	22	36.7	60	49.0	81.7	6	6	100
3	Porcilis PCV (6)	10	0	0	10	6.0	60.0	5	5	100
4	Suvaxyn PCV (7)	15	4	26.7	15	9.0	60.0	14	9	64.3
5	Suvaxyn PCV (6)	14	4	28.6	12	10.0	83.3	6	5	83.3
6	Suvaxyn PCV (6)	12	0	0	12	7.0	58.3	6	2	33.3
7	Suvaxyn PCV (6)	12	0	0	12	4.0	25.0	7	4	57.1
Total		179	30	16.8	177	85	48.0	58	32	55.2

Table 1: Detection of PCV2 DNA in serum, feces and oral fluid. Samples from farms 1 and 2 were tested individually. Samples from farms 3-7 were tested after pooling by 2-5.

Conclusion

On average 55.2% of oral fluid samples tested positive for PCV2 DNA, but the prevalence ranged from 7.1% in farm 1 to 100% in farms 2 and 3. PCV2 DNA was detected in 48% of fecal samples and the prevalence ranged from 0% in farm 1 to 83.3% in farm 5. PCV2 DNA was detected in serum from farms 2, 4 and 5, in 36.7%, 26.7% and 28.6% samples, respectively. On average PCV2 DNA was detected in only 16.8% of serum samples. Further studies are needed to establish the correlation between the presence of PCV2 DNA in different type of pig samples and the efficacy of vaccination protocols.

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The duration period of PRRSV Ab under serum therapy and herd closure

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Introduction Serum therapy with herd closure is a good method for control or eliminating PRRS in sow farm. The F8 farm had 1200 sows in 2014. As the status of PRRS became unstable in 2013 winter, we inoculated serum to sows and gilts on Jan. 18 and 20, and then closed the herd. In some former reports, the antibody will declined in 8 months or 12 months. In order to know the exactly duration period, we fixed some pig for check.
Materials and methods Boars and sows were fixed for monitoring Ab by IDEXX HerdChek* PRRS X3 Kit.
Results The PRRS Ab of some boars occurred negative 3 months later. It takes nearly 14 months that all boars became negative (table 1). The PRRSV Ab of Sow just like the boar, but one sow still kept Ab positive after 15 months (table 2).

Table 1 the fixed boars PRRS S/P value

ID	2/12/2014	4/23/2014	6/20/2014	8/25/2014	11/23/2014	12/29/2014	3/8/2015	3/31/2015
Boar1	1.567	0.783	0.673	0.506		0.344	0.325	0.325
Boar2	3.504	1.955	1.564	0.492	0.61	0		
Boar3	1.507	1.041	0.766	0.471	0.188			
Boar4	0.837	0.251	0.088	0.521	0.018	0.027	0.049	
Boar5	1.837	0.897	0.895	0.694	0.29	0.525		
Boar6		1.047	0.894	0.483	0.322	0.42	0.317	0.315
Boar7	3.537	1.794	1.337	0.505		0.417	0.26	0.26
Boar8		1.206	0.499	0.483	0.42			
Boar9	0.121	0.095	0.05	0.521	0.635	0	0.004	0

Table 2 the fixed sows PRRS S/P value

ID	1/17/2014	3/23/2014	5/23/2014	8/25/2014	11/23/2014	12/29/2014	2/27/2015	4/23/2015
sow4	0.223	1.225	0.62	0.306	0.225	0.357	0.242	0
sow5	0.097	1.143	0.68	0.203	0.065	0.065	0.049	0.08
sow7	0.644	1.262	0.795	0.492	0.387	0.438	0.265	0.192
sow8	0.1	2.827	1.572	0.407	0.17	0.124	0.174	0.144
sow9	0.625	2.02	0.372	0.506	0.46	0.635	0.495	0.274
sow10	0.591	1.501	0.742	0.567	0.28	0.346	0.27	0.241
sow11	0.05	0.798	0.402	0.14	0.093	0.062	0.028	0.029
sow12	0.1	0.817	1.102	0.144	0.098	0.092	0.093	0.071
sow14	0.428	1.798	1.065	0.584	0.585	0.354	0.423	0.301
sow15	0.135	2.193	0.312	0.438	0.322	0.449	0.316	0.234
sow16	0.071	0.877	0.24	0.079	0.04	0.051	0.014	0.042
sow19	0.038	2.61	1.103	0.344	0.227	0.208	0.186	0.281

Discussion The detection PRRS Ab of fixed boar and sows confirmed the previous studies are correct. But very little individual sow or boar still kept PRRS Ab positive more than 15 months. The PRRSv is negative and no PRRS clinical infection. We don't know why some pigs kept the low positive s/p value in the herd. Maybe affected by detection error or the kit or some unknown immunity.

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Development of immunochromatographic strip tests for on-site rapid and early detection of specific antibodies against porcine respiratory reproductive syndrome virus

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Objectives: Porcine reproductive and respiratory syndrome (PRRS) is considered one of the most economically significant swine diseases worldwide. Due to its increasing genetic diversity, a rapid and accurate diagnosis is crucial in laboratory as well as field situation. Although many serological diagnostic methods commonly used to detect PRRSV-specific antibodies show high sensitivity and specificity, specialized equipments and skilled personnel are needed. The objective of this study was to develop and evaluate fast and sensitive point-of-care test using immunochromatographic assay.

Methods: The immunochromatographic strip test (ICST) was developed by type1 and 2 N proteins labeled with colloidal gold to detect PRRSV-specific antibodies. Diagnostic performance was demonstrated with 991 sera from 71 local swine farms and 66 sera from 12 experimentally inoculated pigs by comparing the validity with that of commercial ELISA (IDEXX PRRS X3 ab) using IFA and IgM ELISA as reference standards. To elucidate temporal humoral responses, sera from pigs challenged with field viruses (LMY, PL97-1, and E38) were collected at 0, 7, 14, 28, 39, 52 days post infection (dpi). Additionally, to identify how early these test can detect PRRSV-specific antibodies, sera challenged with prototype viruses (VR2332 and LV) were collected at 0,1, 3, 5, 7, 14 dpi.

Results: The sensitivities of our ICST and commercial ELISA were 97.5% and 97.8%, respectively and the specificities were 91.1% and 92.4%, respectively. More importantly, the ICST could detect PRRSV-specific antibodies as early as 3 dpi, while commercial ELISA could detect PRRSV antibodies from 7 or 14 dpi.

Conclusions: The test results of ICST are generated within approximately 15 min with only 20ul of swine sera. The ICST shows similar performance compared with commercial ELISA and can detect PRRSV-specific antibody in earlier stages of infection. As a simple and accurate test for screening swine sera against PRRSV, we suggest ICST would successfully replace the current commercial ELISA for on-farm use in near future.

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Complete genome sequencing of a genotype 1 subtype 2 PRRSV isolate obtained in Western Siberia

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Purpose. In the present study, we report the complete genome sequencing of a subtype 2 of a Type 1 PRRSV strain. The virus was isolated from lung tissue of aborted foetus from the endemically infected farm in West Siberia, Russia in 2013 and was named Siberian.

Methods. Amplification and sequencing primers were designed by us on the basis of existing GenBank PRRSV sequences available for subtypes 1 and 3 of genotype 1. The resulting PCR fragments covered the entire genome of the virus. Total RNA was extracted and RT-PCR was completed. Sanger sequencing was performed, the coverage at least 2 times. 3' and 5'ends of the genome were amplified.

Results. The full sequence of the PRRSV Siberian isolate genome was 15050 nucleotides in length excluding the poly (A) tail. The genome sequence of the Siberian PRRSV isolate was compared to those of the prototype strains of genotype 1 subtypes 1 and 3, Lelystad and Lena respectively. Full sequence alignment revealed 80,0 and 81,8 % homology, respectively. The Siberian isolate was found to form a monophyletic group with subtype 3 strains. Comparison of ORF1a sequences of the Siberian and Lelystad isolates revealed a deletion 18 amino acids long in the variable region of the NSP2 protein (positions 741-759) and a deletion of one amino acid at position 901. The 3' end of the ORF3 sequence of the Siberian isolate is 10 amino acids shorter than that of the Lena strain and 26 amino acids shorter compared to the Lelystad strain.

Conclusions. We sequenced and analyzed the complete genome sequence of the PRRSV Siberian isolate, which belongs to subtype 2 of European type PRRSV. To our knowledge, this is the first complete genome sequence of a subtype 2 PRRSV-1. This fact is of interest for the perspective of understanding PRRSV evolution and its correlation with geographic distribution of different PRRSV subtypes.

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Identification of immunodominant B-cell linear epitopes present in the nucleocapsid protein of Porcine Epidemic Diarrhea Virus

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Porcine epidemic diarrhea virus (PEDV) is a Coronavirus that causes acute vomiting, anorexia and watery diarrhea in pigs of all ages, with up to 90-95% mortality in suckling piglets. Coronaviruses contain four major structural proteins: spike (S) envelope (E), membrane (M), and nucleocapsid (N). The S protein is further divided into S1 and S2 domains and includes neutralizing epitopes. The N protein binds to viral RNA and provides a structural basis for the nucleocapsid. It is the most abundant and conserved viral protein. In other coronaviruses, N is a target for antibodies, but these antibodies do not possess neutralizing activity. The current study aimed to characterize antibody immune responses to PEDV S1 and N and to identify linear B-cell epitopes within the N protein.

First, we produced recombinant N and S1 proteins in *E. coli* and eukaryotic cells respectively. Second, in-house ELISA has been developed for detection of IgG antibodies against these proteins in pig serum samples. Third, a purified peptide library containing 109 overlapping biotinylated peptides and covering complete N protein sequence was produced. This peptide library was used in PEPSCAN assay to identify linear antigenic epitopes in the N protein.

Twenty serum samples were obtained from a PEDV-positive pig farm in Ontario. All these samples were tested in ELISA using purified recombinant S1 and N proteins and found to be positive. Average ELISA titer against S1 was 1360, and average titer against N was 646. Five serum samples with the highest titer against N were used in PEPSCAN assay. Three epitopes were identified on the N protein sequence that consistently recognized by immune sera of all five pigs.

These findings have direct implications for PEDV diagnostics and eventual eradication as the identified epitopes may represent serological marker candidates for differential (DIVA) PEDV vaccines, derived from infectious cDNA clones.

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Establishment of a SYBR Green I based real time PCR for rapid detection of PRRSV Nsp9 gene and its expression in PRRSV infected cells

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A pair of specific primers targeted to non-structure gene 9(*Nsp*9)of PRRSV was designed and a SYBR Green I fluorescent based real time PCR was developed for the quantization of PRRSV. The melting curve analysis using SYBR Green I dye showed one specific peak, a melting temperature, and no primer dimers peak was observed. No amplification was detected from unrelated virus samples by this method, such as HEV, SIV, PRV. Fine reproducibility was obtained for detecting plasmid DNA with intra-assay. The real-time PCR method developed in this study will be useful for rapid laboratory diagnosis and epidemiology investigation for PRRSV. During the process of virus infecting cells, the expression level of *Nsp*9 increase gradually, it got the highest at 36 h.

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Influence of antiserum of PRRSV to replication in Marc-145 cells

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In order to verify whether hyper-immune serum of PRRSV have an influence on the replication of PRRSV , hyper-immune serum was prepared, PRRSV XH-GD strain were cultured, then centrifuged with high speed, the purified viruses were used to immunize the New Zealand rabbits to raise antibody. New Zealand rabbits were immunized intraperitoneally (i.p.) plus Freund's complete adjuvant. Antiserum was collected from the rabbits that had been placed under terminal halothane anesthesia. Antiserum titer was 1:640, the antiserum was incubated with virus, and then qPCR and TCID50 used to evaluate the titer of virus. The results show that antiserum could inhibit the replication of PRRSV at the mRNA lever, so hyper-immune serum of PRRSV is able to inhibit the replication of PRRSV in Marc-145 cells.

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Preparation and identification of the monoclonal antibodies against Nsp9 protein of Porcine Reproductive and Respiratory Syndrome Virus

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In order to generate monoclonal antibody against the NSP9 protein of PRRSV, the NSP9 protein was expressed in Escherichia coli and subsequently used as an antigen to immunize mice and for the initial screening of hybridomas prepared from the mice for their ability to produce anti NSP9 protein Mabs via an indirect ELISA. Three positive hybridomas were identified in this manner and verified based on the ability of their released Mab to react specifically with both naturally and artificially expressed NSP9 protein in Western Blots. The three hybridomas named 3B17, 3J13, 3F19 were subcloned three times before being introduced intraperitoneally into mice. The three hybridomas could occur with PRRSV-infected Marc-145 cells by indirect immunofluorescence verification. During the process of viral infection, the protein levels of NSP9 gene keep rising, it get highest at 48 h. These antibodies would be of great assistance to elucidate the function of Nsp9 gene.

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Effect of PEDV and PRRSV outbreaks on reproductive performance of commercial sows

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Historically, porcine reproductive and respiratory syndrome (PRRS) has caused major economic impact to the US swine industry from decreased performance in growing pigs and reproductive sows. Since its first reported outbreak in the U.S. in 2013, porcine epidemic diarrhea (PED) has been considered a major problem in the swine industry because of its high mortality rate in piglets. However, little is known about the impact of PED on reproductive performance of sows. Therefore, the objective of this study was to evaluate the impact of PRRS virus (PRRSV) and PED virus (PEDV) outbreaks on the reproductive performance of commercial sows.

The data analyzed for this project were from ten commercial farms located in North Carolina. A total of 21,060 farrowing records on 5,448 multiparous commercial F1 (Landrace x Large White) sows were used. The dataset included phenotypic records on number of piglets born alive (NBA), mummified piglets (MUM), stillborn piglets (NSB), born dead piglets (NBD), piglets weaned (NW) and abortion (AB). Occurrences of PEDV and PRRSV breaks were confirmed by serological results. However, the dates of the PEDV and PRRSV outbreak phases on each farm were determined based on the herd-year-week estimates of the reproductive performance. A total of 6 and 15 outbreaks were identified for PRRSV and PEDV, respectively. The impact of the disease phases on reproductive performance of sows was evaluated in SAS 9.4 in a model including the fixed effects of disease phase (Clean, PRRSV, and PEDV), season, parity, year and farm, and the random effect of sow. An additional model was used to assess the interaction between disease phase and season.

Disease phase had a significant effect on all traits analyzed ($P<0.0001$). Reproductive performance during Clean and PEDV phases was the same ($P>0.05$) for all traits analyzed, except for NW which averaged 9.8±0.05 and 3.2±0.1 piglets weaned for Clean and PEDV phases, respectively. In contrast, reproductive performance during PRRSV was different ($P<0.001$) than the Clean and PEDV phases for all traits. Interestingly, there were 2 occurrences of simultaneous PEDV and PRRSV breaks at the same farm. For all traits but NW, performance during simultaneous breaks was similar to PRRSV ($P>0.05$). For NW, simultaneous breaks showed the lowest ($P<0.0001$) performance, with only 1.8±0.3 piglets weaned. When the interaction of disease phase and season was analyzed, this effect was statistically significant for AB, MUM and NW ($P<0.05$), but not NBA, SB, or NBD ($P>0.05$). However, differences within disease phases were only found for NW, and NW was highest in summer and lowest in fall for both PRRSV and PEDV outbreaks.

These results indicate that PEDV does not have an effect on NBA, SB, MUM, NBD or AB, but does decrease NW. PRRSV affects all reproductive performance traits, although PEDV has a greater effect on NW. When a farm breaks with both PRRSV and PEDV, NBA and SB are statistically similar to a PRRSV break, but MUM, NBD, and NW show a larger effect than either a PRRSV or PEDV break. In addition, these results indicate that there is a compound effect between infection and season of the break.

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Senecavirus A infection in sows, neonates, and market weight gilts with subsequent protective immunity

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Objective: The objectives of this study were to 1) characterize SVA infection in market weight pigs, late-gestation sows, and neonates and 2) examine protective immunity in late-gestation gilts

Materials and Methods: For Part 1 of the study 15 market weight gilts were inoculated with SVA, bled regularly for 2 weeks, and clinical observations were made daily. In addition 10 sows were split into 2 groups. Group A was inoculated at various times pre-farrow (-17, -12, -10, -4, -3) and Group B was inoculated various times post-farrow (2, 3, 7, 7, 14) with their piglets. All animals were bled and swabbed at 0, 7, and 14 days post inoculation (dpi). In addition, piglets were bled pre-colostrum intake. For Part 2 of the study, 12 of the 15 gilts inoculated in Part 1 were bred and challenged again in late gestation. Serum samples were collected from the gilts and piglets along with milk samples. Serum and swab samples were tested for SVA by PCR and a virus neutralization assay was used for serum antibody testing

Results: During Part 1, all market weight gilts developed coronary band vesicles by 5 dpi. Snout lesions appeared 2 days after the first coronary band lesions and only developed in 40% of the gilts. Viremia lasted about a week in most gilts. Lameness was apparent starting on 2 dpi and lasted around 1 week, though feed intake was not affected. On the contrary, of the ten sows inoculated, only one sow developed a vesicle on the snout, though all had evidence of viral replication by PCR. Piglets born to sows infected on -17 and -12 were negative for SVA. Piglets born to the sow infected at -10 were positive for SVA before suckling and in subsequent sampling. Finally, piglets born to sows infected at -4 and -3 were negative at pre-suckle sampling, but positive by PCR in subsequent samplings. Two litters developed a yellow diarrhea often seen with enteric colibacillosis just after birth, but recovered completely in 2-3 days. All sows and piglets infected post-farrowing showed evidence of viral replication, but did not develop any clinical signs. All gilts and sows had increased antibody titers post exposure to SVA. During Part 2, there was no evidence of viral replication in any of the gilts or their piglets. In addition, all milk samples were negative for SVA.

Conclusions: Market weight gilts experimentally infected with SVA developed a clinical picture similar to reports from the field. On the other hand, we were not able to experimentally reproduce clinical signs observed in sow farms naturally infected with SVA, namely neonatal mortality. We did show evidence of infection and viral replication in neonates, but we did not observe increased pre-weaning mortality. Gilts were challenged 5 months after initial exposure in late gestation and we were able to demonstrate protective immunity. Continued experimental studies with SVA will improve understanding of the pathogenesis of SVA and help shape control and prevention measures in the swine industry.

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Phenotypic characterization of a novel HP Italian PRRSV-1 isolate in experimentally infected pigs

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Highly pathogenic (HP) PRRSV isolates are characterized by high viral loads, severe general clinical signs and high mortality. Their genomes share a discontinuous aa deletion in the non-structural protein 2 (nsp2). This investigation is aimed at characterizing clinical, virological, pathological and serological outcomes in conventional pigs experimentally infected with a potential highly pathogenic, Italian PRRSV-1 subtype 1 isolate. The isolate (PR-402014) was obtained from nursery pigs in the course of an outbreak of high post-weaning mortality (up to 50%) associated with severe systemic and respiratory disease. The nucleotide sequence of the ORF5 showed 85.9% homology to LV. The full genome sequence revealed a discontinuous deletion of 42nt and 366nt in the nsp2 region, and a 6nt deletion in the ORF4. To confirm the high pathogenicity of the virus, five conventional pigs of six weeks of age from a PRRSV negative herd were intranasally inoculated with 10^6 $TCID_{50}$/pig PR-402014 (HP) in 2 ml of PBS, 1 ml/nostril (HP group). Moreover, five pigs from the same origin were inoculated with the same dose of a recent Italian PRRSV (PR-012014) isolate. This group (NP group) served as a reference group for the comparison of the obtained findings. At day 3 p.i., two more pigs were added to each group to act as "in contact" pigs. In total 7 pigs/group were considered. Thus, a group of 3 pigs intranasally inoculated with 2 ml of PBS served as negative control. Body temperature and clinical signs (respiratory disorders scored from 0 to 6, appetite, level of consciousness) were monitored daily. Blood and nasal swabs were collected at 0, 3, 7, 10, 14, 21, 28, 35, 42 days p.i. in all experimental pigs. Clinical and virological differences were observed among animals inoculated with the HP and the NP isolates. In particular, high fever (the average temperature was >40°C from day 2 to 24 p.i. peaking up to 41,5°C in some animals), anorexia and depression of the level of consciousness were the prominent signs in pigs inoculated with the HP from day 3 to 28 p.i. Fever in NP animals was constantly lower. Four out of 7 (57%) pigs died in the HP group. The ADWG was 264 g/day for the survivors (3 pigs) in group HP, 345 g/day for those of NP group and 497 in the negative control group. Viremia in HP infected pigs was higher and longer in duration as compared to the NP infected animals. Dead animals from HP group showed severe lymphocyte depletion in the lymphoid tissues and organs and severe interstitial pneumonia. Taken together a) the clinical outcomes of the PRRSV isolate in the field, b) the genome deletions and 3) the experimentally induced severe clinical signs associated with high viremia and pathological lesions in challenged pigs, we can assume that the isolate PR-402014 could be defined as a highly pathogenic PRRSV-1, subtype 1.

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Comparison of morbidity and mortality after challenge with two North American PRRS virus isolates shows marked variation in time course and prevalence of clinical disease between isolates

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Porcine reproductive and respiratory syndrome (PRRS) is the most economically devastating disease of swine worldwide. Significant genetic variation among PRRS virus isolates can correlate to differences in clinical signs and disease progression. The objective of this study was to compare morbidity and mortality of two heterologous North American (Type 2) PRRSV isolates after experimental challenge in nursery pigs. Two experimental populations of approximately 200 commercial crossbred pigs (Pietrain × LW) each were infected with either NVSL-97-7985 (NVSL) or KS-2006-72109 (KS06) and followed for 42 days post-infection (dpi). Overall morbidity after challenge with NVSL or KS06 was 39.2 and 21.6%, respectively ($p = 0.0002$). Mortality rates were also higher after infection with NVSL when compared to KS06 (11.5 and 9.0%, respectively); however, this difference was not statistically significant ($p = 0.51$). The time course of clinical disease post-infection with NVSL was chronic, with clinical signs occurring at a similar rate throughout the course of the trial. In contrast, clinical disease post-infection with KS06 was acute, with clinical signs primarily occurring between 4 and 10 dpi. The mean duration of clinical disease also reflected the chronic and acute disease progression of the two isolates; 11.5 ± 6.0 dpi with NVSL and 4.0 ± 2.1 dpi with KS06 ($p < 0.0001$). Clinical signs of respiratory disease, such as open mouth breathing, dyspnea, tachypnea and nasal discharge, were 11.3 times more likely to occur after challenge with NVSL than after challenge with KS06 ($p < 0.0001$). Infection with NVSL was 3.9 times more likely to reduce body condition during the course of the trial compared to infection with KS06 ($p = 0.001$). Severity of clinical disease correlated with an overall increase in PRRSV replication after challenge with NVSL; total virus load was 153.7 ± 20.3 and 140.3 ± 17.2 for NVSL and KS06, respectively ($p < 0.0001$). Average daily gain (ADG) during the 42 day trial was also significantly lower in pigs challenged with NVSL; 0.43 ± 0.09 kg and 0.45 ± 0.10 kg in pigs challenged with NVSL and KS06, respectively ($p = 0.03$). In this model, challenge with NVSL had significantly higher morbidity, greater virus replication, and decreased ADG due to the chronic duration of disease. However, challenge with KS06 resulted in similar mortality due to acute and severe disease within the first week post-infection. These results provide evidence for the acute and chronic forms of clinical disease that can occur with different PRRSV isolates.

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Cross-reactivity of immune responses against Porcine Reproductive and Respiratory Syndrome virus

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The extent of cross-reactivity of humoral and cell-mediated immunity (CMI) against porcine reproductive and respiratory syndrome virus (PRRSV) are yet to be fully understood. CMI against PRRSV has been described as slow and weak, and it has been hypothesized that expression of interferon (IFN)-gamma by T-cells correlates with reduced viremia and lung lesions after challenge. Protection against challenge is also afforded by neutralizing antibodies. While the overall antibody response against PRRSV is very broad, neutralizing antibodies show high specificity. The objective of our work was to determine the cross-reactivity of T-cells and its correlation with humoral immunity and genetic variability.

To that purpose, two groups of four-week old pigs were either inoculated intramuscularly with PRRSV isolate FL12 (n=12) or left uninfected (n=12). All animals were bled at 0, 14, 28, 42, 63 and 77 days post-infection, serum was collected and peripheral blood mononuclear cells (PBMCs) were isolated. The number of IFN-gamma secreting cells (SC) per million PBMCs was determined by ELISpot using FL12 and nine different PRRSV isolates of varying genome-wide pairwise distance as recall antigens. Antibody responses, total and neutralizing, were evaluated by immunofluorescence and serum viral neutralization assays against five of these PRRSV isolates.

The IFN-gamma SC responses were highly variable between animals against both homologous and heterologous isolates. The overall IFN-gamma SC response was not significantly different among PRRSV isolates, regardless of genetic distance to FL12, and time post-infection. This suggests that the T-cell response against PRRSV is broadly cross-reactive. No association could be drawn between PRRSV isolate genome-wide pairwise distance and the number of IFN-gamma SC. The total antibody response was broad, while the neutralizing antibodies were specific to FL12. Additional studies into PRRSV CMI should be useful in determining whether a highly specific subset of T-cells exists, analogous to neutralizing antibodies in the humoral immune response.

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Changes in the genetic composition of PRRSV quasispecies and its relationship with long and short viral infections

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Replication of RNA viruses is usually mediated by an error-prone RNA-polimerase. The high mutation rate of such RNA-polimerases produces a cloud of mutants in each round of replication. This leads to the formation of quasispecies; namely to groups of related viral genomes competing with other groups in a high mutation environment. This concept of quasispecies is important to understand viral evolution. In PRRSV it is known that vaccination only provides partial protection against the heterologous challenge. This means that vaccinated pigs can be infected although replication of the virus in the vaccinated animals is shorter and of lesser intensity compared to naïve pigs. When this examined in detail for type 1 PRRSV, it can be seen that some vaccinated infected animals have very short viremias (1-3 days) while other pigs develop viremias lasting one or two weeks. It is known that the host's genetic background may play a role on this. The objective of the present work was to assess the variation in the virus across the infection period in vaccinated pigs. To do so, three groups of infected pigs: non-vaccinated (n=6, vaccinated presenting a short-viremia (1-3 days after challenge, n=7) and vaccinated showing a long-viremia (>3 days after challenge, n=4) have been analyzed. After setting up a specific protocol to directly sequence RNA avoiding intermediate PCR steps, pig sera samples were used to infect macrophages. The ARN extracted from the cell culture supernatants were characterized by Next-Generation Sequencing (NGS) using the MiSeq Illumina platform in order to characterize the population diversity and structure of PRRSV. A high proportion of reads (>85%) showed good Phred Quality scores (q>20), coupled with the high coverages reported (>100) indicated the reliability of the reads obtained. Nucleotide and aminoacid differences among groups and with the initial inoculum were screened comparing the nucleotide frequency differences for every polymorphic position by means of a hierarchical nested analysis of molecular variance (AMOVA). A large proportion of nucleotide mutations were not silent, inducing aminoacid changes. Those differences were not evenly distributed along the PRRSV genome, being concentrated in the nsp2, nsp2TF and nsp9 genes, pointing that virus-based factors may influence the differential susceptibility against PRRSV infection within a herd.

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The progression to T cell immunity after infection with porcine reproductive and respiratory syndrome virus

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Although the adaptive response to infection with Porcine Reproductive and Respiratory Syndrome virus (PRRSV) has been analyzed *in vivo*, there has not yet been an explanation for the delay in the occurrence of IFN-gamma secreting cells. Given that PRRSV is able to infect macrophages (Mϕs) as well as CD163+ dendritic cells (DCs), it seems plausible that different antigen presenting cells (APCs) will evoke specific lymphocyte proliferative responses. We hypothesize that macrophages are responsible for the delay in immune protection, whereas DCs are responsible for stimulating IFN-y secreting lymphocyte proliferation. Using GMCSF-derived Mϕs, monocyte derived DCs (MoDCs), and Flt3L-derived bone-marrow dendritic cells (BMDCs), we first compared these cells in vitro in response to infection with PRRSV. Using flow-cytometry, we observed an up-regulation of MHC molecules on CD163+ BMDCs and MoDCs, suggesting their importance in the progression to adaptive immunity. In comparison, the CD163- DCs showed a down-regulation of both MHC molecules. Additionally, we found that levels of MHCI and MHCII expression on the surface of Mϕs infected with PRRSV are both down-regulated. To further characterize the progression to adaptive immunity during PRRSV infection *in vivo*, animals were infected with PRRSV VR-2332 and T cells were isolated over the course of the infection on different dates. By co-culturing MoDCs, macrophages, and BMDCs with T cells from the respective dates, we will analyze the differences in the T cell response to antigen-presentation by either macrophages or DCs. We hypothesize that only the 163+ DCs will be able to stimulate a significant IFN-y cell mediated response. Results from a pilot study in which animals were immunized with the MLV support our hypothesis. ELISPOTs in which PBMCs, from the immunized animals, treated with either inactivated PRRSV or live PRRSV both evoked IFN-gamma responses. However, in the T cell co-cultures, T lymphocyte proliferation was only observed when macrophages were cultured with live but not inactivated PRRSV. This indicates that there is a cell population present in PBMCs that promotes an IFN gamma response to inactivated virus. It seems likely that a subset of dendritic cells is responsible for such a response, which could also provide a theory for the delay in cell-mediated immunity observed *in vivo.*

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Pathological findings at the maternal-fetal interface during the early type 2 PRRS virus infection of late gestation pregnant gilts

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Understanding the pathophysiological mechanisms responsible for fetal death related to porcine reproductive and respiratory syndrome (PRRS) is essential step in designing effective control measures against this costly disease. Our recently completed study of type 2 PRRSV infection at maternal-fetal interface (MFI; uterus plus adherent fetal placenta) 21 days post-inoculation (dpi) revealed that pathological lesions were not compatible with fetal death. However, due to the large number of autolyzed and decomposed fetuses in that study, an association between lesions at the MFI and fetal preservation status was not confirmed. The aim of this present study is to evaluate progression of PRRSV induced pathology in the uterus and fetal placenta during early time points of infection. A total of 15 PRRS virus-naïve, high-health pregnant gilts were intramuscularly and intranasally inoculated with PRRSV (NLSV 97-7895; 1 x 10^5 $TCID_{50}$ total dose) on gestation day 85±1. Five negative control gilts were sham inoculated. Three gilts challenged with PRRSV and one control gilt were euthanized on each of five days post inoculation (dpi 2, 5, 8, 12 and 14). At each time point, MFI samples corresponding to each fetus were formalin-fixed and paraffin-embedded. Histopathology of the MFI was assessed by a pathologist blinded to inoculation status and time points. Severity of inflammation in uterus and fetal placenta was assessed based on percentage of affected tissue: normal, minimal (<10%), mild (10-25%), moderate (25-50%) and severe (>50%). Results of pathological assessment revealed large numbers of PRRSV-induced lesions in the endometrium (Table 1), with the earliest lesion detected on 2 dpi consisting of focal vasculitis. Detachment of fetal placenta from uterus was observed more often in PRRSV infected compared to non-infected samples. On 14 dpi, 64% of PRRSV-infected uterine samples were severely inflamed with diffuse vasculitis and 22% of uterine samples exhibited detachment of fetal placenta. Pathological findings from our study revealed a progression of lesion severity in the maternal-fetal interface starting from 2 dpi to 14 dpi. This project was supported by Genome Canada, Genome Prairie (Saskatchewan Ministry of Agriculture) and Genome Alberta.

Table 1. Pathological lesion severity in endometrium by days of post-inoculation

	PRRSV-infected gilts						**Non-infected gilts**					
dpi	Severity of inflammation in endometrium					Detachments[1]	Severity of inflammation in endometrium					Detachments[1]
	N	Min	Mild	Mod	Sev		N	Min	Mild	Mod	Sev	
2	0/34	23/34	11/34	0/34	0/34	3/34	6/14	7/14	1/14	0/14	0/14	3/14
5	1/43	16/43	23/43	3/43	0/43	6/43	11/13	2/13	0/13	0/13	0/13	0/13
8	0/43	1/43	7/43	27/43	8/43	6/43	10/14	4/14	0/14	0/14	0/14	1/14
12	0/49	0/49	2/49	25/49	22/49	7/49	12/16	4/16	0/16	0/16	0/16	0/16
14	0/36	0/36	2/36	11/36	23/36	8/36	5/14	8/14	0/14	1/14	0/14	1/14

[1] Presence of fetal placental detachments from the uterus. N=normal, Min=minimal, Mod=moderate, Sev=severe

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Pathogenesis and infection dynamics of Senecavirus A in pigs

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Senecavirus A (SVA), a picornavirus of the genus *Senecavirus*, has been recently associated with vesicular disease and neonatal mortality in swine the US and in Brazil. However, many aspects of SVA infection biology and pathogenesis remain unknown. Here, the pathogenesis and infection dynamics and of SVA were investigated in pigs. Twelve finishing pigs (~100 lb) were randomly allocated into two experimental groups as follows: Group 1: Mock-control group (*n = 4*) and Group 2: SVA-inoculated group (*n = 8*). Animals were inoculated oronasally with a contemporary SVA strain and monitored daily for characteristic clinical signs and lesions associated with SVA infection. Viremia was assessed in serum and virus shedding was monitored in oral and nasal secretions and feces. Samples collected on days 0, 3, 5, 7, 10, 14, 21, 28 and 35 post-inoculation (pi) were tested by real-time reverse transcriptase PCR (qRT-PCR) and virus isolation. Clinical signs characterized by lameness and lethargy were first observed on day 4 pi and persisted for 2-10 days. Vesicular lesions were observed on the snout and feet, including coronary bands, dewclaws and sole of inoculated animals. Vesicular lesions were observed between days 4 and 14 pi. Viremia was detected between days 3 and 10 pi, whereas virus shedding was detected between days 1 and 28 pi in oral and nasal secretions and feces. Notably, rRT-PCR and *in situ* hybridization performed on tissues collected on day 38 pi revealed the presence of viral RNA on the tonsil of all SVA infected animals. Serological responses were monitored by virus neutralization and indirect immunofluorescence assays. Animals developed an early neutralizing antibody (NA) response to SVA, with NAs being first detected on day 5 pi and peaking on day 10 pi. High levels of NAs were still detected on day 38 pi. SVA specific IgG antibodies were first detected by IFA on day 10 pi, peaked on day 14 pi and presented a slight decline on days 35 and 38 pi. Results of this study provide important insights about the pathogenesis, infection dynamics, and shedding patterns of SVA in swine.

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The effect of PRRS viral level and isolate on tonsil gene expression 42 days after infection

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The objective of this research was to identify differentially expressed genes (DEGs) and gene ontology-biological process (GO-BP) in tonsils from pigs with either extreme high or low tonsil Porcine Reproductive and Respiratory Syndrome virus (PRRSV) levels 42 days post infection (dpi) with one of two viral isolates, NVSL-97-7985 (NVSL) and KS-2006-72109 (KS06). The data analyzed for this study were from two PRRS Host Genetics Consortium PRRSV infection trials of ~200 commercial nursery pigs each from the same genetic source. At 42 dpi, pigs were euthanized and tonsil samples were collected. Tonsil samples were chosen for RNA-seq based on high or low levels (at least one standard deviation from the mean) of PRRSV present in the tonsil, evaluated by a semi-quantitative PCR assay for PRRSV RNA, resulting in 15 NVSL-high, 13 NVSL-low, 12 KSO6-high, and 10 KSO6-low. After removing transcripts with mean read counts across all samples less than 8 and less than 4 samples with read counts larger than zero, 11,909 genes were determined to be expressed in the tonsil. After backward variable selection built on QuasiSeq, the statistical model for read counts for each gene included PRRSV isolate, tonsil virus class (high/low), the interaction between PRRSV isolate and tonsil virus class, genotype at marker WUR10000125 (WUR), which has been reported to be strongly associated with both weight gain and serum viremia in pigs after infection with PRRSV, and sex as fixed class variables, and RNA integrity number (RIN) as a covariate. Using the QuasiSeq package, 258 DEGs were identified ($q \leq 0.1$) between the two PRRSV isolates, 105 DEGs ($q \leq 0.1$) were identified between the high and low tonsil virus class, and 7 genes were significant ($q \leq 0.1$) for the interaction between PRRSV isolate and tonsil virus class. Using all genes expressed in the tonsil as the reference, GO-BP terms were tested for enrichment in the DEGs using PANTHER. Overrepresented ($p<0.05$) terms among DEGs between the two isolates included immune system process, cell-matrix adhesion, cell-cell adhesion, ectoderm development, cellular component morphogenesis, and signal transduction. The term immune system process was also overrepresented (p=5.97E-03) among DEGs between the high and low tonsil virus class. Taken together, this study suggests that genes involved in the immune system process are correlated with the tonsil virus level for both PRRSV isolates. In future work, the identified DEGs will be further validated and selected to build a biomarker-based classifier for PRRSV resistance. This project was funded by Genome Canada, USDA-ARS, USDA-NIFA grant 2013-68004-20362 and National Pork Board grants #12-061 and #14-223. We would also like to acknowledge contributions from members of the PRRS Host Genetics Consortium.

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A major gene for host response under PRRS challenge is not negatively associated with overall performance in commercial pig lines under non-challenged conditions

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Previous research identified the *GBP5* gene as a major gene for host response to PRRS, for which the single nucleotide polymorphism (SNP) WUR10000125 (WUR) can be used as a tag SNP. The effect of WUR has been validated across breeds, genetic sources, and with different PRRS virus (PRRSV) isolates. However, questions that remain unanswered are: what is the effect of the favorable (B) allele for WUR on economically important traits under non-challenged conditions and why does the B allele have a low frequency (~0.2) in commercial populations? Thus, the objective of this study was to estimate the effect of WUR genotype on selected index traits in commercial pig lines under normal, non-challenged conditions.

Data originated from records collected on four Topigs Norsvin lines: a Landrace maternal line (A), a Large White maternal line (B), a synthetic boar line (C), and a Pietrain boar line (D). Frequency of the B allele ranged from 10 to 22% by line. Pigs were genotyped using either the Porcine SNP60 or SNP80 BeadChip, which included the WUR SNP. Nine traits were analyzed, including total number born, number stillborn, farrowing survival, lactation survival, litter mortality, backfat, daily feed intake, lifetime daily gain, and daily gain during test. The Topigs Selection Index (TSI), indicative of overall performance, was also analyzed. De-regressed estimated breeding values for each trait (except for TSI) were analyzed within line using univariate animal models in ASReml 4.0. PRRS vaccination status (PRRS_vacc; whether/not pigs were vaccinated for PRRS), WUR, and PRRS_vacc*WUR were fitted as fixed effects and genetic relationships were accounted for using pedigree.

For the B line, no difference in farrowing survival was detected between genotypes within the non-vaccinated group, but farrowing survival was numerically greater for AB/BB pigs than for AA pigs within the vaccinated group (PRRS_vacc*WUR; P=0.05). A significant effect of WUR (P<0.001) on litter mortality was detected in the D line, where BB pigs had significantly greater litter mortality than AB or AA pigs. No significant effect of WUR genotype was detected on any of the finishing traits for the maternal lines. In the C line, the B allele was associated with significantly lower lifetime growth rate (P=0.001) and test growth rate (P=0.002), but also lower feed intake (P=0.004). Conversely, the B allele was associated with significantly higher feed intake (P<0.001) and a tendency for higher test growth rate (P=0.09) in the D line. The effect of WUR on TSI was not significant for any of the lines ($P\geq$0.15).

In conclusion, the direction of the WUR genotype effect differed between traits and lines. The favorable (B) allele for host response to PRRS had a favorable effect on farrowing survival in the B line when pigs were vaccinated for PRRS. The B allele was also associated with greater feed intake and a tendency for greater growth in the D line, but the opposite direction of effect was detected for the C line. However, regardless of the effect on individual traits, no effect of WUR on the overall index value was detected for any of the lines. Therefore, selecting for the B allele may result in progeny with increased performance under PRRS challenge without adversely affecting overall TSI. This work was supported by the USDA ARS and NIFA award 2012-38420-19286 and by Topigs Norsvin.

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Porcine reproductive and respiratory syndrome virus (PRRSV) up-regulates IL-8 expression through TAK-1/JNK/AP-1 pathway

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The acute phase of respiratory distress caused by porcine reproductive and respiratory syndrome virus (PRRSV) infection is likely a consequence of the release of inflammatory cytokines in the lungs. IL-8, the main chemokine and activator of neutrophils, might be related in the lung lesions upon PRRSV infection. In this study, we first confirmed that HP-PRRSV induced IL-8 expression in vivo and in vitro. Subsequently, we showed that JNK and NF-κB pathways were required for the enhancement of IL-8 expression. JNK and NF-κB pathways were indeed activated upon PRRSV infection, as evidenced by JNK and IκB phosphorylation. We further verified that PRRSV activated TAK-1 was essential in JNK and NF-κB pathway activation and IL-8 expression. Moreover, we revealed an AP-1 binding motif in the cloned porcine IL-8 (pIL-8) promoter, and deletion of this motif abrogated the pIL-8 promoter activity. Additionally, the AP-1 subunit c-Jun was found to be critical for the activation of porcine IL-8 promoter by PRRSV. Our findings suggest that PRRSV-induced IL-8 production is likely through the activation of TAK-1/JNK/AP-1 pathway.

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Genetic evaluation of reproductive performance during PRRS/PED outbreaks

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Porcine reproductive and respiratory syndrome (PRRS) is one of the most infectious swine diseases in the world, resulting in over $600 million dollars of economic loss in the U.S. alone. More recently, the U.S. swine industry has been having additional major economic losses due to the spread of porcine epidemic diarrhea (PED). However, information regarding the amount of genetic variation for response to diseases in reproductive sows is still very limited. Therefore, the purpose of this study was to quantify differences in genetic parameters for reproductive performance within PRRS and/or PED challenged and non-challenged environments.

Performance data and a five-generation pedigree were available from 10 commercial farms in North Carolina. A total of 21,060 farrows from 5,448 crossbred (Large White x Landrace) multiparous sows were used for analyses. Traits analyzed included abortions (AB), number of piglets born alive (NBA), number of stillborn piglets (SB), number of mummified piglets (MUM), number born dead (NBD), and number weaned (NW). Occurrences of PED and PRRS breaks were confirmed by serological results. However, the dates of the PED and PRRS outbreak phases on each farm were determined based on the herd-year-week estimates of the reproductive performance. A total of 6 and 15 outbreaks were identified for PRRS and PED, respectively. Genetic parameters (heritabilities and correlations) were estimated for each phase (Clean, PRRS, and PED) separately, in a model including the fixed effects of season, year, and farm, and the random effect of animal. A covariate of number of weaning events was added for the NW trait. For the Clean phase, a random permanent environmental effect was fit in the model to account for the repeated records. Genetic correlations between traits were estimated within and between disease phases. Traits with a large number of zeros (SB, MUM, and NBD) were analyzed as the natural log of the phenotype + 1. Analyses were done in ASReml4.

Heritability estimates for the Clean phase ranged from 0.01±0.003 (MUM) to 0.23±0.04 (AB), for the PRRS phase ranged from 0.05±0.07 (SB) to 0.29±0.06 (AB), and for the PED phase ranged from 0.01±0.02 (SB) to 0.38±0.06 (AB). Genetic correlations within the PRRS phase ranged from -0.97±0.46 to 0.82±0.44 for NBD with NBA and MUM, respectively. Within the PED phase, genetic correlations were estimated from -0.62±0.82 to 0.98±0.38 for MUM with NW and NBD, respectively. In general, estimation of genetic correlations between phases for the same traits showed convergence problems. However, interesting genetic correlations were found, such as the low estimate (0.36±0.17) for NW between the Clean and PED phases, indicating that NW in these phases are two genetically different traits, and the overall high estimates (>0.80) between PRRS and PED phases for most traits, indicating that, although different diseases, response to these diseases are genetically similar.

These are the first reports on genetic variation for response to PED infection in reproductive sows. These results indicate that there is a sizable genetic variation for response to PED, and that the selection for increased NW during PED outbreaks will not impact NW performance in clean environments. In addition, response to PED and PRRS seems to be genetically the same for reproductive traits.

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Genetically edited pigs lacking CD163 show no resistance following infection with the African Swine Fever Virus isolate, Georgia 2007/1

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African swine fever is a highly contagious, often fatal disease of swine for which there is no vaccine or other curative treatment. The macrophage marker, CD163, is a putative receptor for African swine fever virus (ASFV). The objective of this study was to evaluate the requirement of CD163 using a genetically edited pig model. Pigs possessing a complete knockout of CD163 on macrophages were inoculated with Georgia 2007/1, a genotype 2 isolate. Knockout and wild type pen mates became infected and showed no differences in clinical signs, mortality, pathology or viremia. There was also no difference following *in vitro* infection of macrophages. The results do not rule out the possibility that other ASFV strains utilize CD163, but demonstrate that CD163 is not necessary for infection with the Georgia 2007/1 isolate. This work creates opportunities to focus on alternative ASFV receptors and entry mechanisms. Understanding these virus-host interactions is important for designing better antiviral strategies against ASF.

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Porcine reproductive and respiratory syndrome virus takes advantage of host intercellular mitochondria transferring pathway for cell to cell spreading of the infection

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Our recent study showed that intercellular nanotube connections can serve as an alternative pathway for cell to cell spreading of PRRSV infection (Guo et al., 2016, J. Virology, 90(10):5163-75). Here, we further studied the mechanisms of nanotube formation during PRRSV infection and cellular organelles involved in the transportation of PRRSV infectious materials. We found that PRRSV infection can induce the formation of intercellular nanotube connections between infected and uninfected MARC-145 cells in the early stage of infection. Co-culturing PRRSV-infected cells with uninfected cells rescued PRRSV-induced cell necrosis. Mitochondria, an important regulator for virus-induced danger signaling, can be observed transferring from uninfected cells to PRRSV-infected cells. Importantly, impaired formation of nanotubes or ethidium bromide and uridine treated cells carrying defective mitochondria were unable to rescue infected cells from necrosis in the co-culture system. Confocal microscopy analysis showed that mitochondria-associated molecules in the antiviral signaling pathways, including MAVS and RIG-I, were co-localized with the mitochondria and transported through the nanotubes from uninfected to infect cells. Furthermore, PRRSV nsp1alpha, nsp1beta, and nsp4 were detected to be associated with mitochondria and transported from infected to uninfected cells through the nanotubes. Our results suggest that transferring of functional mitochondria through nanotubes rescued the PRRSV-induced cell necrosis in the early stage of infection. On the other hand, PRRSV takes advantage of this intercellular pathway, in which mitochondria could be utilized as a cargo to transport viral infectious materials for cell to cell spreading of the infection.

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Evaluation of fetal and maternal gene expression responses to reproductive porcine reproductive and respiratory syndrome virus infection

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Porcine Reproductive and Respiratory Syndrome virus (PRRSV) infection causes reproductive failure in pregnant females. It is mainly characterized by late-term abortions, early farrowing, fetal death, and an increase of weak born fetuses which can result in elevated pre-weaning mortality. Our group has used a pregnant gilt model (PGM) to probe the mechanisms of PRRSV-induced reproductive failure. Our original model (PGM1) tested effects at 21 days post infection (dpi) in pregnant gilts and their fetuses, inoculated at 85 +/- 1 day gestation (DG). Our new PGM2 uses 85 DG gilts that were sham (control; n=5) or type 2 PRRSV (strain NVSL 97) inoculated (n=15). Gilts were euthanized at 2, 5, 8, 12, and 14 dpi and fetal preservation status evaluated. Blood and tissue samples were collected to measure viral load to determine when the virus crosses the placental barrier and infects the fetuses. For each fetus, the thymus was collected as well as the maternal-fetal interface (MFI) which was separated into maternal endometrium and fetal placenta; all samples were snap frozen. To characterize factors regulating the effects of temporal movement of PRRSV across the MFI and gain insight into the mechanisms of PRRSV pathogenesis we will analyze gene expression in these tissues using Nanostring gene expression technology, testing samples from 4 time points (5, 8, 12, 14 dpi). We will compare data from sets of fetuses from each negative control gilt (NEG) and from each of the 3 PRRSV inoculated gilts [matching PRRSV negative, uninfected (UNINF) with infected (INF) from the same litter] based on fetal serum and thymus PRRSV viral load. RNA will be prepared from maternal endometrium, fetal placenta and thymus from each selected fetus. For Nanostring PCR, >220 genes were selected for expression analyses. These gene codesets were based on data from past PRRSV infection response studies, in cell cultures, growing pigs, and PGM1 RNAseq studies, analyzed using Ingenuity Pathway Analysis (IPA) and KEGG Pathway Database. The critical gene sets and pathways that were significantly associated with post-PRRSV infection response included signaling pathways associated with interferons, TREM1, HMGB1, B cell/T cell receptors, Toll-like receptors, and apoptosis/mitosis, etc. The codeset also tested for genes related to endometrium and placenta tissue remodeling and epithelial integrity and permeability. Overall this data should reveal mechanisms involved in PRRSV transmission from the gilt to some, but not all, of her fetuses and highlight genes which predict prevention of in utero fetal PRRSV infection. Funding provided by Genome Canada, Genome Prairie (Saskatchewan Ministry Agriculture), Chinese Scholarship Council fellowship, and USDA ARS.

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SAP domain in nsp1-beta of porcine reproductive and respiratory syndrome virus (PRRSV) correlates with interferon suppression in cells and pathogenesis in pigs

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Porcine reproductive and respiratory syndrome virus (PRRSV) is an arterivirus whose translation is cap-dependent and occurs in the cytoplasm of infected cell. In the present study, we show the subversion of host cell mRNAs translation by PRRSV during infection. PRRSV blocked the host mRNA nuclear export to the cytoplasm, and it was common in both European genotype and North American genotype of PRRSV. For PRRSV, nsp1-alpha, nsp1-beta, and N were nuclear proteins, and of these, nsp1-beta was found to play a pivotal role for host mRNA nuclear retention. A SAF-A/B, Acinus, and PIAS (SAP) motif was identified in nsp1-beta with a consensus sequence of 126-LQxxLxxxGL-135. Mutations were introduced in the SAP domain and the mutants were examined for their subcellular localization, inhibition of host cell mRNA nuclear export, and suppression of host protein synthesis. In site hybridization unveiled that L126A, R128A, R129A, L130A, and L135A were unable to cause nuclear retention of host cell mRNAs. PRRSV nsp1-beta was shown to inhibit the type I IFN response, and the above mutants were unable to inhibit the IFN production and signaling pathways. Using the infectious clone for PRRSV and reverse genetics techniques, SAP mutant viruses were generated. Infectious viruses were recovered for vK124A, vL126A, vG134A, and vL135A, but vR128A, vR129A, and vL130A were non-viable. Among the viable mutants, vL126A and vL135A lost the ability to suppress the IFN production in cells, suggesting that the SAP domain in nsp1-beta of PRRSV is crucial for type I IFN suppression. To investigate the role of SAP domain in nsp1-beta of PRRSV for viral pathogenesis, piglets of 3-week-old were infected intramuscularly with SAP mutant viruses. Pigs infected with vL126A or vL135A exhibited less severe clinical signs with lower and shorter durations of viremia comparing to pigs infected with wild-type PRRSV. The titers of neutralization antibody were higher in vL126A- or vL135A-infected pigs than those of control pigs. When examined for viral persistence in the tonsils, two of ten pigs in the vL135A-infection group were PRRSV-negative, and the remainders were positive for PRRSV. Reversion to wild-type sequence occurred in all ten pigs in the vL126A group and seven of eight pigs of the vL135A group. Only one of the eight pigs in the vL135A group remained unchanged. These data show that the SAP domain in nsp1-beta of PRRSV contributes to viral pathogenesis.

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Contribution of PRRSV minor glycoproteins to a protective immune response in swine

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Determining the role of PRRSV minor glycoproteins in the induction of a protective immune response is an area of PRRSV research that may have an impact on vaccine development. GP2, GP3, and GP4 form a trimer on the surface of the virion. GP2 and GP4 interact with CD163, the main host cell receptor for PRRSV infection, and because GP3 is part of a trimer it may be interacting with the receptor as well. Previous work by many laboratories has shown minimal cross-protection between Type 1 and Type 2 PRRSV. With this knowledge, GP2, GP3 and GP4 of a Type 2 infectious clone were cloned into a Type 1 infectious clone, and this virus was used to determine the contribution of the minor glycoproteins to a protective immune response. Chimeric virus was recovered, and we determined that the chimeric virus was sensitive to neutralization, indicating that neutralizing antibodies are directed against GP2, GP3, and GP4. This chimeric virus was then used in an animal experiment to evaluate the contribution of GP2, GP3, and GP4 to protective immunity in pigs. Neutralizing antibodies against the chimeric virus and the Type 2 parental virus, and GP2, GP3, and GP4 specific IFN-gamma secreting cells were detected prior to challenge and increased after challenge. Viremia after challenge was lower in the chimeric virus group compared to the PBS and Type 1 PRRSV controls. Tissue viral load in the lung was lower for the chimeric virus group compared to the control groups, while the tonsil and lymph node viral loads were similar across all groups. The chimeric virus group had lower lung pathology scores than the control groups. Animals immunized with chimeric virus developed neutralizing antibodies and antigen-specific T cells that recognized GP2, GP3, and GP4 peptides; however, GP2, GP3, and GP4 conferred only partial protection against challenge.

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Porcine deltacoronavirus induces caspase-dependent programmed cell death

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Porcine deltavoronavirus (PDCoV), a member of the genus *Deltacoronavirus* in the family *Coronaviridae* of the order *Nidovirales*, is a newly emerged swine enteric coronavirus causing severe clinical diarrhea and intestinal pathological damage in piglets. As a novel identified viral pathogen, numerous aspects of virus-host interactions have been largely undeciphered. As a first step toward understating the effect of PDCoV on cells, we sought to investigate whether PDCoV induces programmed cell death (PCD) *in vitro* and to elucidate mechanisms associated with the process of PCD after PDCoV infection. PDCoV-infected cells showed evidence of apoptosis including DNA fragmentation and phosphatidylserine exposure. In addition, caspase-3, the main effector caspase, was activated in PDCoV-infected cells up to 24 h post-infection (hpi), indicating the cascade of caspase activation in relation to PDCoV-induced apoptotic cell death. Furthermore, the use with Z-VAD-FMK, a pan-caspase inhibitor, affected PDCoV replication and inhibited virus-induced apoptosis, suggesting that a caspase-dependent pathway is involved in the process. Since caspases appear to be essential factors in PDCoV-induced cell death, we tried to assess the release of cytochrome c (CytC), which is proapoptotic protein to execute caspase proteolytic cascade-dependent intrinsic apoptosis, from mitochondria to the cytosol by mitochondrial outer membrane permeabilization. A number of coronaviruses, including porcine epidemic diarrhea virus, are known to trigger PCD through an apoptosis inducing factor (AIF)-mediated pathway. Thus, we further aimed to investigate whether mitochondrial AIF translocate to the nucleus during the course of PDCoV infection. We also examined effects of cyclosporin A (CsA), an inhibitor of cyclophilin D (CypD) that is the major component of the mitochondrial permeabilization transition pore (mPTP), and *N*-phenylmaleimide, an AIF inhibitor, on PDCoV infection and virus-induced apoptosis. Results and discussion of *in vitro* assessment for those pharmacological treatments will be presented. Taken together, our results indicate that a caspase-dependent pathway plays a central role in PDCoV-induced apoptotic cell death.

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Resolution of genotype 1 PRRSV attachment on bone marrow-derived dendritic cells

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Porcine sialoadhesin (pSn) and CD163 have been thought the two main receptors mediating uptake and genome release of porcine reproductive and respiratory syndrome virus (PRRSV), and heparan sulphate (HS) facilitating initial attachment. To further evaluate the role of HS/pSn/CD163, the attachment on bone marrow-derived dendritic cells (BMDCs) by three genotype 1 PRRSV isolates 3249, 3262 and 3267 (with distinct immunobiological properties) was conducted. Firstly, BMDCs were digested with 10 U/ml heparinase I for 60 min at 37 ℃ to remove cell surface HS. Thereafter, each viral isolate was added at a multiplicity of infection (m.o.i.) of 3, incubating for 90 min on the ice. Attachment was subsequently quantified by flow cytometry (FC), and colocalization of virus and receptors was analysed by confocal microscopy. For FC, cells were fixed and underwent an indirect staining for PRRSV. According to the relative mean fluorescence index (MFI), isolates 3249 and 3267 generated higher MFIs while isolate 3262 scarcely attached on BMDCs. After HS removal, binding of 3249 was not significantly changed compared to reduction by 92% and 87.5% of 3262 and 3267, respectively. For single-cell imaging, a four-color fluorescence confocal staining PRRSV/pSn/CD163/DAPI was developed. As a result, attachment of 3249 was seen on $pSn^{+}CD163^{+}$, $pSn^{+}CD163^{-}$, $pSn^{-}CD163^{+}$ as well as $pSn^{-}CD163^{-}$ BMDCs, without obvious difference in fluorescence intensity between each subset. Even if on pSn^{+} cells, many virions did not colocalize with pSn. This pattern was not affected by HS removal. Isolate 3267 also attached on the four subsets but HS removal sharply decreased its attachment. For isolate 3262, very few viral particles were detected even without heparinase treatment, which conflicted with its efficient replication on BMDCs. These preliminary results indicate 1) HS plays different roles in mediating attachment of different type 1 PRRSV isolates on BMDCs. 2) Besides HS/pSn/CD163, BMDCs probably possess other potential receptors for type 1 PRRSV entry. 3) Alternative entry pathways independent of receptors for isolate 3262 may exist on BMDCs.

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IFN-lambda preferably inhibits PEDV infection of porcine intestinal epithelial cells compared to IFN-alpha

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Unlike type I interferons targeting many types of cells and organs in host, interferon lambda (IFN-L) is recently ascribed to primarily act on the mucosal epithelial cells and exhibits robust antiviral activity on mucosal surface. Porcine epidemic diarrhea virus (PEDV) causing high morbidity and mortality in piglets is an economically important enteropathogenic coronavirus. Here we demonstrated that both recombinant porcine IFN-L1 (rpIFN-L1) and rpIFN-L3 displayed powerful antiviral activity against PEDV in Vero E6 and intestine epithelial cell line-IPECJ2, and IFN-L1 inhibited both two genotypes of PEDV (genotype 1 CV777 strain and genotype 2 LNCT2 strain). rpIFN-L1 primarily controlled viral infection at the early stage of infection and showed more antiviral activity in IPEC-J2 than Vero E6. The anti-PEDV activity accounted for the antiviral IFN-stimulated genes (ISGs) (ISG15, OASL, MxA, and IFITMs) in IEC induced by rpIFN-L1. In addition, rpIFN-L1 exhibited more antiviral activity against PEDV in IEC than porcine IFN-alpha, which was consistent with the results that rpIFN-L1 triggered higher levels of ISGs (ISG15, OASL, MxA) in IEC than porcine IFN-alpha. Therefore, our data provide the first experimental evidence that porcine IFN-L has the ability to suppress PEDV infection of IPEC-J2 and might provide a new therapeutic to control PEDV infection in piglets.

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PRRSV nsp5 downregulates expression of antiviral genes by suppressing phosphorylation of STAT2

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Porcine reproductive and respiratory syndrome (PRRS) is an important disease causing severe economic losses in the swine industry worldwide. PRRSV has the ability to suppress innate immune signaling during infection, and elucidation of viral mechanism for innate immune modulation has been of interest. In the present study, we found that nonstructural protein 5 (nsp5) of PRRSV was an additional antagonist for antiviral innate immunity. The luciferase reporter assays using the ISRE-luc reporter, nsp5 was found to inhibit the ISRE promoter activity. When activation of STATs was examined by immunofluorescence in nsp5-expressing cells, STAT2 nuclear localization was specifically inhibited and this inhibition was mediated by the reduced phosphorylation of STAT2 as shown by Western blot. In contrast, STAT1 and STAT3 were normally translocated to the nucleus even in the presence of nsp5, suggesting that the STAT2 activity was specifically modified by nsp5. These results suggest that PRRSV nsp5 is involved in interfering the host antiviral innate immune response during infection. The present study contributes to a better understanding of the molecular basis of host cells process manipulated by PRRSV nsp5.

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Temporal movement of type 2 porcine reproductive and respiratory syndrome virus across the maternal-fetal interface

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Porcine reproductive and respiratory syndrome virus (PRRSV) infection within the uterus and at the maternal-fetal interface (MFI) is poorly understood. The aim of this study was to characterize the temporal movement of PRRSV by measuring viral load in the MFI, fetal tissues, and fetal and gilt serum at five time points after experimental inoculation of pregnant gilts. Using 20 gilts on day 85±1 of gestation, 15 were inoculated with 1 x 10^5 $TCID_{50}$ PRRSV (NVSL 97-7895) and 5 were sham-inoculated with sterile media (CTRL). At 2, 5, 8, 12, and 14 days post infection (dpi) three of the inoculated gilts plus one control were euthanized. Pre-and post-inoculation serum, and reproductive lymph node were collected from gilts, along with a section of MFI adjacent to the umbilical stump of each fetus. The placenta was manually separated from the endometrium for testing. After the preservation status of each fetus was determined, serum, thymus, spleen, mesenteric lymph node, umbilical cord, and amniotic fluid were collected. Viral RNA was extracted from samples using commercial kits. Probe based reverse-transcriptase quantitative PCR (qRT-PCR) targeting PRRSV NVSL 97-7895 was performed to assess viral load in samples. Gilt serum at 0 dpi, and all samples from CTRL gilts and their fetuses were negative for PRRSV. Average PRRSV RNA concentration (target log_{10} copies/uL) in gilt serum was 4.4 (2 dpi), 5.9 (5 dpi), 5.7 (8 dpi), 5.0 (12 dpi), and 3.1 (14 dpi). In the endometrium and fetal serum, qRT-PCR results were categorized as: RNA not detected (NEG; Cq>40), detectable but not quantifiable (DNQ), positive (POS: concentration >1.1 log_{10} copies/uL), and compared across day of termination (Table 1). The main findings were that the endometrium is largely infected by 2 dpi and the first evidence of fetal infection (based on serum PCR) was on 5 dpi. Fetal compromise was first observed on 8 dpi and increased progressively through 14 dpi.

Table 1: PCR and fetal preservation results by day of termination.

DPI	ENDOMETRIUM			FETAL SERUM			FETAL PRESERVATION		
	NEG	DNQ	POS	NEG	DNQ	POS	VIA	MEC	DEC
2	5/34 15%	7/34 20%	22/34 65%	34/34 100%	0/34	0/34	34/34 100%	0/34	0/34
5	0/43	2/43 5%	41/43 95%	24/43 56%	18/43 42%	1/43 2%	43/43 100%	0/43	0/43
8	0/43	1/43 2%	42/43 98%	23/43 53%	14/43 33%	6/43 14%	42/43 98%	0/43	1/43 2%
12	0/49	0/49	49/49 100%	7/47 15%	13/47 28%	27/47 57%	45/49 92%	0/49	4/49 8%
14	9/36 25%	0/36	27/36 75%	14/34 41%	9/34 26%	11/34 33%	21/36 58%	13/36 36%	2/36 6%

POS = positive; DNQ = detectable; but not quantifiable; NEG = negative; VIA = viable; MEC = meconium stained; DEC = decomposed; DPI = day post infection.

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Pigs vaccinated with PRRSFLEX EU at two- or three-weeks of age that did not show sero-conversion are protected by an immunologic recall answer after artificial challenge

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Porcine Reproductive and Respiratory Syndrome (PRRS) Virus is one of the major pathogens in pigs that have a significant economic impact on the swine industry worldwide. Vaccination against PRRSV has been demonstrated as an effective tool to control clinical signs related to infection. In the field sero-conversion is a common readout of successful vaccination, and animals that do not sero-convert have a questionable status in terms of protection.

In this study piglets were vaccinated on a commercial farm at two- or three-weeks of life, or not vaccinated as control animals. At 10-weeks of life 25/26 pigs of each group were artificially challenged with a heterologous field strain. Ten days post challenge the animals were euthanized and necropsied. At necropsy pigs PRRS induced lung lesions were scored according to previously established methods. Piglets were blood sampled on the day of vaccination, before challenge and the day of necropsy. All serum samples were analysed for PRRSV antibodies assayed by IDEXX 3x-ELISA. RNA of PRRSV was quantitatively detected in serum by Real Time PCR. A subset of 10 animals per group was tested for cellular immunity.

Before challenge, at 10 weeks of live, a total of 13 out of 51 vaccinated animals (25%) were tested negative for PRRS antibodies by ELISA (cutoff SP < 0,4) (‘non-responders‘; 6 animals vx. at 2-weeks of life and 7 animals vx. at 3-weeks of life). By chance, only three of the ‘non-responders’ were pre-selected for immunologic analysis. All but one control animals were tested negative for PRRS antibodies as the maternally derived antibodies had phased out.

At necropsy the vaccinated ‘non-responders’ did show a recall answer both for humoral and cellular immunity and had significant higher amounts of antibodies and PRRS specific IFN-gamma producing cells. Also, the mean amount of lung lesions was reduced by 40% and to semilar extent in both “responding” and “non-responding pigs in both of the vaccinated groups.

In conclusion, although some vaccinated animals did not show a sero-conversion after vaccination at two or three weeks of life, they were protected by the vaccine upon a heterologous challenge with a virulent field strain, both, by means of antibodies and cellular immunity.

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Antiviral potency and functional novelty of porcine Interferon-Omega subtype

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Innate immune interferons (IFNs), particularly type I IFNs, are primary mediators regulating antiviral immunity. These antiviral cytokines have evolved remarkable molecular and functional diversity to confront ever-evolving viral threats. Pigs have the largest and an expanding type I IFN family consisting of nearly 60 functional genes that encode seven IFN subtypes including multigene subtypes of IFN-alpha and omega. Whereas subtypes such as IFN-alpha and beta have been widely studied, the unconventional IFN-omega subtype has barely been investigated. We have evolutionarily defined the porcine IFN family, and preliminarily showed that porcine IFN-omega subtype has evolved several novel features including, (1) a signature multi-gene subtype expanding particularly in bats and ungulates, (2) emerging isoforms that have much higher antiviral potency than typical IFN-alpha, (3) cross-species high antiviral (but little anti-proliferative) activity in cells of humans and other mammalian species, and (4) potential action through non-canonical signaling pathways. This study is focused on antiviral potency of porcine IFN-omegas investigating their evolutionary and functional diversity, signaling specificity, and optimization of novel antivirals against devastating viral diseases. This project will, for the first time in an animal species, establish state-of-the-art procedures for efficient characterization of the molecular and functional spectrums of unconventional IFNs, which will further IFN-based novel antiviral design.

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Genetic variation for antibody response to a range of pathogens in commercial replacement gilts

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Replacement gilts sourced from multiplier herds are usually introduced into commercial herds following acclimation and vaccination procedures that aim to expose these naïve animals to pathogens (or antigens), such as the strains of PRRSV, PCV2, and other typical swine diseases that are present in the herd. The objective of this study was to estimate genetic parameters for antibody response to several pathogens measured at different stages of production in commercial replacement gilts.

The data set used included phenotypes and genotypes (40K SNPs) on 2479 F1 replacement gilts that were sourced from 17 high-health multipliers from 7 genetic sources. Gilts, in groups of 10 to 63 in size, were introduced into 22 commercial farms with historical cases of natural disease challenges. Blood samples were collected at arrival (D0) on the farms, at 40.1±14 days after arrival (post-acclimation; PA), and at parities 1 (P1) and 2 (P2). Serum was extracted and used for quantification of antibodies to PCV2, swine influenza virus (SIV), *Mycoplasma hyopneumoniae* (MH), and 8 serotypes of *Actinobacillus pleuropneumoniae* (APP; 1, 2, 3, 5, 7, 10, 12, and 13) using commercially available tests. For each serological test, the data set was split into 5 subsets based on the proportion of seroconverted animals within each group: 0, 25, 50, 75, and 100%. Heritabilities were estimated for each trait, time point, and proportion of seroconverted animals within each group. The model used for estimation of heritabilities included the fixed effect of group and a genomic relationship matrix of 3535 individuals. All analyses were performed in ASReml4.

Heritability estimates ranged from 0.03 (PA, 0%) to 0.32 (D0, 75%) for SIV, and from 0.07 (D0, 0%) to 0.35 (P2, 75%) for MH. For APP, the only scenario analyzed was for 0%, as few animals were positive for a given serotype. Heritability estimates ranged from 0.1 (PA) to 0.24 (P2) for APP1, 0.06 (P1) to 0.13 (D0) for APP2, 0.18 (P2) to 0.31 (D0) for APP3, 0.07 (P1) to 0.31 (PA) for APP5, 0.11 (P2) to 0.22 (PA) for APP7, 0.19 (P2) to 0.25 (PA) for APP10, 0.05 (P1) to 0.18 (D0) for APP12, and 0.15 (P1) to 0.29 (P2) for APP13. Heritability estimates for PCV2 were close to zero.

These results indicate that there is substantial genetic variation in response to a range of pathogens in commercial replacement gilts following standard acclimation procedures. The only that was not heritable in this study was antibody response to PCV2. Overall, heritability estimates for all other traits increased with the proportion of seroconverted animals but estimates varied by stage of production and serology test. Thus, selection for changing the immune responsiveness in replacement gilts is possible. Financial support from Genome Canada, the Canadian Swine Health Board, and PigGen Canada is appreciated.

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Modulation of NF-kB activity for innate immune evasion by nonstructural protein 1 of Porcine Epidemic Diarrhea Virus

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Porcine epidemic diarrhea virus (PEDV) is an emerged virus in the US and has become endemic posing significant economic concerns. We previously showed that PEDV possessed an ability to suppress type I IFN production. Of the identified ten viral IFN antagonists, nonstructural protein 1 (nsp1) was one of the most potent viral proteins. Nsp1 inhibited IRF3 signaling pathway for IFN suppression by degradation of CREB-binding protein in a proteasome-dependent manner in the nucleus. In the present study, we found that PEDV efficiently replicated in a porcine epithelial cell line and confirmed the suppression of type I IFN production in these cells. PEDV blocked p65 nuclear localization in virus-infected cells and did not activate the NF-κB pathway at early time post-infection. PEDV was further found to significantly suppress the PRDII promoter activity, which suggests that PEDV inhibits NF-kB activity and suppress type I IFN production. PEDV also suppress the expression of NF-kB-mediated pro-inflammatory cytokines at early time post-infection, but induced at later time post-infection. Of the ten IFN antagonists, nsp1, nsp3, nsp14, nsp15, ORF3, E, and N protein were found to inhibit NF-kB-mediated IFN production. Nsp1 inhibited NF-kB activity and potently suppressed the production of pro-inflammatory cytokines. Nsp1 was further found to block the p65 nuclear localization and interfered the phosphorylation and degradation of IKB-alpha. A series of nsp1 mutants were made according to the high-order structure prediction to identify motifs important for suppression of NF-kB activity. Interestingly, mutations of the conserved residues altered their cellular distributions and subverted their NF-κB suppressive activity, which suggests that conserved high-order structures are crucial for nsp1-mediated NF-kB activity. Our study shows that PEDV modulates NF-κB activity in a time-dependent manner and nsp1 is the NF-kB antagonist for suppression of both IFN and early production of pro-inflammatory cytokines.

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PRRSV interference with cytokine-mediated JAK/STAT signaling

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PRRSV infection is characterized by prolonged viremia and elicitation of inadequate protective immune responses featured by delayed onset and low level of neutralizing antibodies and weak cell-mediated immunity. One of the possible reasons for the weak protective immune response is that PRRSV interferes with cytokine signaling and innate immunity. Many cytokines initiate function by binding to specific receptors on cells to activate Janus kinases (JAK)-signal transducers and activators of transcription (STAT) signal pathway. STATs are a family of transcription factors that regulate cell growth, differentiation, proliferation, apoptosis, immunity, inflammatory responses, and angiogenesis. There are seven mammalian STAT proteins (STAT1, 2, 3, 4, 5a, 5b, and 6). Each STAT member responds to a defined set of cytokines. It is known that lymphocyte development and differentiation rely on cytokines, many of which signal via JAK/STAT pathway to exert their biological effects. Due to the importance of JAK/STAT signaling in the immune response, it is often antagonized by viruses, including PRRSV. The objective of this research was to define the mechanisms of PRRSV interference with JAK/STAK signaling. We discovered that PRRSV inhibits interferon-activated JAK/STAT signaling by blocking nuclear translocation of STAT1/STAT2/IRF9 heterotrimer, and IL-6/IL-10-activated JAK/STAT3 signaling by inducing degradation of STAT3 protein. PRRSV nsp1beta is responsible for the inhibition of JAK/STAT1/STAT2 signaling by downregulating importin alpha5, which is known to mediate nuclear import of the STAT1/STAT2/IRF9 heterotrimer. Interestingly, substitution of the amino acid residue valine 19 of nsp1beta with isoleucine abolished its capability to reduce the importin, whereas nsp1beta of a vaccine MLV strain has no effect on the importin but gains the function after mutation of isoleucine 19 to valine. PRRSV nsp5 is found to reduce STAT3 protein level via ubiquitin-proteosome degradation pathway. The C-terminal portion of nsp5 is required for the inhibition of STAT3 signaling. STAT3 is known to play critical roles in cell growth, proliferation, differentiation, immunity and inflammatory responses. These results indicate that PRRSV may evade the host innate antiviral response and thwart the development of protective adaptive immunity by interfering with cytokine-mediated JAK/STAT signaling.

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The unfolded protein response induced by porcine reproductive and respiratory syndrome virus infection of alveolar macrophages is involved in immune dysregulation

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Porcine reproductive and respiratory syndrome virus (PRRSV), an important swine pathogen, infects alveolar macrophages causing dysregulated interferon (IFN)-alpha and tumor necrosis factor (TNF)-alpha production through a mechanism(s) yet to be resolved. We show that alveolar macrophages infected with PRRSV secrete reduced quantities of IFN-alpha following the cells' subsequent exposure to synthetic dsRNA. This diminution did not correlate with less IFNA1 gene transcription but rather with two events occurring late in infection indicative of translational attenuation, namely the activation of eukaryotic translation initiation factor 2 (eIF2)alpha and the appearance of stress granules. In contrast, the rapid production of TNF-alpha in response to lipopolysaccharide (LPS) was suppressed or enhanced depending on when the stimulation of the PRRSV-infected alveolar macrophages was initiated. If introduction of this agonist was delayed until 6 h post-infection (hpi), to enable eIF2alpha phosphorylation by the stress sensor RNA-like endoplasmic reticulum kinase (PERK), inhibition of TNF-alpha synthesis was observed, presumably due to translational repression. However, a synergistic response, due to earlier NFkB activation apparently via another stress sensor, inositol-requiring enzyme (IRE)-1alpha, was noted if LPS exposure began 4 h earlier at 2 hpi, prior to the onset of eIF2alpha phosphorylation. These results indicate that, depending on when after PRRSV infection an alveolar macrophage encounters LPS, the asynchronous actions of two distinct branches of the unfolded protein response (UPR), IRE-1alpha and PERK, to virus-infection is associated with an increase or decrease TNF-α production via the activation of NFkB or eIF2alpha, respectively. PPRSV pneumonias frequently become complicated with secondary bacterial infections triggering severe inflammation, lung dysfunction and death. The presence of high levels of TNF-alpha in lungs afflicted with PRRSV-bacterial co-infections might be the result of the activation of NFkB in PRRSV-infected alveolar macrophages via the IRE-1alpha. The nonconforming robust TNF-alpha response to bacterial products promoted by PRRSV would mediate severe inflammation and lung damage.

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Evaluation of the novel subunit porcine reproductive and respiratory syndrome (PRRS) vaccine against PRRSV in piglets and sows

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A Pseudomonas exotoxin (PE)-based chimeric subunit vaccine system was developed using a reverse vaccinology (RV) technique. The plasmids chosen for this vaccine contain four PE-PRRS chimeric sequences from the porcine reproductive and respiratory syndrome virus (PRRSV) combined with a ligand moiety and Pseudomonas exotoxin deleted domain III (PE (DIII)), and a carboxyl terminal moiety that includes a polypeptide with amino acid sequence KDEL (K3). PRRSV-negative piglets vaccinated with this construct demonstrated significantly lower ($P < 0.05$) mean rectal temperatures, respiratory scores, lung lesions and presence of PRRSV nucleic acids within interstitial pneumonia, as well as reduced type 1 or type 2 PRRSV viremia compared to unvaccinated challenged pigs. The PE-PRRS combination vaccine induced PRRSV-specific INF-gamma cellular immunity and complement neutralizing antibody in pigs. Further, a field trial of this vaccine to was conducted to evaluate the immune response of pregnant sows following vaccination in a PRRSV positive farm. Results indicate increased sow reproductive performance associated with reduced viremia assessed by RT-PCR analysis. And it also stimulated maternal immune response associated with reduced viremia in the piglets. The data presented supports the claims that the commercialized novel PRRS sub-unit vaccine is an effective tool in the control of the disease based on the presentation of the Pseudomonas exotoxin (PE-K3) carrier in combination with PRRSV conserved epitopes against heterologous PRRS viruses.

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A GP5 mosaic T-cell vaccine for Porcine Reproductive and Respiratory Syndrome Virus is immunogenic and confers partial protection to pigs

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Objectives: Evaluate T-cell epitope mosaic DNA vaccines to protect swine against genetically and antigenically diverse PRRSV strains.

Methods: Two mosaic DNA vaccines that encode mosaic PRRSV GP5 derived from 748 genotype II ORF5 sequences were constructed. The mosaic DNA vaccines were tested in pigs in three pilot vaccination/challenge trials. Gene gun, electroporation and complexed to liposomes were utilized as delivery systems in these trials. T-cell responses were evaluated by lymphocyte proliferation assay using the MTT method and the expression of interferon-gamma and IL-10 mRNA measured in virus-stimulated PBMCs by real-time PCR using the delta-delta method. Antibody responses were monitored in vaccinated animals by indirect-ELISA. Protection was evaluated by measuring viral copy numbers in serum and tissue samples and lung lesion scores.

Results: Mosaic vaccines were shown to be functional and immugenic. Significantly higher levels of proliferative responses were detected in virus-stimulated peripheral blood mononuclear cells of GP5-Mosaic-vaccinated pigs compared to control pigs in both Trials 1&2. In Trial 2, significantly higher levels of interferon-γ mRNA and lower levels of IL-10 mRNA were detected in GP5-Mosaic-vaccinated pigs as compared to control pigs. Virus-specific antibodies were higher in GP5-Mosaic-vaccinated animals than in control animals in Trials 2&3. The antibodies were neutralizing. In Trial 3, there were significant differences between mosaic-vaccinated and control animals in the expression of interferon-gamma mRNA by virus-stimulated PBMCs at 21, 35 and 48 day post vaccination ($p<0.05$). Expression levels of mRNA of other cytokines are being investigated. Significantly higher levels of interferon-gamma mRNA were detected in PBMCs collected from mosaic-vaccinated animals than those in control animals by divergent strains stimulation.

Conclusions: The data shows that vaccination induced both humoral and cellular immune responses in both positive control and mosaic-vaccinated pigs but not in control animals, confirming their immunogenicity. Significantly higher levels of interferon-gamma mRNA were detected in PBMCs collected from mosaic-vaccinated animals compared to those of control animals against diverse PRRSV strain stimulation, which indicated that mosaic vaccines could induced broad immune responses towards diverse strains but not controls.

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Field evaluation of a modified-live PRRS vaccine in an unstable herd in Northwest Mexico

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Introduction: For more than two decades, porcine reproductive and respiratory syndrome virus (PRRS) has caused severe economic losses to the Mexican pork industry. The disease is widespread and serological surveys demonstrated that farms have been infected since 1992. Herd-to-herd biosecurity and PRRS specific control programs vary among swine operations in northwestern Mexico. Efforts to eradicate the disease through regional control and depopulation of herds have yielded mixed results and acute outbreaks are still common. Furthermore, viral dissemination between farms is high, resulting in the emergence of unique strains due to recombination and evolution. The preferred approach for PRRS control in this region has been to maintain a uniform level of immunity through a combination of vaccination and serum inoculation. However, these practices have been unable to uniformly stop PRRS circulation and disease outbreaks still occur.

Objective: To evaluate the efficacy in young pigs of a recently approved PRRS vaccine (Prime Pac® PRRS, MSD Animal Health, Boxmeer, Netherlands) in a highly PRRS challenged, multi-strain affected operation located in northwestern Mexico by comparison with the farm's previous vaccination program. The specific goal for the Prime Pac PRRS vaccination was to improve mortality and productivity parameters of nursery pigs raised in this operation.

Material and Methods: The study was conducted in a nursery site that received the weekly production from a 1,800 sow farm. The study involved 14 weekly groups and a total of 6,923 pigs; 7 groups and 3,415 pigs that were vaccinated at 3 weeks of age with a competitor vaccine (previous program) and 7 subsequent groups and 3,408 pigs that received Prime PAC PRRS at 14 days of age. The pigs were housed in the nursery for 6-7 weeks. Production parameters evaluated in the nursery phase included mortality and cull rates, daily weight gain and feed conversion.

Results: Mortality rate improved following the implementation of Prime Pac PRRS from 18.65% to 3.91%, a difference of 14.74%, and a 79.0% reduction. Daily gain improved by 18.7% (353 to 419 grams/day) while feed conversion improved by 15.8% (1.65 to 1.39). The rate of cull pigs declined from 3.73% to 0.90%, a difference of 2.83% and a 75.9% reduction.

Conclusion: Vaccination is an important tool for controlling PRRS in endemically infected herds. In this operation, Prime Pac® PRRS significantly impacted farm profitability due to the reduced mortality and cull pig rates, increased daily weight gain and improved feed conversion compared with the previous program.

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Comparative serological response after an inactivated EU-typed PRRS vaccination in Korea

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Introduction

Porcine reproductive and respiratory syndrome virus (PRRSV) causes reproductive failure in sows and respiratory disease in young pigs. Prevention of PRRS neonatal infections by passive colostrum and lactogenic immunity transferred from the sow has been shown to be dose dependant. The aim of this study was to compare with and assess the PRRS-specific serologic response after sow vaccination with an inactivated EU-typed PRRS vaccine and its passive transfer to piglets, by serum neutralization (SN) test, enzyme-linked immunosorbent assay (ELISA), and indirect fluorescent antibody (IFA) test in Korean field conditions.

Materials and methods

The study was carried out in an EU-typed PRRSV negative 600-sow farm located in Boryeong city South-Korea. Eight sows randomly chosen were vaccinated (V) with PROGRESSIS® (Merial, Lyon, France) 9 weeks before farrowing and revaccinated 3 weeks later. As a non-vaccinated control group (NV), 8 other sows were injected with saline according to the same schedule. From each of the 16 sows, 5 piglets per sow were selected to be tested. All sows were bled on day D-63, D-42, D0 (farrowing day) and D26, and 5 of their newborn piglets were bled on day D7, D14 and D26 after birth. SN test antibody titers of all sera were analyzed, with PRRSV Lelystad strain, and MARC-145 cells. ELISA antibody titers of all sera were analyzed using an ELISA kit(IDEXX Laboratories. Inc., Westbrook, USA). IFA antibody titers of all sera were analyzed, with Lelystad strain, and MA104 cells. T-test and Mann-Whitney U test of SPSS statistics 21 (IBM Corp., USA) were used for statistical significance($P<0.05$).

Results

The results are as follows: Table 1 and 2.

Table 1. EU-PRRSV-specific antibody titers of the sows (M±SD)

Sows		Day -63	Day -42	Day 0	Day 26
SN	V	0 (±0)	1.13 (±0.81)	2.63 (±0.49)	1.88 (±0.81)
	C	0.25 (±0.46)	0 (±0)	0.25 (±0.46)	0 (±0)
	P value	0.167	0.105	0.001	0.010
ELISA	V	0.12 (±0.08)	0.67 (±0.46)	0.81 (±0.56)	0.75 (±0.52)
	C	0.16 (±0.12)	0.17 (±0.12)	0.17 (±0.12)	0.19 (±0.13)
	P value	0.382	0.009	0.005	0.000
IFA	V	1.81 (±0.14)	2.08 (±0.15)	2.62 (±0.14)	2.34 (±0.16)
	C	1.83 (±0.12)	1.83 (±0.12)	1.85 (±0.12)	1.85 (±0.13)
	P value	0.721	0.130	0.000	0.010

Table 2. EU-PRRSV-specific antibody titers of the piglets (M±SD)

Piglets		Day 7	Day 14	Day 26
SN	V	2.62(±0.26)	1.59(±0.20)	0.32(±0.20)
	C	0.32(±0.24)	0(±0)	0(±0)
	P value	0.000	0.000	0.011
ELISA	V	1.08(±0.21)	1.01(±0.20)	0.60(±0.20)
	C	0.20(±0.11)	0.22(±0.12)	0.19(±0.12)
	P value	0.000	0.000	0.000
IFA	V	2.67(±0.21)	2.23(±0.20)	2.00(±0.20)
	C	1.83(±0.11)	1.83(±0.12)	1.78(±0.12)
	P value	0.000	0.000	0.003

Discussion and conclusion

All three methods' antibody titers of the vaccinated sows significantly increased to Day0 and then slightly decreased. Otherwise, the control sows remained low. Antibody titers of piglets of the vaccinated group were significantly higher than those of the control group at every sampling point and decreased over time as expected. In this study, PROGRESSIS® was shown to induce high level of antibodies in the sows that are well transferred to their piglets, and SN test, ELISA, and IFA were useful to detect EU-PRRSV antibody.

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Serum and mammary secretion antibody responses in PEDV-exposed gilts following PEDV vaccination

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Purpose: Since there is little possibility that PEDV will be eradicated in the near future, reliable methods to prevent and/or control its effects are needed. In the sow herd, this implies monitoring/maintaining levels of immunity sufficient to protect neonatal pigs. The objective of this study was to compare antibody responses in previously PEDV-exposed gilts to vaccination.

Methods: PEDV antibody-positive gilts (n = 36) in a commercial production system were randomly assigned to 1 of 5 vaccination treatments and sampled as described in Table 1.

Trt*	Vaccination treatment	Animals	Sampling
1	Unvaccinated (control)	5 gilts	1. Serum at 5 weeks pre-farrow
2	1 ml IM - 2 weeks pre-farrow	6 gilts	2. Serum and colostrum ≤ 24 hr
3	1 ml IM - 5 and 2 weeks pre-farrow	8 gilts	post farrowing
4	2 ml IM - 2 weeks pre-farrow	7 gilts	3. Milk at 3, 10, and 21 days post
5	2 ml IM - 5 and 2 weeks pre-farrow	7 gilts	farrowing

*Treatment 2, 3 - *Harrisvaccines™ PEDV Vaccine;* 4, 5 - *Zoetis PEDV Vaccine, Killed Virus*

Thirty-three gilts completed the study, i.e., farrowed viable litters and provided a full complement of samples. Serum, colostrum, and milk samples were tested by PEDV whole virus (WV) IgG and IgA ELISAs and for neutralizing antibody by PEDV fluorescent focus neutralization assay (FFN).

Initial analyses found no significant differences in outcomes between 1 vs 2 doses of either Vaccine A or B. Therefore, the data were analyzed on the basis of 3 treatment groups: 1) no vaccine (controls); 2) PEDV vaccine A; and 3) PEDV vaccine B. Thereafter, a nonparametric one-way ANOVA was used to test for differences among treatments for IgG, IgA, and FFN by sample type (serum, colostrum, milk). A mixed-effects repeated measures model was used to analyze the difference between treatment groups for IgG, IgA, and FFN by sample type.

Results: Gilt serum antibody responses at 5 weeks pre-farrow, i.e., pre-vaccination, were not different ($p > 0.05$). Controls (no vaccine) had significantly lower antibody responses than vaccinates for most tests and specimens. IgG responses in serum and colostrum from gilts vaccinated with B were higher than controls and gilts vaccinated with A ($p < 0.01$). IgA and neutralizing antibody responses were not different between gilts vaccinated with Vaccine A and B.

Conclusions: Compared to unvaccinated controls, vaccination increased IgG, IgA, and neutralizing antibody levels in gilts in all diagnostic specimens tested.

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Interaction between ORF2 protein of porcine circovirus type 2 and C1QBP enhances phagocytic activity

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Porcine circovirus type 2 (PCV2) is non-enveloped, icosahedral, small DNA virus with a single-stranded circular DNA genome. PCV2 infection often impairs host immunity, with the subsequent development of multifactorial postweaning multisystemic wasting syndrome (PMWS) due to secondary infections. Among four major open reading frames (ORFs) of PCV2, ORF1, which is also termed the "rep" gene, encodes viral replicase and ORF2 (the "cap" gene) encodes capsid protein. ORF3 and ORF4 encode non-structural genes that may modulate the phenotype of host cells. In this study, we cloned pig C1QBP cDNA and determined its complete cDNA sequence. Then, we showed that the direct interaction between the C1QBP and PCV2 ORF2 led to increasing stability of C1QBP by inhibiting ubiquitin-mediated proteasomal degradation of C1QBP. Increased stability of the C1QBP by the interaction with PCV2 ORF2 further enhanced phagocytic activity of porcine macrophages through the phosphoinositol-3-kinase (PI3K) signaling pathway. This evidence may explain the molecular basis of how PCV2 ORF2 enhances phagocytic activity of host macrophages.

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Development of porcine epidemic diarrhea virus vaccines derived from a virulent Korean strain

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Massive outbreaks of PEDV re-emerged in South Korea in 2013–2014 and rapidly swept across the country, causing tremendous financial losses to producers and customers. Despite the availability of PEDV vaccines in the domestic market, their protective efficacy in the field is still being debated. The unsatisfied effectiveness of current vaccines appears to result from antigenic and genetic differences between vaccine and field epidemic strains, raising the need for new vaccine development using the PEDV isolate prevalent in the field. We first aimed to produce an inactivated killed vaccine using a cell culture-propagated KNU-141112 epidemic strain and evaluate its effectiveness in nursery piglets. Pregnant sows were immunized intramuscularly with the inactivated adjuvanted monovalent vaccine at 6 and 3 weeks prior to farrowing. Six-day-old piglets born to vaccinated or unvaccinated sows were challenged with the homogeneous virus. The administration of the inactivated vaccine to sows greatly increased the survival rate of piglets challenged with the virulent strain, from 0% to approximately 92% (22/24), and significantly reduced diarrhea severity including viral shedding in feces. In addition, litters from unvaccinated sows continued to lose body weight throughout the experiment, whereas litters from vaccinated sows started recovering their daily weight gain at 7 days after the challenge. Furthermore, strong neutralizing antibody responses to PEDV were verified in immunized sows and their offspring, but were absent in the unvaccinated controls. Altogether, our data demonstrated that durable lactogenic immunity was present in dams administrated with the inactivated vaccine and subsequently conferred critical passive immune protection to their own litters against virulent PEDV infection. In addition, a virulent Korean PEDV strain was serially propagated in Vero cells for up to 100 passages for attenuation to develop a modified live virus vaccine. During cell adaptation process, we were able to isolate 4 deletion (DEL) mutants with 8 to 10 amino acid changes distributed throughout the genome. Results of animal inoculation studies to assess the virulence of the cell-adapted PEDV DEL strains will be discussed.

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Pathogenic and genomic characteristics involved in porcine alveolar macrophage passages of an attenuated PRRSV nsp2 DEL strain CA-2-P100

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PRRSV is a globally ubiquitous swine viral pathogen and a major economic plague worldwide. We previously reported the attenuated phenotype in inoculated pigs and amino acid mutations of a cell-adapted CA-2-P100 (100th passage of the virulent type 2 Korean PRRSV nsp2 DEL strain CA-2 in MARC-145 cells) However, some of pigs challenged with CA-2-P100 remained viremia-negative and seronegative to PRRSV throughout the trial, suggesting that the virus might be over-attenuated. In the present study, a high-passage derivative of CA-2, CA-2-P100, was serially propagated in cultured porcine alveolar macrophage (PAM) cells for up to 20 passages (CA-2-P100+PAM20). Animal inoculation studies were conducted to assess and compare *in vivo* effects of CA-2-P100 and CA-2-P100+PAM20 strains in the natural host. There were no noteworthy differences in virulence between two cell-adapted viruses, with exhibiting normal weight gain, body temperatures, and lung lesions comparable to the control group. No pigs in the virus-infected groups shed virus nasally, orally or rectally throughout the experiment. However, CA-2-P100+PAM20 infection resulted in consistently higher levels of viremia in pigs compared to CA-2-P100 infection. Furthermore, all pigs inoculated with CA-2-P100+PAM20 developed viremia and seroconverted to PRRSV. In addition, we determined the whole genome sequences of PAM-passage derivatives of CA-2-P100. The nsp2 111-1-19 DEL signature was completely retained for 20 passages in PAM cells, whereas no other deletions or insertions arose during the additional PAM adaptation process. However, CA-2-P100+PAM20 contained 36 random nucleotide mutations that resulted in 14 amino acid changes throughout the genome, suggesting that these genetic drifts provide a possible molecular basis correlated with the PAM-adapted phenotype *in vivo*. Altogether, our data indicate that the PAM-passage CA-2-P100+PAM20 strain is a promising candidate for developing a safe and effective live PRRSV vaccine.

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An interferon inducing PRRSV vaccine candidate protects against challenge with a heterologous virulent type 2 strain in a conventional pig model

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Recently, an interferon inducing PRRSV vaccine candidate strain A2MC2 was demonstrated to be attenuated and induce neutralizing antibodies. The objective of this study was to determine the efficacy of passage 90 of A2MC2 (A2P90) to protect pigs against challenge with moderately virulent PRRSV strain VR-2385 (92.3% nucleic acid identity with A2MC2) and highly virulent atypical PRRSV MN184 (84.5% nucleic acid identity with A2MC2). Forty 3-week old pigs were randomly assigned to five groups including a NEG-CONTROL group (non-vaccinated, non-challenged), VAC-VR2385 (vaccinated, challenged with strain VR-2385), VR2385 (challenged with strain VR-2385), VAC-MN184 (vaccinated, challenged with strain MN184) and MN184 group (challenged with MN184 virus). Vaccination was done at 3 weeks of age followed by challenge at 8 weeks of age. No viremia was detectable in any of the vaccinated pigs, however, by the time of challenge, 15/16 vaccinated pigs had seroconverted based on ELISA and had neutralizing antibodies against a homologous strain with titers ranging from 8 to 128. Infection with VR-2385 resulted in mild-to-moderate clinical disease and lesions. Vaccination reduced VR-2385 viremia and nasal shedding, which was significantly lower than VR2385 group. Vaccination also reduced macroscopic and microscopic lung lesions associated with PRRSV VR-2385. Infection with MN184 resulted in moderate-to-severe clinical disease and lesions with significantly higher levels of viremia and virus shedding and reduced weight gain compared to NEG-CONTROLS and VAC-VR2385 pigs. Vaccination had little protective effect against MN184 challenge. Under the study conditions, the A2P90 vaccine strain was attenuated without detectable shedding and provided protection against VR-2385 challenge.

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A PRRSV candidate vaccine based on the synthetic attenuated virus engineering approach is attenuated and effective in protecting against homologous virus challenge

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Rapid production of attenuated farm-specific homologous vaccines is a feasible alternative to commercial vaccines. In this study, attenuation and efficacy of a codon-pair de-optimized candidate vaccine generated by synthetic attenuated virus engineering approach (SAVE5) were tested in a conventional growing pig model. Forty pigs were vaccinated intranasally or intramuscularly with SAVE5 at day 0 (D0). The remaining 28 pigs were sham-vaccinated with saline. At D42, 30 vaccinated and 19 sham-vaccinated pigs were challenged with the homologous PRRSV strain VR2385. The experiment was terminated at D54. The SAVE5 virus was effectively attenuated as evidenced by a low magnitude of SAVE5 viremia for 1-5 consecutive weeks in 35.9% (14/39) of the vaccinated pigs, lack of detectable nasal SAVE5 shedding and failure to transmit the vaccine virus from pig to pig. By D42, all vaccinated pigs with detectable SAVE5 viremia also had detectable anti-PRRSV IgG. Anti-IgG positive vaccinated pigs were protected from subsequent VR2385 challenge as evidenced by lack of VR2385 viremia and nasal shedding, significantly reduced macroscopic and microscopic lung lesions and significantly reduced amount of PRRSV antigen in lungs compared to the non-vaccinated VR2385-challenged positive control pigs. The nasal vaccination route appeared to be more effective in inducing protective immunity in a larger number of pigs compared to the intramuscular route. Vaccinated pigs without detectable SAVE5 viremia did not seroconvert and were fully susceptible to VR2385 challenge. The SAVE approach was successful in attenuating PRRSV strain VR2385 and protected against homologous virus challenge. Virus dosage likely needs to be adjusted to induce replication and protection in a higher percentage of vaccinated pigs.

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Efficacy of Ingelvac PRRS® MLV against a heterologous PRRSV 1-7-4 RFLP challenge

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The use of Ingelvac PRRS® vaccines can significantly reduce lung lesions following challenge with heterologous isolates (86-94% ORF5 nucleotide similarity) in the three-week-old pig respiratory challenge model. However, the efficacy of Ingelvac PRRS® MLV vaccine against current virulent PRRSV isolates, such as RFLP 1-7-4, has not been reported to date. This experiment was designed to evaluate the efficacy of two commercially available PRRSV vaccines in a three-week-old pig respiratory challenge model, using a heterologous RFLP 1-7-4 field isolate from 2014.

Materials and Methods: At approximately three weeks of age (Day 0 of the study), 154 PRRSV naïve piglets pigs were randomized into groups, and intramuscularly vaccinated with 2 ml of either a placebo (challenge controls n=64), Ingelvac PRRS® MLV (n=45) or Fostera® PRRS (n=45). Pigs were housed in rooms by group during the vaccination period. At day 28 of the study (D28), all pigs were comingled and challenged with 2.0 mL intramuscularly and 2.0 mL intranasally (1 mL per nostril) with $10^{4.6}$ $TCID_{50}$/mL of PRRSV RFLP 1-7-4. Serum samples, weights, and temperatures were collected periodically from D0 through termination of the study on D42. On D42 (14 days post-challenge), all pigs were necropsied and lungs were scored for the presence of macroscopic lesions and BALF samples were collected. Serum samples were tested by RT-PCR for the presence of viremia and by ELISA for the presence of anti-PRRSV antibody. A subset of samples were assayed by bead-based multiplex assay for multiple cytokines including IFN-alpha. Data were analyzed using Generalized and Linear Mixed Models. Pairwise comparisons between groups were conducted as appropriate using a level of confidence of 0.05 to indicate statistical significance.

Results: Table 1 summarizes lung lesions (percentage) for each group. Table 2 summaries average daily weight gain (ADWG) for the post-challenge period by group. The percentage of vaccinated animals with detectable amounts of INF-alpha at D29 and D35 was significantly lower than the controls ($p \leq 0.05$). Additional data analysis is in progress at the time of abstract preparation.

Table 1. Day 42 Percent Lung Lesions (Median)

Group	Treatment	Lung Lesions (%)
1	Ingelvac PRRS® MLV	8.4[a]
2	Fostera® PRRS	12.9[a]
3	Placebo	25.4[b]

[a] significantly different from the placebo at $P \leq 0.05$

Table 2. Post-challenge ADWG

Group	Treatment	ADWG (lbs)
1	Ingelvac PRRS® MLV	0.61[a]
2	Fostera® PRRS	0.49[a]
3	Placebo	0.24[b]

[a] significantly different from the placebo at $P \leq 0.05$

Conclusion: The pigs vaccinated with Ingelvac PRRS® MLV had significantly reduced lung lesions, and increased ADWG, in comparison to placebo vaccinated pigs, following challenge with a recent PRRSV RFLP 1-7-4 isolate. In addition, vaccination with Ingelvac PRRS® MLV resulted in a significantly lower percentage of animals with an IFN-alpha response as compared to placebos at D29 and D35.

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Evaluation of PRRSV challenge dose in vaccinated pigs

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The infectious dose of PRRSV has been shown to be very low, therefore highly infectious. The objective of this study was to evaluate the effect of PRRSV challenge dose in vaccinated pigs.

Materials and Methods: The study was performed in ninety, three-week-old pigs from a PRRS naïve and PCR negative source. Groups 1-5 (n=10) were vaccinated (Day 0) with Ingelvac PRRS® MLV (2ml IM). Forty pigs served as matched non-vaccinated challenge controls (NVC-Groups 1-4; n=10 per group). Groups 1-4 were challenged on Day 28 intranasally with 2.0 ml of virulent PRRSV SDSU-73 at 4log, 3log, 2log or 1log$_{10}$TCID$_{50}$/ml, respectively. Group 5 was not challenged. Temperature (Day 28-42), viremia and ADWG (Day 28-70) were evaluated and statistically analyzed.

Results: At all challenge doses, Ingelvac PRRS® MLV vaccinated pigs demonstrated a significant decrease in days pyrexic compared to NVC groups ($P<0.05$). At PRRSV challenge doses of ≤2logs, the average temperatures and days pyrexic of the vaccinated challenged pigs were similar to the non-challenge control (Table 1).

Table 1. Mean Number Days Pyrexic Post-Challenge

Group	4log	3log	2log	1log	Non-Challenge
Ingelvac PRRS® MLV	4.4[1]	4.2[1]	1.0[1]	1.4[1]	1.8
NVC	11.2	8.8	10.0	6.0	-

1 Statistically significant difference ($P < 0.05$) in number days pyrexic between Ingelvac PRRS® MLV and Challenge Control groups based on model prediction.

As compared to the NVC, there was a significant increase in ADWG ($P<0.05$) in the 3, 2 and 1log groups, and at $P<0.07$ in the 4log group. ADWG in vaccinated groups challenged with ≤2logs of PRRSV were numerically similar to the ADWG of control. There was a measurable negative impact on ADWG in the NVC groups with no difference across all challenge doses (Table 2).

Table 2. Average Daily Weight Gain (lbs)

Group	4log	3log	2log	1log	Non-Challenge
Ingelvac PRRS® MLV	1.41	1.29[1]	1.70[1]	1.64[1]	1.67
NVC	1.18	1.06	1.15	1.23	-

1 Statistically significant difference ($P < 0.05$) in ADWG between Ingelvac PRRS® MLV and Challenge Control groups based on model prediction.

Vaccinated pigs demonstrated fewer percent PCR positive pigs than NVC pigs at all challenge doses. As challenge dose decreased the percentage of viremic pigs in vaccinated groups decreased, with viremia in vaccinated pigs challenged with ≤2logs similar to the non-challenge control. At all challenge doses, the NVC pigs show similar post-challenge viremia profile.

Discussion: In this study, at all challenge doses, Ingelvac PRRS® MLV vaccinated pigs demonstrated a reduction in post-challenge viremia, temperature and increased ADWG as compared to NVC pigs. Based on challenge dose (≤2logs), the consequences in vaccinated pigs were similar to non-challenged pigs. The post-challenge viremia and ADWG of NVC pigs were similar across all challenge doses, indicating a measurable negative impact. Implementation of vaccine for PRRS control can mitigate the consequences of PRRSV infection subsequently improving health and performance.

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How to pick the right strain of PRRSv for a vaccine... Or for an outbreak at a concentrated animal feeding operation (CAFO)

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We have developed an immunoinformatics tool to identify the best PRRSv vaccine to use for herd-specific PRRSv outbreaks. Like many RNA viruses, PRRSv has considerable genetic and antigenic variability that has resulted in the vaccine and the outbreak strain being not well matched. The widely used 'whole gene' approach fails to gauge cross-reactivity. This is because it does not consider the T cell epitopes that are presented to the immune system, and whether they are conserved between the vaccine and the challenge strain. We developed an Epitope Content Comparison (EpiCC) tool to solve this issue and better define the degree of conservation between PRRSv vaccines and circulating strains. This tool will be used to identify the best vaccine to use for herd-specific PRRSv outbreaks.

We have previously developed a set of Swine Leukocyte Antigen (SLA)-restricted epitope prediction tools (PigMatrix). We further modified this tool to define relatedness based on T cell epitope content. Using this new tool (EpiCC) we screened 20 complete genomes from PRRSv and three modified live virus (MLV) vaccines. We identified epitopes predicted to bind to common class I and class II SLA alleles. These epitopes were compared and an epitope-based relatedness score (EpiCC score) was calculated. We observed epitope content variability across proteins and these EpiCC scores can be used to classify PRRSv strains based on their T cell epitope content.

EpiCC gives pork producers and vaccine researches an objective approach to aid in vaccine selection when a PRRSv strain is introduced into a herd, and to select the appropriate viral epitopes for incorporation into a MLV vaccine.

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Pigs immunized with a novel E2 subunit vaccine are protected from subgenotype heterologous Classical Swine Fever Virus challenge

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Background: Classical swine fever (CSF) or hog cholera is a highly contagious swine viral disease. CSF endemic countries have to use routine vaccination with modified live virus (MLV) vaccines to prevent and control CSF. However, it is impossible to serologically differentiate MLV vaccinated pigs from those infected with CSF virus (CSFV). The aim of this study is to develop a one-dose E2-subunit vaccine that can provide protection against CSFV challenge. We hypothesize that a vaccine consisting of a suitable adjuvant and recombinant E2 with natural conformation may induce a similar level of protection as the MLV vaccine.

Methods: Our experimental vaccine KNB-E2 was formulated with the recombinant E2 protein (Genotype 1.1) expressed by insect cells and an oil-in-water emulsion based adjuvant. 10 pigs (3 weeks old pigs/group) were immunized intramuscularly with one dose or two doses (3 weeks apart) KNB-E2, and 10 more control pigs were administered normal saline solution only. Two weeks after the second vaccination, all KNB-E2 vaccinated pigs and 5 control pigs were challenged with 5x105 TCID50 CSFV Honduras/1997 (Genotype 1.3, 1 ml intramuscular, 1 ml intranasal).

Results: It was found that while control pigs infected with CSFV stopped growing and developed high fever (>40^{o}C), high level CSFV load in blood and nasal fluid, and severe leukopenia 3 – 14 days post challenge, all KNB-E2 vaccinated pigs continued to grow as control pigs without CSFV exposure, did not show any fever, had low or undetectable level of CSFV in blood and nasal fluid. At the time of CSFV challenge, only pigs immunized with KNB-E2 developed high levels of E2-specific antibodies and anti-CSFV neutralizing antibodies.

Conclusions: Our studies provide direct evidence that pigs immunized with one dose KNB-E2 can be protected clinically from CSFV challenge. This protection is likely mediated by high levels of E2-specific and anti-CSFV neutralizing antibodies.

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Maternally derived antibody mediated protection against porcine epidemic diarrhea virus on piglets via the different ways of immunity provides in sows following by the classical and variant strain challenges

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The study was conducted to investigate the efficacy of the maternally derived antibody (MDA) raised against two different routes of PEDV immunization in the induction of lactogenic immunity as measured by ELISA IgG/IgA and VN titers of colostrum at 0 day-post-parturition (DPP) and milk at 3 DPP. In addition, protection in piglets against oral challenge was measured using severity of clinical disease, shedding periods with RT-PCR, and, villous height to crypt ratio (VCR) at 4 day-post-challenge (DPC). Thirty primiparous sows free of PEDV were randomly allocated into three groups of 10 sows each. Three groups included Negative (Neg), Feedback (FB) using piglet intestines feedback, and intramuscular vaccinated (IV). Neg was left as control. FB was orally administrated with feedback at 11 and 13 weeks of gestation (WG). IV was intramuscularly vaccinated with attenuated PEDV vaccine at 11 and 13 WG. Colostrum and milk samples were collected at 0 and 3 DPP and assayed for antibody response by viral neutralization assay (VN) and ELISA IgG/IgA. In each group, 2 piglets per sow were weaned at 3 days of age and orally challenged with either genogroup 1a (G1; n = 10) or genogroup 2a (G2; n = 10) isolates of PEDV. Mortality was recorded and all pigs were necropsied at 4 DPC. VCR was determined. The MDA results demonstrated that the IV group had significantly higher VN titers than FB and Neg in both colostrum and milk samples (Table 1). In contrast, FB had significantly higher level of IgA compared to other two groups. Neg had no detectable antibody response in colostrum and milk samples throughout the study. All piglets in Neg died at 4 DPC following challenge. All piglets in IV group displayed severe clinical disease leading to necropsied at 4 DPC. In contrast, following G1 and G2 challenge, mortality in FB was 80 and 30%, respectively. Piglets in FB group had significantly lower VCR in G2 challenge that that of G1 challenge. These results indicate that the G2 variants, compared to the G1 variants, were more virulence to those negative pigs. Intramuscular vaccinated with the G1 was only partial protection against G1 challenge, but not the G2 challenge. In contrast, the feedback of G2 variants are more suitable to protect against both variants.

Experimental groups		Villous height/ crypt depth ratio (VCR)			VN		ELISA IgG		ELISA IgA	
		Duodenum	Jejunum	Ileum	0 DPP	3 DPP	0 DPP	3 DPP	0 DPP	3 DPP
Neg	G1	1.59^{a} (0.17)	1.19^{a} (0.08)	1.24^{a} (0.12)	0^{c} (0)	0^{c} (0)	0.02^{c} (0.01)	0^{c} (0)	0.01^{c} (0)	0.01^{c} (0.01)
	G2	0.79^{b} (0.08)	1.02^{a} (0.07)	0.99^{b} (0.10)						
FB	G1	0.76^{b} (0.03)	0.58^{b} (0.08)	0.87^{b} (0.03)	1.8^{b} (0.39)	1.8^{b} (0.33)	0.87^{b} (0.19)	0.60^{b} (0.18)	1.16^{a} (0.08)	0.88^{a} (0.11)
	G2	1.16^{a} (0.04)	1.15^{a} (0.07)	1.13^{a} (0.07)						
IV	G1	1.49^{a} (0.06)	0.97^{b} (0.05)	1.13^{a} (0.08)	6^{a} (0.21)	5.4^{a} (0.27)	1.62^{a} (0.08)	0.62^{b} (0.10)	0.56^{b} (0.04)	0.39^{b} (0.05)
	G2	1.55^{a} (0.08)	1.41^{a} (0.07)	1.18^{a} (0.08)						

Table 1 VCR, VN, IgG and IgA values of each experimental groups (Neg, FB and IV) and treatments (G1 and G2) in this study.

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Intranasal immunization of pigs with porcine reproductive and respiratory syndrome virus-like particles plus 2'3'-cGAMP VacciGrade™ adjuvant exacerbates viremia after virus challenge

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Porcine reproductive and respiratory syndrome virus (PRRSV) causes reproductive failure in pregnant sows and acute respiratory disease in young pigs. It is a leading infectious agent of swine respiratory complex, which has significant negative economic impact on the swine industry. Commercial markets currently offer both live attenuated and killed vaccines; however, increasing controversy exists about their efficacy providing complete protection. Therefore, there is a pressing need for a safe and effective vaccine to control and prevent this devastating disease.

We generated VLPs by expressing the glycoprotein 5 (Gp5), envelope protein (E), membrane protein (M) and nucleocapsid protein of PRRSV using the flashBAC™ baculovirus expression system. After two intranasal immunizations of pigs with phosphate-buffered saline (PBS), VLPs, or VLPs with 2'3'-cGAMP VacciGrade™ adjuvant, immunogenicity and protection efficacy were evaluated after virus challenge at two weeks after boost immunization. No PRRSV N specific antibody or Gp5 epitope specific antibody was detected in all animals prior to challenge. N protein specific antibody was detected in all animals at day 10 after challenge, but no significant difference was observed between the vaccinated and control groups. However, a significant increase in serum IgG and IgA specific to VLPs was observed at day 7 after challenge only in the VLPs plus the 2'3'-cGAMP VacciGrade™ group, suggesting that the adjuvant may boost the recall immune response against VLPs. It seemed to correlate with a higher interferon-alpha in the serum in the VLPs plus the adjuvant group. Surprisingly, a significantly higher viremia was observed in the VLPs and VLPs plus the adjuvant groups compared to the control group. A transient slight increase in the interferon-gamma and IL-10 in the serum was observed in all groups at day 3 after challenge, but no significant difference between the groups was observed. The average rectal temperature was significantly higher at day 10 after virus challenge in the control group than the VLPs plus adjuvant group. Similarly, a slightly milder lung histological lesion was observed in the VLPs plus adjuvant group compared to the VLPs group. Overall, the intranasal immunization of PRRSV VLPs plus adjuvant exacerbates viremia. A stronger interferon-alpha and a milder histological lesion were observed in the VLPs plus 2',3'cGAMP adjuvant group. Future studies should be focused on incorporating other viral proteins of PRRSV into VLPs and improving VLPs assembly efficiency. Additionally, different dose of VLPs, different adjuvant and route of vaccination such as intramuscular injection should be explored further to fully assess the feasibility of such a vaccine platform for PRRSV control and prevention.

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A sow farm PRRS elimination with serum therapy and herd closure

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Introduction Serum inoculation (therapy) with herd closure is a good method for control or eliminating PRRS in sow farm. The F8 farm had 1200 sows in 2014. The status of PRRS became unstable in 2013 winter. According with clinical signs, we decided inoculate serum to sows and gilts, and then closed the herd.

Materials and methods The PRRSV positive serum from F8 farm, was detected no classical swine fever and pseudorabies virus. We introduced 6 months gilt before serum acclimation. The herd was inoculated (10μl serum/head) by intramuscular injection on Jan. 18 and 20, respectively. Then we closed the herd and monitor the serum by ELISA.

Results There was little effect on the breeding performance during the acclimation period. Sow abortion began at Jan.19 and ceased at Jan.23, there was only 10 sow abortion together. The PRRS antibody positive rate of boar, sow herd, nursey and finish gradually decreased when the time passed. The S/P ratio of PRRS antibody levels also gradually decreased ,the rate of PRRS Ab negative pigs risen, the boar, sow, nursery and finish became PRRS Ab negative (Table 1).

Table 1 the detection of PRRS S/P value

item	year	boar	sow	gilt	piglet	nursey	finish
samples	2014	266	471	75	52	264	530
	2015	247	408	221	725	441	221
	2016(6)	75	231	283	538	391	1002
s/p>0.4 positive	2014	60%	52%	45%	19%	14%	13%
	2015	2%	24%	1%	5%	0%	0%
	2016(6)	3%	13%	1%	1%	0%	0%
s/p average value	2014	0.71	0.62	0.48	0.30	0.19	0.23
	2015	0.06	0.27	0.04	0.10	0.04	0.01
	2016(6)	0.05	0.16	0.05	0.06	0.04	0.02

Discussion Serum therapy and herd closure are useful tool for control and eliminating PRRS. In order to improve the success, we should introduce more than 6 months gilt and acclimate the gilts at the same time. The serum must be free of PRV and CSFV, or it will cause greater loss. Serum therapy and herd closure is not always successful, there are many unpredictable factors. Sometime it is a dilemma when we decide whether utilize serum inoculation for the herd or not. However, as long as really know the health status of the farm and planned well, strengthen farm biosecurity at the same time, the opportunity of PRRS elimination will become much higher, just like this case.

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Abortions when applied serum therapy in PRRS unstable sow farms

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Introduction Serum inoculation (therapy) is a good method to control and maintain the PRRSV stable. We usually use it for gilt acclimation. But sometimes the sow farm becomes PRRS unstable, such as much higher abortion rate than normal in gestation sows, and surveillance the PRRSV from weak piglets in farrowing room and/or abortion sows. If we continuously monitor the virus shed from weak piglet and off-feed sows for 3 weeks, and get the sequence of PRRSV. We should adopt some strategies for controlling the PRRS.

Materials and methods The PRRSV positive serum from every own farm, was detected no classical swine fever and pseudorabies virus. The herd was inoculated 1 or 2 times (1-10μl serum/head/time) by intramuscular injection. We applied serum therapy in PRRS positive unstable sow farm 11 times from 2007 to 2106. The sow scale of 8 farms are ranging from 400 to 2200.

Results We collect the abortion data form 2007 to 2016. The data include when we applied the serum injection, how many times injection we applied, when the abortion took place, which day was the peak day and when the abortion was ceased. We also calculated the number of days corresponding to the abortion events (see table1). Analyzed the 11 time abortions, we can see the abortion will begin from 0 to 4 days after injecting the serum, the average days is 1; the peak abortion range from 4 to 9 days, the average days is 6.2; the ends abortion from 6 to 13 days, the average days is 10.4.

Table 1 serum inoculation and the duration period of sow abortion

Farm code	Date of happening					days		
	SI*1 date	SI*2 date	AT# start	AT# peak	AT# end	start	peak	duration
F1	7/14/2007	7/16/2007	7/16/2007	7/20/2007	7/27/2007	2	6	13
F1	6/30/2013	7/2/2013	6/30/2013	7/6/2013	7/12/2013	0	6	12
F5	2/26/2011	2/28/2011	2/26/2011	3/4/2011	3/11/2011	0	6	13
F4	8/7/2007	\	8/7/2007	8/14/2007	8/18/2007	0	7	11
F4	3/8/2011	3/10/2011	3/12/2011	3/17/2011	3/21/2011	4	9	13
F3	9/12/2007	\	9/12/2007	9/17/2007	9/23/2007	0	5	11
F2	9/14/2007	\	9/15/2007	9/20/2007	9/23/2007	1	6	9
F8	1/18/2014	1/20/2014	1/19/2014	1/22/2014	1/24/2014	1	4	6
F6	4/9/2014	4/11/2014	4/12/2014	4/15/2014	4/17/2014	3	6	8
F6	3/26/2016	3/30/2016	3/26/2016	4/1/2016	4/2/2016	0	6	7
F7	3/30/2016	4/2/2016	3/30/2016	4/6/2016	4/10/2016	0	7	11
#AT=abortion *SI=serum inoculation					average	1.0	6.2	10.4

Discussion Serum therapy is a good method for controlling PRRS .The duration period of abortion induced by serum therapy is nearly 10.4 days. Compared to some reports, it is much shorter than using MLV. Whether we use serum therapy for sow herd or not, it is a dilemma. Sometime the abortion is as higher as 20%, but sometime as lower as 0.2%.

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Micro-emulsion adjuvants for swine viral vaccines: Application to a recombinant CSF vaccine

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Classical swine fever (CSF) is a highly virulent disease in pigs caused by a Pestivirus, which causes high mortality and can therefore have dramatic impacts on the productivity of pig industry. Vaccination against CSF has been successfully implemented using live attenuated vaccines. Recombinant viral vaccines are a safe alternative which allow the differentiation between infected and vaccinated animals. However they usually also have a decreased efficacy and thus need strong adjuvants. Here we demonstrate the safety and efficacy of a recombinant E2 CSF vaccine based on a micro-emulsion adjuvant.

3 groups of 10 40-day-old pigs received 2 injections of 1ml 20 days apart. Group 1 was immunized with a recombinant E2 vaccine formulated with the microemulsion adjuvant Montanide IMS 1313 VG (IMS), Group 2 with a recombinant E2 vaccine formulated with the polymer adjuvant Montanide Gel 01 (Gel). The control group received 2 injections of saline solution. For safety assessment, clinical signs after vaccination were recorded in all groups. Body temperature after vaccination and body weight during the trial were measured. For efficacy assessment, blood samples were collected at D0, 20, 40, 80 and 120 after injection and ELISA titrations and virus neutralization (VN) tests were performed on the pig sera. Animals were slaughtered at D120. This trial was repeated in 3 different farms in South Korea.

No severe clinical signs were observed. Animals showed some degree of depression right after vaccination. Pyrogenicity was lower than 0.7°C, and temperature and behavior of all animals were back to normal 24h after vaccination. There were no significant difference in the body weight of vaccinated and control animals at any time during the trial.

Antibody and virus neutralization titers were significantly higher in the IMS vaccinated group than in other groups at all time points during the trial in all farms. ELISA measurements showed that 100% of IMS vaccinated animals had protective levels of IgG at 40 days post injection. At 120 days post injection, 97% of IMS vaccinated animals showed protective levels of IgG. Virus neutralization tests showed that 100% of IMS vaccinated animals had protective VN titers at 40 dpi. At 120 dpi 70% of IMS vaccinated animals had protective VN titers.

This study shows that Montanide™ IMS adjuvants combined with recombinant CSF swine vaccine can induce lasting protective immune response until market age in pigs, while preserving the safety properties of the vaccine.

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Attenuate highly pathogenic Porcine Reproductive and Respiratory Syndrome virus by incorporating target site of hematopoietic-specific microRNA into viral genome

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Incorporation of target sequences of tissue- or cell-enriched microRNAs into the viral genome can be used to restrict off-target spread of virus. And infection in pulmonary alveolar macrophage (PAM), the host cell of porcine reproductive and respiratory syndrome virus (PRRSV), is critical for PRRSV pathogenicity and immunosuppression. To attenuate the highly pathogenic PRRSV by restricting viral replication in PAM, the target sequence of hematopoietic-specific miR-142 that is highly-expressed in PAMs was incorporated into PRRSV genome by using reverse genetic operation. Then, the in *vitro* and in *vivo* replication capability and pathogenicity for piglets of the rescued chimeric virus were systematically analyzed and compared with its parental backbone virus RvJXwn.

A viable chimeric virus designed as RvJX-miR-142t, with 22nt miRNA-142 target sequence replacing same length fragment of Nsp2 coding region, was first successfully rescued. And the multistep growth curve showed that the chimeric RvJX-miR-142t and RvJXwn have the same growth prosperities in MARC-145 cells. However, as expected, the replication of RvJX-miR-142t was seriously impaired in PAMs with significantly lower titers compared with that of RvJXwn at all time points. Especially, as much as 10^4 times peak titers difference could be observed between these two viruses.

Then the pathogenicity of the chimeric virus was further investigated in animal inoculation test. The results showed that the body temperature in RvJX-miR-142t-infected group raised slowly, and did not reach 41 ℃ until the 16 day post inoculation (dpi), accompanied by a significantly higher ADG than that of RvJXwn-infected group ($P < 0.001$). The clinical symptoms of piglets in RvJX-miR-142t-infected group were also significantly lower than that of RvJXwn-infected group ($P < 0.001$), and the mortality decreased to 2/6, with only two piglets died at 19 dpi. As well, the virus loads of RvJX-miR-142t-infected piglets were obviously lower than that of RvJXwn group on 3, 5, 7 dpi ($P < 0.001$). Meanwhile, the seroconversion for antibodies to PRRSV was later than that of RvJXwn group. Moreover, during the acute phase in the first 7 dpi, lung lesions of piglets in RvJX-miR-142t-infected group were much milder than that of RvJXwn group, with significantly lower lung lesions scores than that of RvJXwn group ($P < 0.01$).

Taken together, the results above demonstrated that incorporation of miR-142 target sequence into RvJXwn impaired the replication of PRRSV in its host cells and reduce its pathogenicity in piglets, correspondingly. This study provided a novel method for limiting PRRSV's tropism and driving viral attenuation.

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Dissection of complex molecular interactions between important animal nidoviruses and the host

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The long-term goal of our research program is to better understand molecular mechanisms of interactions between animal nidoviruses and their hosts in order to develop new strategies for effective control of viral infections. The present research project is focused on emerging swine pathogens of unprecedented economic significance, such as the porcine reproductive and respiratory syndrome virus (PRRSV) and the porcine epidemic diarrhea virus (PEDV). The PEDV and PRRSV are responsible for severe economic losses and considered as the primary emerging livestock pathogens worldwide. Insufficient understanding of virus-host interactions impedes the development of effective animal vaccines against PRRSV and PEDV.

Host-virus interactions are highly dynamic and may involve multiprotein complexes. Earlier, our group employed biochemical and proteomics approaches to identify virus-host multiprotein complexes, and showed that their composition is controlled by the virus either by direct recruitment of or by binding to host proteins. Consequently, characterization of the composition of PRRSV and PEDV and identification of the host proteins that are specifically encapsidated into or bound to virions are important for our further understanding of virus-host interactions. To accomplish this objective, we produced and purified PRRSV and PEDV using both the simian cell cultures that are routinely used for virus production and PRRSV/PEDV natural target cells. We hypothesized that the composition of PRRSV and PEDV virions and virus-host molecular complexes will reflect changes in environmental conditions (e.g., pH, activities of host proteases, and tissue-specificity). Furthermore, we hypothesized that the tight homeostatic balance between host cell and virus defines the fate of infection and pathogenesis. Proteomics is the best method to directly characterize the multimolecular complexes important for virus entry and pathogenesis. We examined the composition of progeny virions in order to identify cellular proteins that are associated with or encapsidated into viral particles using state-of-the-art mass spectrometry (MS) strategies, including a high-resolution hybrid Quadrupole-Orbitrap MS. The present study has demonstrated the incorporation of cellular proteins in PRRSV and PEDV virions. Further investigations are needed to evaluate the role of individual cellular proteins in the viral replication, assembly, and pathogenesis.

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Cleavage of cytochrome c1 by the PRRSV 3C-like protease leads to shedding of an apoptosis inducer

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Porcine reproductive and respiratory syndrome (PRRSV) is an important pathogen of swine and represents a major threat to the worldwide swine production. PRRSV-induced cell apoptosis contribute critically to viral pathogenesis but the molecular details have remained yet understood. In this report, we show that the 3C-like protease of PRRSV interacts with the mitochondrial inner membrane protein cytochrome c1 (cyto.c1) and induces its proteolytic cleavage. Importantly, the cleavage of cyto.c1 results in release of a strong cell apoptosis inducer that causes mitochondrial fragmentation, leading to cell apoptosis. Time course analysis of PRRSV infection revealed that this cleavage is consistent with the timing of the 3C-like protease expression and the onset of caspase-3 activation. Further RNAi silencing experiments revealed that cyto.c1 is critical for PRRSV-induced apoptosis. Taken together, the cleavage of cyto.c1 by PRRSV 3C-like protease is a critical trigger of cell apoptosis. Our studies provide an important piece of mechanistic clues of PRRSV-induced cell apoptosis and also indicate a novel mechanism for the 3C-like proteases of positive-stranded RNA viruses in induction of cell apoptosis.

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A novel mechanism of protein-stimulated trans-activation of ribosomal frameshifting in porcine reproductive and respiratory syndrome virus: implication in improved vaccine development

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Viruses have evolved various non-canonical translation mechanisms, like programmed ribosomal frameshifting (PRF), to overcome some of the restrictions posed by host cell ribosomes and - for example - express multiple proteins from a single mRNA. Arteriviruses utilise PRF to direct the efficient expression of two alternative proteins from the nsp2-coding region of their replicase gene. The PRF signal involved, unusually, lacks an obvious stimulatory RNA secondary structure and induces both –2 and –1 PRF, to produce an nsp2 variant with an alternative C-terminal domain (nsp2TF) and a truncated version of nsp2 (nsp2N), respectively. In the genome of porcine reproductive and respiratory syndrome virus (PRRSV), the minimal PRF signal maps to a 34-nt region including a slippery sequence (GG_GUU_UUU) and downstream conserved C-rich motif. Strikingly, efficient –2/–1 PRF also depends on the nsp1β replicase subunit [Fang et al. (2012), Proc. Natl. Acad. Sci. USA 109:e2920 and Li et al. (2014), Proc. Natl. Acad. Sci. 111:e2172-81]. In addition to this viral trans-activator, PRF requires the participation of cellular poly(C) binding proteins (PCBPs). *In vitro* translation and RNA binding assays revealed that a complex of nsp1β and PCBP binds to the genomic mRNA downstream of the slippery sequence, where it mimics the action of the more typical RNA pseudoknot-type of PRF stimulators [Napthine et al. (2016), Nucleic Acids Res., 44(12):5491-503]. This unprecedented viral PRF signal provides new insights on the modulation of ribosomal elongation by *trans*-acting protein factors. On the other hand, it prototypes a new class of virus-host interactions. Frameshift knockout mutants of PRRSV were attenuated *in vivo*. In comparison with wild-type virus, the frameshift knockout mutants stimulated earlier IFN-α production in infected pigs, and the upregulation of innate immune gene expression was correlated with reduced viral load in animals. Our data strongly implicate the PRF products in viral immune evasion and provides a basis to explore –2/–1 PRF inactivation in vaccine development.

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Identification of CD163 domain involved in the infection with Type II Porcine Reproductive and Respiratory viruses

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Porcine Reproductive and Respiratory Syndrome has been shown to be one of the most economically destructive diseases affecting swine worldwide. In the U.S. alone, recent estimates indicate losses to the national swine herds of $664 million annually from 2005-2010. Efforts to solve this issue have granted a breadth of knowledge revealing details of how the virus infects the host. CD163, present on macrophages and cells of the monocyte lineage, has been shown to play a critical role in infection. Physiologically, CD163 functions as a scavenger receptor for the hemoglobin-haptoglobin complex. CD163 is composed of nine scavenger receptor cysteine-rich (SRCR) domains. There are two 35-amino-acid proline-serine-threonine (PST)-rich regions, one between domains six and seven, and one between domain nine and the transmembrane region and cytoplasmic tail.

In this study, CD163 constructs containing an EGFP fluorescent tag and bearing serial deletions of SRCR domains were produced in order to determine which domains are important for permissiveness to Type II PRRSV. HEK293T cells, which do not support PRRSV infection, were transfected with the CD163 constructs. Transfection was confirmed by visible expression of the CD163-EGFP fusion protein. The proper expression of each CD163 construct was also evaluated by Western blot, using an anti-EGFP antibody for the detection of the fusion protein. The permissiveness of transfected cells for PRRSV was tested using recombinant PRRS viruses expressing a red fluorescent protein (RFP). Successful infection was detected by the presence of red fluorescence in a green fluorescing cell.

The infection experiments revealed that all the constructs containing domain 5 were able to sustain infection by Type II PRRSV while all the constructs that lacked domain 5 were not permissive to infection. This included constructs that had the first 5, 6, and 8 N-terminal SRCR domains deleted. Thus, the presence of domain 5 is a key component in achieving viral infection. Finer mapping studies need to be conducted by making smaller and smaller deletions in this target region to determine the smallest deletion needed to block infection by Type II PRRS viruses.

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Cloning and sequence analysis of Nsp9 gene of Porcine Reproductive and Respiratory Syndrome Virus FS strain

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In order to evaluate function of Nsp9 gene, the target gene of porcine reproductive and respiratory syndrome virus (PRRSV) FS strain was amplificated and sequenced after being cloned into the pMD18-T vector. The physical and chemical properties, homology, hydrophilicity, surface probability plot, antigenic index, secondary structure and subcellular localization were predicted by various softwares. The results showed that the length of Nsp9 was 1 929 bp, its predicted molecular weight was 70.5 ku and pI was 8.04, and it was unstable protein. There were many antigen sites, and the flexibility and hydrophilicity of Nsp9 were ideal. The study showed that Nsp9 possessed potential antigenicity, and it fits for preparation of monoclonal antibodies. The results of subcellular location showed that it may exist in the cytoplasm. Nsp9 of FS strain shared 96.9 % to 98.9% amino acid homology with other strains. Some amino acid mutations were found between the parent strains and vaccine strains, and insertions and deletions could be found among the European strains and the American strains. Whether these insertions and deletions correlate with the virulence and polymerase needed further research.

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Construction and identification of Nsp9-deficient clone of porcine reproductive and respiratory syndrome virus (PRRSV) XH-GD strain

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Nonstructural protein 9 (Nsp9) is one of the most conserved nonstructural proteins in porcine reproductive and respiratory syndrome virus (PRRSV). The major role of NSP9 remains unclear. To further identify the function of Nsp9 in PRRSV, reverse genetic manipulation was performed and an infectious PRRSV cDNA clone with Nsp9-deficient mutants were constructed to verify the function of Nsp9. The results revealed that the PRRSV clones deficient of Nsp9, cannot be rescued suggesting that Nsp9 is critical to the replication of PRRSV. These results may provide the basis for the functional study of this nonstructural protein.

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Influence of Nsp9 between of highly pathogenic PRRSV and low pathogenic PRRSV to replication of PRRSV

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In order to verify the influence of Nsp9 gene between highly pathogenic PRRSV and low pathogenic PRRSV to replication of PRRSV, plasmids pIRes2-EGFP-Nsp9-XH-GD and pIRes2-EGFP-Nsp9-CH-1R containing whole Nsp9 gene were transfected into Marc-145 cells, then cells were infected with PRRSV XH-GD strain at a MOI of 1, TCID50 was used to evaluate viral titer, qPCR and western blot were conducted to evaluate expression of PRRSV N protein. The results showed that the level of N protein in the cells that were transfected with typical PRRSV CH-1R Nsp9 gene was higher than that of the highly pathogenic PRRSV group in the mRNA level, in the protein level, it was same as the mRNA level, and virus titer was also higher than of highly pathogenic PRRSV group. So the conclusion is that Nsp9 gene of low pathogenic PRRSV strain CH-1R is more beneficial to the replication of PRRSV than that of highly pathogenic PRRSV strain XH-GD in the Marc-145 cells.

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Influence of Nsp9 to replication of PRRSV in MARC-145 cells

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In order to evaluate whether Nsp9 could enhance the replication of PRRSV, plasmids pIRES2-EGFP-Nsp9 containing whole Nsp9 genome were transfected into Marc-145 cells, qPCR and western blot were used to evaluate its titer and expression after PRRSV was inoculated, the results showed that level of N protein in the transfected Nsp9 cells was higher than control group, 1.5times of the control group. Meanwhile, the protein level was same as the mRNA level, N protein both at the mRNA and protein level were increased with the increase of plasmids. So the conclusion is that Nsp9 gene could enhance replication of PRRSV, and it was closely related with replication of PRRSV.

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Subcellular localization analyisi and function prediction of PRRSV NSP9 protein

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PRRS is one of the most serious diseases that are harmful to pig industry and NSP9 gene encodes RNA dependent RNA polymerase (RdRp) of PRRSV. Plasmids containing NSP9 gene were transfected into BHK cells and Marc-145 cells in order to confirm the subcellular localization of NSP9 gene and verify whether PRRSV infection could affect its localization through indirect immunofluorescence microscopy. The results show that NSP9 gene was located in the cytoplasm in BHK cells and Marc-145 cells. NSP9 genes are mainly distributed in the cytoplasm ; NSP9 gene gradually transfers to the nucleus after PRRSV infection, and the area was also gradually increased. The research laid a foundation for the replication of PRRSV.

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Substitution between highly pathogenicial PPRSV and low pathogenicial PPRSV with Reverse Genetics System

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The Nsp9 gene of porcine reproductive and respiratory syndrome virus (PRRSV) codes the RNA dependent RNA polymerase, which play a big part in the virus replication. However, whether Nsp9 gene influences the virulence is unclear. To determine the interaction of Nsp9 with virulence and speed of viral replication, cell tropism, the Nsp9 sequences of vaccine strain CH-1R were cloned, ligated it to a virulent strain of the experimental XH-GD infectious clone after restriction enzyme digestion, and transformed the virus under the basis of the reverse genetics. Following by virus rescue, the virus can be successfully saved. Biological characteristics of the virus were explored, titers of saved virus were significantly higher than the growth rate and the parental strain XH-GD, but lower than vaccine strain CH-1R, while plaques similar in size, the polymerase activity of the vaccine virus CH-1R is higher than the virulent strain XH-GD.

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Modeling the transboundary survival of foreign animal disease pathogens in contaminated feed ingredients

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Objective: To model the survival of foreign animal diseases in feed ingredients shipped from Asia to the US using surrogate viruses.
Materials & Methods: Based on the Swine Health Information Center pathogen matrix, 10 FAD viral pathogens were identified as significant risks to the US swine industry. For the purpose of the study, a surrogate virus was selected to represent each pathogen: FMDV (SVA), CFV (BVDV), PRV (BHV-1), ASFV (Vaccinia), Nipah virus (CDV), SVDV (PEV) and VEV (FCV). Other selected pathogens included PRRSV 174, PCV2 and VSV. Using a transboundary model (1), feed ingredients known to be imported from China to the US (organic & conventional soybean meal, soy oil cake, DDGS, lysine, choline, vitamin D, pork sausage casings, and various pet foods) were inoculated (5g ingredient+100uL virus). Controls included complete feed (surrogate or saline) and stock virus (positive control, no feed matrix). Samples were incubated in an environmental chamber for 37 days programmed with T and % RH data recorded from China to the US during December 2012 through January 2013 (SeaRates.com). Samples were tested by PCR, VI and bioassay at day 2, 8, 25 and 37 PI.
Results: Testing of the FMDV, CSFV and PRV surrogates indicated the survival of SVA and BHV-1 at 37 DPI. Both surrogates survived in conventional soybean meal and soy oil cake. SVA also survived in lysine, pet food, Vit D, complete feed and casings. Positive controls did not survive. BVDV was negative at 37 DPI, independent of ingredient.
Discussion: These preliminary results suggest that contaminated feed ingredients could serve as vehicles for FAD introduction to the US, supporting our PEDV data. Phase 2 has begun, consisting of surrogates for ASFV, VEV and Nipah Virus along with PRRSV (174). New data will be shared if selected for presentation.

(1). Dee S, et al. Modeling the transboundary risk of feed ingredients contaminated with porcine epidemic diarrhea virus *BMC Vet Res,* 2016, 12:51

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Isolation and characterization of porcine deltacoronavirus from pigs with diarrhea in China

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Porcine deltacoronavirus (PdCoV) (family Coronaviridae, genus Deltacoronavirus) is an emerging swine enteropathogenic coronavirus that causes symptoms of acute diarrhea and vomiting. It is a significant threat to the pig industry. In this study, a molecular-based method was used to investigate the prevalence of PdCoV and characterize the aetiologic agents that induce diarrhea in pigs in China. The RT-PCR results indicated that porcine epidemic diarrhea virus (PEDV) is the most common porcine enteric virus isolated with PdCoV. Furthermore, the prevalence of PEDV is more common than PdCoV in 12 provinces of China. A total of 4 different PdCoV strains were isolated using swine testicular (ST) cells. Phylogenetic analysis of the complete genome revealed that the N and S protein sequences of the four PdCoV isolates were most closely related to PdCoVs from Korea and the US. With no way of predicting an outbreak of PdCoV in China and there being no vaccine available to prevent infection, extensive surveillance for PdCoV is critical in order to define the epidemiology and evolution of PdCoV. An effective vaccine is urgently needed to prevent widespread emergence of this disease in China.

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Leveraging data across a large geographic area to increase context and understanding of swine viral residence and transmission in smaller regions

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Area Regional Control (ARC) projects have been successful helping producers and veterinarians understand the local risk for PRRSV introduction into herds and coordinating disease control efforts at a local level. One weakness of ARC projects is that while they provide granularity at the local level, they do not provide a broad context for current and potential sources of new viruses to that region. To address that information gap we established a network (coined Illinois Swine Health Network or ISHN) of ARC projects, producers that had sites both within and outside of ARC projects and other producers that are in proximity to ARC projects. The goals of the network are: 1) to develop the data collection methods, infrastructure and collaborations between producers, veterinarians, and technical experts, 2) to facilitate dynamic, real time estimates of the risk of disease introduction into a pig farm, 3) to facilitate the development and deployment of optimum prevention strategies for herds, local production ecosystems and regional production ecosystems.

Since inception in June of 2014, ISHN has enrolled 572 individual sites. Each site has a robust set of metadata including, geo-location, production type, size, and Prem ID. The focus has been on collecting all PRRSV and Influenza Virus A sequences obtained from the enrolled sites along with their associated metadata (Date, etc.). Each participant (ARC, veterinary clinic or production system) maintains its own dataset of sequences to allow for individual local analysis. Using Disease BioPortal (www.bioportal.ucdavis.edu, Univ. CA-Davis), the ISHN aggregates these datasets and provides analytics for the entire network. Standard reporting is provided to participating veterinarians routinely. As of July 1, 2016, ISHN contains 1978 unique PRRS sequences and 508 unique IAV - HA sequences. Additional target gene sequences (NA, M, etc.) are also contained in the database but are not routinely analyzed. Future work includes capturing animal movement data to provide better context for disease movement patterns and integrating poultry sites to understand cross species IAV movement.

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Estimating the costs of Porcine Reproductive & Respiratory Syndrome (PRRS) and return on investment of interventions with a PRRS economic simulator

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Porcine reproductive and respiratory syndrome (PRRS) is among the diseases with the highest economic impact in pig production worldwide. Holtkamp et al. (2013) estimated annual losses due to the disease in the USA as high as $664 Mio. Yet, the economic impact of the disease at farm level is not well understood as, especially in pig herds chronically infected with PRRS virus, losses caused are often not obvious for farmers and veterinarians. Furthermore, the vast number of options to control PRRS makes it difficult for farmers and veterinarians to decide on the economically most efficient strategy for their farm. Aim of this study was to develop an economic model to estimate the costs of PRRS and the cost-efficiency of different control strategies for an individual farm. In a production model simulating the production of different farm types, batch systems, etc., an epidemiological model was integrated to estimate the impact of PRRS infection on health and productivity parameters, depending on PRRS severity. Based on this, financial losses were calculated in gross margin and partial budget analysis. This cost model was extended to incorporate different intervention strategies: a) depopulation / repopulation (D/R), b) close & roll-over (C&R), c) test & removal (T&R), d) mass vaccination of sows (MS), e) MS and vaccination of piglets (MSP), f) vaccination of sows according to the status of reproduction (6-60), g) 6-60 and vaccination of piglets (6-60P), h) improvement of biosecurity and management (BSM), and combinations of h) with d) – g). Data on the effects of PRRS infection and of each intervention were obtained through literature review and expert opinion. Economic efficiency of the different control strategies was assessed over a period of 5 years through investment appraisals, and the resulting expected value (EV) indicated the most cost-effective strategy. The final calculator was coded as a stochastic model in Excel add-in @RISK 6.3.1 (Palisade Corporation, Newfield, New York, USA). In a moderately affected herd (moderate deviations in all health and productivity parameters from what could be expected in an average negative herd), total median losses per year were estimated as being $-495,775. The intervention strategies with the highest median EV were 1) C&R ($1,261,120), 2) MSP ($1,247,520) and 3) 6-60P ($1,226,990). In a slightly affected herd, median annual losses were $-249,915, and the most cost-efficient strategies according to their median EV were 1) MSP ($807,777), 2) 6-60P ($797,442) and 3) MS ($743,273). Results indicate that losses in affected herds can be considerable and that the expected benefits of interventions and the most efficient strategy depend on the farm individual situation, e.g. disease severity. The model can provide a better understanding of the economic impact of PRRS in a farm and the need for interventions. It is a valuable tool for farmers and veterinarians to facilitate decision on the most economically efficient intervention strategy.

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Spatiotemporal detection and localization of type 2 porcine reproductive and respiratory syndrome virus at the maternal-fetal interface of late gestation pregnant gilts

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Porcine reproductive and respiratory syndrome virus (PRRSV) infection causes severe reproductive failure characterized by high fetal mortality leading to substantial economic losses to the swine industry. The mechanism of PRRSV-induced fetal death needs further studies to explore PRRSV transmission across the maternal-fetal interface (MFI). The localization of PRRSV antigen at various time points post-inoculation is important to identify the mechanisms used by the virus to breach the MFI. An immunofluorescence (IF) technique was used for the spatiotemporal detection of type 2 PRRSV across the MFI in 20 pregnant gilts on day 85±1 of gestation. Type 2 PRRSV (NVSL 97-7895) was used to inoculate 15 gilts (1 x 10^5 $TCID_{50}$ total dose) at 85 days of gestation. Five gilts were sham-inoculated with sterile culture media (CTRL). Chronological IF detection of PRRSV in MFI was conducted in three inoculated gilts and one control gilt euthanized at 2, 5, 8, 12, and 14 days post infection (dpi). Samples of MFI were collected from the area adjacent to the umbilical stump of each fetus and frozen for cryosectioning. The images were obtained using CellSens® software and an Olympus® IX83 microscope equipped with a high resolution Zyla sCMOS camera. To date we have analysed transplacental PRRSV transmission in randomly selected fetuses obtained at day 5, 8, 12 and 14 dpi in both PRRSV inoculated and corresponding CTRL gilts. Five-micrometer cryosections were used for single IF detection and localization of PRRSV-positive cells in the MFI. Three major focus areas were categorized: endometrial connective tissues (including uterine glands and blood vessels), the interface (junction of endometrium and fetal trophoblasts) and fetal placental structures (mesenchymal cells and placental blood vessels). Results obtained from our preliminary work show that the majority of PRRSV was localized in the endometrial connective tissues and the interface at 5 and 8 dpi, whereas the detection of PRRSV was more localized in the fetal placental side at 12 and 14 dpi. IF labelling at 14 dpi revealed the majority of fetal placental blood vessels were infected with PRRSV-positive cells, which was not observed at 5, 8 and 12 dpi. The PRRSV infected cells at 12 and 14 dpi were also more abundant than 5 and 8 dpi and localized in a very consistent “lined up” fashion along the fetal placental border. Further investigation is in progress to perform double and triple IF staining to focus on specific maternal/fetal cells and connective tissue structures that PRRSV is potentially exploiting for active transmission from dam to fetuses leading to reproductive failure. This project was supported by Genome Canada, Genome Alberta and Genome Prairie (Saskatchewan Ministry of Agriculture).

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Using machine learning to predict swine movements with application to the control of infectious diseases

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Background: Direct or indirect contact between farms is one of the most important factors influencing the spread of infectious diseases in food animals, including the US swine industry. Understanding an industry's structural network of contacts is prerequisite to plan for efficient production strategies and, for effective disease control measures. Unfortunately, systematic collection of contact data between farms is difficult and, thus, such information is often unavailable.

Objectives: Here, we first summarized frequency and distance of movements within two partial networks of swine producing facilities in Minnesota, and, second, developed a methodology utilizing that incomplete information to estimate a complete contact network in a region in which a voluntary swine disease control program has been implemented.

Methods: A machine learning technique, referred to as Random Forest (RF), which is an ensemble of independent classification trees, was used to estimate the probability of pig movements between farms and/or market sites located in two counties in MN. Once calibrated and tested, the model was used to predict animal movements in sites located across 34 Minnesota counties (RCP-N212).

Results: Agreement between observed and expected movements in the model was maximized using a 0.85 probability threshold. Variables that were important in predicting pig movements included distance between sites, ownership, and production type of the origin and destination. Using a weighted-Kernel approach to describe spatial variation in centrality measures of the predicted network, we also show that the south-central region of the study area exhibited high spatial-aggregation of pig entries and exits. This area also seemed to be a hot spot for some swine diseases, which would be expected for an area engaging in large quantities of animal movements.

Conclusions: The information provided here will help to design and implement control strategies in the region. Additionally, the methodology here may be used to estimate contact networks for other livestock systems when only incomplete information is available.

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Epitope mapping of monoclonal antibodies against emerging porcine circovirus subtype 3

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Porcine circovirus (PCV) has been causing significant economic losses to the swine industry worldwide. Recently, novel subtype 3 (PCV3) has been identified in field cases with porcine circovirus-associated disease (PCVAD). Development of specific diagnostic reagents and assays are important for controlling this emerging pathogen. In this study, we generated a panel of monoclonal antibodies (mAbs) against the capsid proteins of PCV3. Four mAbs were selected for characterization in various diagnostic assays. The antigenic epitopes recognized by these mAbs were further mapped with full-length and C-terminal truncated capsid proteins of PCV3. MARC-145 cells were transfected with a plasmid DNA expressing full-length or a fragment of capsid protein, and indirect immunofluorescence assay was used for detecting the mAb reactivity. The results showed that mAbs 29-1, 40-84, and 47-1 recognized epitopes located at amino acid (aa) 59–140 of the capsid protein. These mAbs were further tested in Western blot using cell lysates of MARC-145 cells that express full-length of PCV3 capsid protein. The mAbs 14-1 and 40-84 reacted with the capsid proteins from cell lysates, but no reactivity was detected for other mAbs, suggesting that mAbs 14-1 and 40-84 recognized linear epitopes, while the others mAbs recognized the conformational epitopes. Further mapping of the individual epitope and testing the mAb cross-reactivity with other PCV subtypes are currently going on in our laboratory. This panel of mAbs provides a useful tool for PCV diagnostics and pathogenesis studies.

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Development of novel chimeric vaccine and delivery system for classical swine fever virus

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Classical swine fever virus (CSFV) is highly contagious to pigs. Although it has been eradicated from the US and many other countries, biosecurity measures, including efficient vaccines, are critical to assure a CSFV-free status. CSFV vaccines are available, but modified live virus (MLV) vaccines may pose concerns on biosecurity issues in CSFV-free countries, while subunit vaccines have limitations on stimulation of sufficient levels of immunity. A viral vector vaccine would be able to overcome these limitations. In this study, a modified live porcine reproductive and respiratory syndrome virus (PRRSV SD95-21 MLV) was used as a viral vector backbone to express immunogenic E2 protein of CSFV. Using the infectious clone of SD95-21 MLV, the CSFV E2 gene was inserted between non-structural and structural genes, which was transcribed as an additional subgenomic RNA. Upon transfection of cells with this plasmid, the progeny virus "PRRSV-E2" was obtained. To eliminate the need for a cold chain, DNA vaccine approach was used, in which nanoparticles composed of branched amphiphilic peptide capsules (BAPCs) were employed as the DNA delivery agent. Transfection of DNA-BAPC nanoparticles in MARC-145 cells recovered infectious viruses. Subsequently, DNA vaccination and BAPCs delivery approach were evaluated using a nursery pig model. Pigs were immunized by PRRSV-E2 chimera in a form of DNA-BAPC nanoparticles (group 1), DNA without nanoparticles (group 2), live recombinant chimeric virus (group 3), or mock-inoculated as a control (group 4). Viral RNA was detected by nested RT-PCR from group 1 and group 3 pigs at 7 days post inoculation, while virus specific antibody response was detected by 3 weeks post-infection. This study developed a chimeric dual user candidate vaccine for both PRRSV and CSFV. The chimeric vaccine platform and DNA delivery system established in this study could be applied to other emerging and transboundary swine pathogens in the future.

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Identification of African swine fever virus p30 antigenic epitopes after experimental infection

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African swine fever virus (ASFV) is the etiologic agent of a devastating disease of swine for which there is no available commercial vaccine. The ASFV has a multilayer virion composed of at least 50 proteins and contains a double stranded DNA genome of 170-190 Kbp encoding for more than 100 polypeptides. Kollnberger and colleagues identified p30 among the 12 most antigenic proteins, and Gomez-Puertas and colleagues showed that p30 induces neutralizing antibodies. There is little information on the p30 antigenic epitopes recognized by sera from ASFV infected swine. Identification of epitopes is important for the development of diagnostic tools and vaccines. The aim of our study was to identify antigenic epitopes on p30 using sera from pigs immunized with an alphavirus based replicon particles expressing p30 (RP-30) and then infected with the attenuated ASFV strain, OURT88/3. Ten pigs were immunized with RP-30 and boosted after three weeks. Six non-immunized pigs were included as controls. All sixteen pigs were inoculated by intramuscular injection with OURT88/3 at 10^4 $TCID_{50}$/ml one week after the last immunization. Pigs were euthanized by 21 days post infection (DPI) with OURT88/3. Temperature and clinical signs were recorded daily until the end of the study. For epitope mapping, five overlapping p30 fragments and p30 whole protein expressed in *E.coli* were used as antigen for ELISA, and sera from pigs at days 0 (before inoculation with OURT88/3) and at 17 DPI were tested. All day 0 sera from the 10 immunized pigs showed high reactivity with the p30 whole protein, 3 sera showed reactivity above background with the p30 region between amino acids (aa) 61 and 91, and 1 sera reacted with the region between aa 91 and 110. Overall, no strong immune dominant epitopes are elicited after vaccination with RP-30.

As expected, no reactivity against p30 fragments nor the whole protein was detected for sera at day 0 from the non-immunized pigs. All sera from 17 DPI reacted with p30 whole protein, and 5 sera from the immunized group reacted with the p30 region between aa 91 and 130, while 1 reacted weakly with the region between aa 111 and 130. One out of 6 sera from the non-immunized group reacted with the region between aa 91 and 130. Among 8 sera that did not react with any p30 fragment, 2 of those pigs had high average clinical score and temperature starting from the second week post infection and were euthanized 2 days before the end of the study. Three pigs had low average clinical score and temperature throughout the study, and the remaining three had average clinical score of around 2 or below. In conclusion, we have identified p30 epitopes recognized after ASFV experimental infection, however a clear role for those epitopes in the pathogenesis of ASFV has not yet been established. Future studies will be conducted to test the serum samples for neutralizing activities, as well as to investigate the role of other immunogenic proteins.

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