



Swine Health Information Center

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OUR LATEST INFORMATION ON PROTECTION OF US SWINE HERD HEALTH

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SHIC/AASV H5N1 IAV Webinar Addresses Global Influenza Surveillance and Risk to Swine

The Swine Health Information Center, in collaboration with the American Association of Swine Veterinarians, hosted a webinar on influenza A viruses on Friday, April 19, 2024. The goal of the webinar was to understand the threat HPAI H5N1 poses to domestic livestock species and to inform producers of actions that can be taken to prevent infection on-farm. This article includes an overview of influenza A viruses, global and domestic distribution of the virus, IAV swine surveillance programs, and research outcomes for HPAI H5N1 experimental infection in swine. A second article summarizing information including an overview of influenza A viruses, global and domestic distribution of the virus, IAV swine surveillance programs, and research outcomes for HPAI H5N1 experimental infection in swine [can be found here](#). The webinar garnered high interest with 1341 registrants and 921 joining the webinar live from 30 countries.

The webinar recording is available [here](#).

Dr. Amy Baker, research veterinary medical officer at the USDA National Animal Disease Center, started the presentations with an overview of influenza A virus in swine. Influenza A has a negative strand

RNA genome, is enveloped, and contains two major surface glycoproteins – hemagglutinin (H) and neuraminidase (N). Dr. Baker said influenza A is prone to rapid evolution by two main processes – genetic mutation and reassortment - and that the virus escapes population immunity by antigenic drift and/or shift. With reassortment, influenza A evolution can lead to antigenic shift which was seen in the 2009 H1N1 pandemic in humans.

Dr. Baker said influenza is constantly changing and shared that wild waterfowl are a native host for the virus. Influenza from waterfowl has the potential to infect swine and those same viruses can also interact with humans and poultry. During her presentation, Dr. Baker highlighted how several species, including pigs, birds, wild mammals, and humans, have the potential to serve as mixing vessels and share the influenza A virus among mammalian species.

Dr. Baker reviewed the ongoing USDA IAV surveillance in swine stating that this system has been active since 2009. Viruses identified at veterinary diagnostic laboratories are initially screened for the presence of IAV through PCR. The current testing methodology can detect the different H and N glycoproteins including H5N1. Cases that meet specific criteria can then be added into the surveillance for further whole genome sequences. Three sample streams are

incorporated into the current surveillance system, including 1) case-compatible swine accessions to the NAHLN laboratories, 2) swine population samples epidemiologically linked to a human case of IAV, and 3) swine exhibiting influenza-like illness at commingling events such as fairs or exhibition events. Goals of the surveillance system are to monitor the genetic evolution of endemic IAV in swine and make influenza isolates from swine available for research. Further, goals include establishing a data management system for genetic analysis to facilitate the development of relevant diagnostic reagents, updating diagnostic assays, and identifying proper isolates for vaccine seed stock.

The ongoing surveillance system helps to address the human/swine influenza A interface. Dr. Baker noted that human influenza A greatly influences the pathogen's diversity in swine due to interspecies transmission from humans to swine. Surveillance of influenza viruses assists with the One Health approach to understand swine influenza A hemagglutinin and neuramidase diversity in the US and globally. Human variant cases from swine hemagglutinin clades are detected globally and monitored by the World Health Organization Collaborating Centres of the Global Influenza Surveillance and Response System. The USDA Swine Surveillance system provides valuable information regarding the evolution of the virus within the US to benefit swine and human populations. Dr. Baker highlights the public health-animal health collaboration within the influenza community as a success story. While the current HPAI H5N1 panzootic is a concern for swine health and human pandemic preparedness, robust surveillance and disease investigation are the foundation for improving intervention strategies for animal and public health, Dr. Baker concluded.

Dr. Bailey Arruda, research veterinary medical officer with the USDA Agricultural Research Service at the National Animal Disease Center in Ames, began her presentation by discussing the differences between HPAI H5N1 and low pathogenic avian influenza. The HPAI designation refers to a specific clinical presentation in poultry based on the ability of the virus to replicate outside of the gastrointestinal tract. She said there have been multiple introductions of HPAI from 2021 to present

with viruses of European descent being maintained in the US.

A change in global HPAI epidemiology due to unprecedented detections of the virus in many different mammalian species has increased research interest and concern regarding the potential for mammalian adaptation of the virus. Dr. Arruda shared HPAI detections in wild birds are on the rise and incidence in commercial poultry flocks are continuing as well. Swine adapted influenza A infection in the US is common in commercial production and routinely monitored, per data from the SHIC-funded swine disease reporting system and the USDA surveillance.

To understand the risk of HPAI, it is important to note that multiple adaptations of the influenza A virus are required to overcome species restriction, stated Dr. Arruda.

In one study led by Dr. Arruda and colleagues to characterize the divergent pathology and transmission among avian and mammalian origin isolates of HPAI H5N1 in swine, they discovered that overt clinical signs were not observed in pigs after experimental challenge. All isolates caused lung lesions consistent with influenza A virus infection, but differences included the variability of lesion severity across strains, the antigen distribution and cells affected, and only mammalian isolates had limited nasal shedding and partial transmission to direct contact pigs.

In another recently completed study with full analysis pending, research observed that HPAI H5N1 strains vary in their clinical presentation post exposure in pigs. Based on results from this study, HPAI may need to be considered for the differential list when pigs present with neurologic clinical signs.

From research outcomes, Dr. Arruda stated that pigs are at risk from hemagglutinin H5 circulating strains and reassortment with endemic swine strains is a concern. She also stated that risk is higher for incursion into swine located in backyard multi-species or transitional outdoor pig farms that include the presence of poultry and/or wild waterfowl species. Finally, risk of incursion into conventional confinement swine operations in the US is likely low, but awareness and precautions are critical.

Influenza A viruses are constantly evolving and pose a risk to domestic livestock species. To address and mitigate the impact of emerging influenza strains for producers, SHIC and AASV collaborated to provide this influenza A virus webinar with the latest information on influenza in domestic livestock species. Prevention efforts should focus on actions to reduce biosecurity risks including the use of outbreak investigation tools to identify biosecurity hazards at the farm. Understanding the status of influenza in US pig populations through targeted surveillance provides information on virus evolution, distribution and support of diagnostic tests and vaccines. Influenza viruses present a challenge for swine health and production and tools exist to reduce the impact this disease can have on pork producers.

SHIC/AASV H5N1 IAV Webinar Addresses Dairy Experience and Biosecurity on Swine Farms

The Swine Health Information Center, in collaboration with the American Association of Swine Veterinarians, hosted a webinar on influenza A viruses on Friday, April 19, 2024. The goal of the webinar was to understand the threat HPAI H5N1 poses to domestic livestock species and to inform producers of actions that can be taken to prevent infection on-farm. This article includes an overview of the clinical presentation and epidemiology of the multi-state dairy herd outbreak and a review of biosecurity considerations for swine farms to mitigate risks of HPAI H5N1. A second article summarizing information including an overview of influenza A viruses, global and domestic distribution of the virus, IAV swine surveillance programs, and research outcomes for HPAI H5N1 experimental infection in swine [can be found here](#). The webinar garnered high interest with 1341 registrants and 921 joining the webinar live from 30 countries.

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Dr. Jamie Jonker, chief science officer with the National Milk Producers Federation, shared information on the diagnosis of HPAI H5N1 in domestic livestock. The first confirmation of H5N1 in a dairy herd was in Texas on March 25, 2024. As

of the date of the webinar, 29 herds in eight states had confirmed HPAI H5N1 detections including Texas, New Mexico, Kansas, Idaho, South Dakota, Michigan, Ohio, and North Carolina. As of May 1, 36 herds in nine states confirmed HPAI H5N1 detection.

Affected dairy cows are typically multiparous in production at over 150 days in milk. About 10% of this population are affected in impacted herds with no mortality. Affected cows exhibit decreased activity with a drop in rumination and decline in feed intake. Milk yield drops with a change in milk consistency to a thicker, often yellowish to brown color resembling colostrum. Flakes can periodically be observed in milk which are most often associated with mastitis. Severely affected cows have all quarters impacted while others have just one or two quarters affected. There is a widespread increase in milk conductivity, also a typical indicator of mastitis. Affected herds take just four to six days to reach peak incidence, then clinical signs taper off at 10 to 12 days. However, it takes around 45 days for full herd recovery. Affected cows are managed symptomatically as there are no current treatments or vaccines approved for use in dairy cattle.

Dr. Jonker pointed to migratory birds as the likely source of HPAI H5N1 infection in dairy cows as well as subsequent animal movements. He also shared information about commercial poultry herds in the vicinity of impacted dairies being diagnosed with HPAI since March 25, including one egg layer in the Texas panhandle and three egg layers in Michigan. Research on virus transmission is needed to understand areas of risk and to identify potential management and mitigation steps. Additional research needs include understanding the long-term health and production implications for infected mature lactating dairy cattle and characterizing the impact in young-stock and dry cows.

Due to the HPAI outbreaks in dairy herds, a new emphasis is being placed on biosecurity on dairy farms to reduce the risk of introduction and infection. Dr. Jonker described the challenges of dairy farms' typically open design and areas of concern for disease introduction. USDA, American Association of Bovine Practitioners, National Milk Producers Federation, FARM, and Secure Milk Supply are all providing guidance and resources

to dairy farms in these biosecurity efforts. Human workers can also be at risk of infection, with upper respiratory protection (eyes, nose and mouth mucosa) being important after a dairy caretaker presented with symptoms of conjunctivitis after exposure. The CDC is providing additional guidance for animal caretaker protection to prevent potential exposure.

Dr. Derald Holtkamp of Iowa State University shared perspectives on what the HPAI H5N1 situation means for biosecurity on swine farms. While these outbreaks do not signal novel biosecurity hazards for swine farms, it can change the prioritization of hazards to be addressed relative to wildlife. Dr. Holtkamp talked about the biosecurity hazards posed by wild birds and other animals inside and around swine barns, compost facilities, storage sheds, and other facilities including the perimeter buffer areas.

Water, food, and shelter including trees/windbreaks can act as attractants for wild birds. To implement control measures, attractants should be removed or protected from wild bird access. This includes cleaning up spilled feed daily, eliminating bird nesting and roosting sites, controlling rodents, removing wild animal habitats, using bird netting to prevent access inside swine barns, repairing curtains where needed, and draining ponds. Biosecurity control measures to eliminate nests and roosting sites near air inlets and entry points into swine farms is especially important. Harassment of birds to deter contact is also possible through lasers and loud noises. The potential use of lethal control measures for birds should always be carefully considered with assistance from the USDA Wildlife Services before being implemented.

Contaminated feed sources are another area of concern. Ingredient sources, including DDGs, feed storage facilities and feed mill biosecurity all need to be assessed for potential biosecurity hazards. In some cases, bovine-derived feed ingredients are used in swine rations including whey, milk replacers, dairy by-products, and raw milk potentially fed to show pigs. To address these factors, Dr. Holtkamp recommends an audit of ingredient sources, storage, and off-site processing. Bird-proofing and rodent control in these feed manufacturing and storage facilities are necessary.

Surface water used as a source of drinking water for pigs is another biosecurity hazard. Surface water control measures included avoidance or water treatment with chlorine, acidifiers, iodine or peroxide. Proximity to nearby poultry and dairy farms and the related operational connections of third-party service providers (equipment repairs, supply deliveries, etc.) raise additional concerns for biosecurity hazards.

Dr. Holtkamp shared information regarding the SHIC-funded Standardized Outbreak Investigation Program. This consistent approach to identify, assess, and prioritize biosecurity hazards can be used to conduct outbreak investigations or to proactively conduct a biosecurity hazard analysis. To request access to this free tool, send an email to soip@iastate.edu.

Influenza A viruses are constantly evolving and pose a risk to domestic livestock species. To address and mitigate the impact of emerging influenza strains for producers, SHIC and AASV collaborated to provide this influenza A virus webinar with the latest information on influenza in domestic livestock species. Prevention efforts should focus on actions to reduce biosecurity risks including the use of outbreak investigation tools to identify and prioritize biosecurity hazards at the farm. Understanding the status of influenza in US pig populations through targeted surveillance provides information on virus evolution, distribution and support of diagnostic tests and vaccines. Influenza viruses present a challenge for swine health and production and tools exist to reduce the impact this disease can have on pork producers.

SHIC Highlights Ongoing Influenza A Surveillance in US Swine Herds

Part of SHIC's mission to protect and enhance the health of the US swine herd includes identifying emerging disease threats through surveillance and monitoring. The recent detection and confirmation by USDA of HPAI H5N1 in domestic livestock raises concerns regarding the emerging threat and potential risks to swine herds. In collaboration with AASV, SHIC recently hosted a [webinar on HPAI in livestock](#) which highlighted the ongoing surveillance of influenza A viruses in swine. IAV monitoring is important for early detection of newly emerging strains, to track changes in known viruses over time, and for informing response to an emerging threat. Current influenza monitoring in US swine populations include the [SHIC Domestic Disease Monitoring Reports](#) and the [USDA Influenza A Swine Surveillance Program](#).

Supported by funding from SHIC, the [Swine Disease Reporting System](#) monitors and provides monthly Domestic Disease Monitoring Reports on the detection of IAV from swine samples submitted to participating veterinary diagnostic laboratories. Samples submitted to the six participating VDLs represent >96% of swine samples being tested in the US. The report highlights the detection of IAV by PCR, including the number of IAV submissions tested over time, the percent of positive submissions by age, a comparison of expected versus actual percent of positive submissions for seasonal trends, and the IAV subtype detected by PCR. Further, the IAV subtype distribution and location is now available through the new IAV state-level monitoring dashboard. Additionally, confirmed disease diagnosis for influenza A from porcine tissue cases received at ISU VDL is also available in the report. These combined reports provide tools to aid veterinarians and producers in timely identification of IAV in their herds and to determine if the influenza A positive cases are above expected in their region. Information from surveillance is necessary to guide prevention and control efforts including evaluation of the use of vaccines within the herd. The SDRS report is included in the monthly SHIC newsletters and can be found online [here](#).

In conjunction with IAV monitoring by VDLs, USDA monitors IAV from multiple surveillance streams

and provides additional information regarding these viruses. The USDA Influenza A Swine Surveillance Program was initiated after the 2009 H1N1 influenza pandemic. A visual showing the diagnostic criteria for inclusion on the program is available [here](#). Goals of the surveillance program include monitoring the genetic evolution of endemic IAV in swine to better understand endemic and emerging influenza virus ecology, making influenza isolates from swine available for research, and establishing a data management system to facilitate genetic analysis of these isolates and related information. Additional goals include selecting the proper isolates for the development of relevant diagnostic reagents, updated diagnostic assays, and vaccine seed stock products. Samples submitted for influenza detection through this Program can originate from sick pig cases submitted to a VDL, samples from pigs at the pig/human interface, such as fairs and exhibitions, and from IAV strains collected from pigs with a link to confirmed isolation of IAV in a human case.

Influenza viruses that have been identified through specific IAV case criteria at the VDLs can be included in the USDA IAV Swine Surveillance Program. Producer data is anonymized with information such as age/production stage of animals sampled, sample type, subtype, and region of origin within the US. Samples that are PCR positive can be further evaluated by virus isolation, subtype sequencing, and whole genome sequencing. Information generated by the Surveillance Program is publicly reported here and a tool for the visualization of aggregate IAV data developed by the USDA ARS National Animal Disease Center is available [here](#).

The American Association of Swine Veterinarian's [position statement on influenza A viruses](#) includes the statement, "It is the position of the AASV that we...recommend pork producers, swine veterinarians and diagnostic laboratories actively participate in IAV surveillance programs that provide information regarding IAV evolution and epidemiology."

The recent detection of influenza A virus H5N1 in livestock highlights the potential for influenza viruses to infect different species and the necessity for routine monitoring of influenza-like illness and

maintaining good biosecurity practices in swine herds. Daily evaluation of pig health is important to rapidly identify early signs of an influenza outbreak such as increased coughing, difficulty breathing, nasal or ocular discharge, fever, lethargy and reduced feed intake. When pigs are sick, producers should work with their herd veterinarian to submit samples for testing to a veterinary diagnostic laboratory. Ongoing surveillance, at the VDL and in cooperation with USDA, is important to assist in identifying influenza detection trends for the national swine herd, to ensure veterinary diagnostics and vaccines are effective, and to determine the best strategies for prevention, management, and control.

SHIC-Funded MSHMP Project Fills PDCoV Epidemiologic Information Gap

In February 2014, porcine deltacoronavirus emerged in the US nearly one year after the initial detection of porcine epidemic diarrhea virus, further impacting the US swine industry. Dr. Mariana Kikuti with the Morrison Swine Health Monitoring Project at the University of Minnesota, along with colleagues Drs. Catalina Picasso-Risso and Cesar Corzo, conducted a Swine Health Information Center-funded study to fill the gaps in current epidemiologic information regarding PDCoV post-introduction.

MSHMP data available between January 2015 and December 2023 were analyzed, representing approximately 60% of the US breeding herd. During the study period, 244 PDCoV outbreaks occurred across 186 sites from 22 production systems in 16 different states. Yearly cumulative PDCoV incidence ranged from 0.44% in 2017 to 4.28% in 2023. Research findings underscore the importance of continued monitoring and control measures to mitigate the impact of PDCoV in the US.

Read the published study [here](#).

PDCoV causes atrophic enteritis in neonatal piglets, leading to acute watery diarrhea, malabsorption, dehydration, and death. In 2014, upon initial emergence, data from laboratory testing indicated PDCoV was detected in 25-30% of samples submitted from clinically affected pigs, with cases

being reported across >10 states. In reporting from US veterinary diagnostic laboratories, PDCoV occurrence is described as the percentage of positive case submissions. Since laboratory submissions more frequently represent clinically affected cases, the probability of testing positive is typically greater than the general swine population.

In the current study, researchers utilized data available from producer participants who report PDCoV weekly status to MSHMP. Data from the participating breeding herds was utilized to calculate the yearly cumulative incidence of PDCoV as an estimation of disease occurrence across the general breeding population. Providing a unique dataset, MSHMP includes the weekly status of herds both clinical and nonclinical for diarrheal disease.

Since January 2015, results of the study showed a total of 244 PDCoV outbreaks have been reported to MSHMP, originating from 186 sites, belonging to 22 production systems, and located across 16 US states. During the entire nine-year period (2015-2023), 140 herds reported one PDCoV outbreak, 36 herds reported PDCoV twice, eight reported it three times, and two herds reported PDCoV outbreaks four times. For sites that experienced more than one PDCoV outbreak during the study period, the interval between outbreaks had a median interval of 2.11 years, ranging from two months to almost five years.

PDCoV case locations were divided into West, Midwest, Northeast and South. Most cases occurred in the South (69.9%) and the Midwest (24.7%), with the remaining cases located in the West (1.6%) and Northeast (0.5%). While most cases occurred in the Midwest in 2015 and 2016, a change occurred in 2017 when most cases originated in the South. The yearly cumulative PDCoV incidence ranged from 0.44% in 2017 to 4.28% in 2023.

Researchers noted that no standardized classification of PDCoV status has been proposed that would allow an estimate of disease prevalence fluctuations over time. Further, the absence of universally adopted standardized criteria for declaring a herd negative post-outbreak also hampers the ability to have a comprehensive understanding of an outbreak's duration. "Efforts

to standardize monitoring and classifying a herd as negative after an outbreak should be made if the goal is to better understand the disease dynamics,” investigators wrote. While PDCoV occurs at a much lower frequency than other important swine diseases such as PEDV, this study provides evidence that PDCoV is still present in US breeding herds and that incidence has increased when compared to early years immediately post-introduction. The findings from this study highlight the importance of continued monitoring of PDCoV in US breeding herds to note changes in occurrence and that focus on control measures is needed to limit the impact on US swine production.

SHIC/FFAR JEV Request for Research Proposals Nets 26 Responses

The Swine Health Information Center and Foundation for Food & Agriculture Research (FFAR) leveraged funds to develop a \$1 million research program to enhance US prevention, preparedness, and response capabilities for Japanese encephalitis virus (JEV), a transboundary emerging disease risk for US swine. Announced in February 2024, the partnership between SHIC and FFAR invited proposals to be submitted by qualified researchers to address 13 JEV research priorities. Proposals were due April 15, 2024, and a total of 26 research proposals from 23 different institutions, including international organizations, were received and will undergo competitive review for funding recommendation.

JEV is an emerging disease transmitted by infected mosquitoes and identified as a priority for North American prevention and preparedness through global swine disease monitoring. In 2022, an outbreak of JEV genotype IV spread rapidly across new geographic regions of Australia affecting breeding swine herds and causing reproductive failure, delayed farrowing, stillbirths, mummified fetuses, abortions, and weak piglets. The US is currently negative for this mosquito-borne virus which has waterbirds as a natural reservoir host but is capable of infecting pigs, humans, and horses.

Recently completed, [a SHIC-funded economic assessment](#) on the impact of a JEV introduction

to the US reports that 32% of the US sow herd would be at-risk for JEV infection and that resulting sow herd losses would range from 1-2% of production. Assuming no increase in prices due to the diminished output, the assessment says economic losses to the US pork industry would be between \$306 million and \$612 million. Coupled with the recent outbreak in Australia, this economic assessment highlights the need for close investigation of this emerging disease and its potential for incursion and establishment in the US.

Responding to this emerging disease risk, SHIC and FFAR joined efforts to form the JEV Research Program with a goal of generating new knowledge for US pork producers on JEV prevention, preparedness, and mitigation. The 26 JEV proposals received in response to this Program will undergo a competitive review process by a task force comprised of pork producers, veterinarians, allied industry, academic researchers, and government scientists. Proposals will be reviewed for their value to US pork producers, application to identified research priorities, scientific soundness, timely completion of objectives, efficient use of funds, level of impact on swine health, and industry-wide benefit.

Proposals were requested to address one or more of 13 research priorities for JEV: 1) transmission and epidemiology, 2) mosquito control, 3) diagnostics, 4) communication, 5) surveillance, 6) compatible cases, 7) challenge models, 8) vaccines, 9) cross-protection, 10) competent vectors, 11) role of wildlife, 12) novel hosts, and 13) viral sequencing. Proposal information and the detailed list of research priorities can be found [here](#).

Upon review, project awards are expected to be announced in the summer of 2024. Projects demonstrating the most urgent and timeliness of completion, providing the greatest value to pork producers, and showing efficient use of funds are prioritized for funding. Results will be shared with producers and veterinarians as soon as they become available.

Research investments are necessary to prevent JEV incursion, ensure rapid detection of JEV if introduced, inform stakeholder response, mitigate production losses on the sow farm, identify effective

control measures, and develop clear messaging to consumers on the safety of pork. Outcomes from the funded proposals will provide critical information that producers, veterinarians, and industry stakeholders can use to better prevent incursion and develop preparedness plans if JEV is identified in the US.

The Foundation for Food & Agriculture Research (FFAR) is a non-profit organization established in the 2014 Farm Bill to build public-private partnerships that fund bold research addressing food and agriculture challenges. SHIC and FFAR collaborated with the Pork Checkoff to fund the Wean-to -Harvest Biosecurity Research Program now underway.

SWINE DISEASE MONITORING REPORTS

The Swine Health Information Center, launched in 2015 with Pork Checkoff funding, protects and enhances the health of the US swine herd by minimizing the impact of emerging disease threats through preparedness, coordinated communications, global disease monitoring, analysis of swine health data, and targeted research investments. For more information, visit <http://www.swinehealth.org> or contact Dr. Sundberg at psundberg@swinehealth.org.

DOMESTIC

This month's Domestic Swine Disease Monitoring Report brings the new SDRS PCR dashboard. The new dashboard is a compilation of all the PCR data for the eight pathogens monitored by the project that will be publicly available, enabling our audience to look at the trends of detection over time by specimen, category, and geographic location. Also, the report brings information about the record of PRRSV ORF5 sequences detected as L1C.5 (variant) for the month of April (355). Since its emergence, L1C.5 has never had this amount of detection in a month, except in November of 2022 (405). The majority of the sequences were from wean-to-market sites (190). Also, some specific regions such as Iowa, South Dakota, Indiana, and Illinois have a PRRSV percentage of positive submissions above the expected. For enteric coronaviruses, PEDV and PDCoV positivity continued to decrease during April, achieving low levels of positivity. However, in the state-level monitoring, the overall positivity continues above the expected for PEDV in Kansas and PDCoV in Minnesota and Missouri. PCV3 substantially increased positivity for the sow farm category, where 63% of submissions were positive. At the ISU-VDL, there were consecutive alarms of the increased number of confirmed diagnoses for PRRSV in tissue cases. Podcast hosts talked with Dr. Cameron Schmitt (Pipestone) about Influenza A virus monitoring and control strategies.

[VIEW REPORT](#)

GLOBAL

In the May report, read about new African swine fever outbreaks in Italy triggering the expansion of restriction zones I and II in Parma province and raising concern regarding the international markets' response. The first report of ASF in domestic pigs in Bulgaria since early 2022 is detailed. Learn about Crimean-Congo Hemorrhagic Fever; a recent report presents evidence of seropositivity in wild boar and Iberian pigs. Classical swine fever has been confirmed in Eastern Russia, the first report of the disease since August 2020. Physical border checks are implemented in the United Kingdom for EU-imported, medium-risk animal products. Days before new biosecurity checks on EU imports were set to begin, over 3.4 tonnes of illegal meat were seized at the Port of Dover.

[VIEW REPORT](#)