Antimicrobial susceptibility of *Actinobacillus pleuropneumoniae, Bordetella bronchiseptica, Pasteurella multocida,* and *Streptococcus suis* isolated from diseased pigs in the United States and Canada, 2016 to 2020

Michael T. Sweeney, MS; Lacie A. Gunnett, BS; Dipu Mohan Kumar, MVSc, PhD; Bryce L. Lunt, PhD; Lucina Galina Pantoja, DVM, PhD; Donald Bade, BS; Chandra Machin, BS

Summary

Objective: To report the *in vitro* susceptibility to veterinary antimicrobials of *Actinobacillus pleuropneumoniae, Bordetella bronchiseptica, Pasteurella multocida*, and *Streptococcus suis* isolated from diseased pigs in the United States and Canada from 2016 to 2020.

Materials and methods: *In vitro* broth microdilution susceptibility testing for minimal inhibitory concentration values were performed using ten antimicrobials (ampicillin, ceftiofur, danofloxacin, enrofloxacin, florfenicol, penicillin, tetracycline, tilmicosin, trimethoprim-sulfamethoxazole, and tulathromycin) with *A pleuropneumoniae* (n = 250), *B bronchiseptica* (n = 602), *P multocida* (n = 874), and *S suis* (n = 1223) following methods and susceptibility breakpoints approved by the Clinical and Laboratory Standards Institute.

Results: *Actinobacillus pleuropneumoniae* isolates were 100% susceptible to ceftiofur, florfenicol, and tulathromycin and *P multocida* isolates were 100% susceptible to ceftiofur. High rates of susceptibility (95% to > 99%) were observed for *A pleuropneumoniae* to tilmicosin; for *P multocida* to ampicillin, enrofloxacin, florfenicol, penicillin, tilmicosin, and tulathromycin; for *S suis* to ampicillin and florfenicol; and for *B bronchiseptica* to tulathromycin. Tetracycline exhibited low susceptibility rates against *A pleuropneumoniae* (0% to 10.6%), *P multocida* (23.2% to 38.2%), and *S suis* (0.8% to 2.1%). No susceptibility of *B bronchiseptica* to ampicillin (0%) and low rates of susceptibility to florfenicol (3.9% to 15.2%) were also observed.

Implications: Under the conditions of this study, the predominant pathogens associated with swine respiratory disease in the United States and Canada, *A pleuropneumoniae, B bronchiseptica, P multocida,* and *S suis* collected during 2016 to 2020, display high rates of susceptibility to most veterinary antimicrobials.

Keywords: swine, surveillance, antimicrobial susceptibility, respiratory disease

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Resumen - Susceptibilidad antimicrobiana de *Actinobacillus pleuropneumoniae, Bordetella bronchiseptica, Pasteurella multocida,* y *Streptococcus suis* aislados de cerdos enfermos en los Estados Unidos y Canadá, 2016 a 2020

Objetivo: Reportar la susceptibilidad *in vitro* a los antimicrobianos veterinarios de *Actinobacillus pleuropneumoniae*, *Bordetella bronchiseptica*, *Pasteurella multocida*, y *Streptococcus suis* aislados de cerdos enfermos en los Estados Unidos y Canadá de 2016 a 2020.

Materiales y métodos: Se realizaron pruebas de susceptibilidad por microdilución en caldo *in vitro* para valores de concentración inhibitoria mínima utilizando diez antimicrobianos (ampicilina, ceftiofur, danofloxacina, enrofloxacina, florfenicol, penicilina, tetraciclina, tilmicosina, trimetoprim-sulfametoxazol, y tulatromicina) con *A pleuropneumoniae* (n = 250), *B bronchiseptica* (n = 602), *P multocida* (n = 874), y *S suis* (n = 1223) siguiendo métodos y puntos de corte de susceptibilidad aprobados por el Instituto de Estándares Clínicos y de Laboratorio.

Resultados: Los aislados de *A pleuropneumoniae* fueron 100% sensibles a ceftiofur, florfenicol, y tulatromicina y

MTS, LAG, DMK, BLL: Zoetis, Kalamazoo, Michigan.

LGP: Zoetis, Parsippany, New Jersey.

DB, CM: Microbial Research, Inc, Fort Collins, Colorado.

Corresponding author: Michael T. Sweeney, Global Therapeutics, Zoetis, 333 Portage St, Kalamazoo, MI 49007; Tel: 269-359-9533; Email: **michael.t.sweeney@zoetis.com**.

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los aislados de *P multocida* fueron 100% sensibles a ceftiofur. Se observaron altos porcentajes de susceptibilidad (95% a > 99%) de *A pleuropneumoniae* a la tilmicosina; para *P multocida* a ampicilina, enrofloxacina, florfenicol, penicilina, tilmicosina, y tulatromicina; para *S suis* a ampicilina y florfenicol; y para *B bronchiseptica* a tulatromicina. La tetraciclina mostró bajos porcentajes de susceptibilidad frente a *A pleuropneumoniae* (0% a 10.6%), *P multocida* (23.2% a 38.2%), y *S suis* (0.8% a 2.1%). No se observó susceptibilidad de *B bronchiseptica* a ampicilina (0%), y también se observaron bajos porcentajes de susceptibilidad a florfenicol (3.9% a 15.2%).

Implicaciones: Bajo las condiciones de este estudio, los patógenos predominantes asociados con la enfermedad respiratoria porcina en los Estados Unidos y Canadá, *A pleuropneumoniae*, *B bronchiseptica*, *P multocida*, y *S suis* recolectados durante 2016 a 2020, muestran altos porcentajes de susceptibilidad a la mayoría de los antimicrobianos.

Résumé - Sensibilité aux antimicrobiens d'*Actinobacillus pleuropneumoniae, Bordetella bronchiseptica, Pasteurella multocida*, et *Streptococcus suis* isolés de porcs malades aux États-Unis et au Canada, de 2016 à 2020

Objectif: Rapporter la sensibilité *in vitro* aux antimicrobiens vétérinaires d'*Actinobacillus pleuropneumoniae*, *Bordetella bronchiseptica*, *Pasteurella multocida*, et *Streptococcus suis* isolés chez des porcs malades aux États-Unis et au Canada de 2016 à 2020.

Matériels et méthodes: Des tests de sensibilité par microdilution en bouillon *in vitro* pour les valeurs de concentration minimales inhibitrices ont été effectués à l'aide de dix antimicrobiens (ampicilline, ceftiofur, danofloxacine, enrofloxacine, florfénicol, pénicilline, tétracycline, tilmicosine, triméthoprime-sulfaméthoxazole, et tulathromycine) avec *A pleuropneumoniae* (n = 250), *B bronchiseptica* (n = 602), *P multocida* (n = 874), et *S suis* (n = 1223) selon les méthodes et les seuils de sensibilité approuvés par le Clinical and Laboratory Standards Institute.

Résultats: Les isolats d'*A pleuropneumoniae* étaient sensibles à 100% au ceftiofur, au florfénicol, et à la tulathromycine, et les isolats de *P multocida* étaient sensibles à 100% au ceftiofur. Des taux élevés de sensibilité (95% à > 99%) ont été observés pour *A pleuropneumoniae* à la tilmicosine; pour *P multocida* à l'ampicilline, l'enrofloxacine, le florfénicol, la pénicilline, la tilmicosine, et la tulathromycine; pour *S suis* à l'ampicilline et au florfénicol; et pour *B bronchiseptica* à la tulathromycine. La tétracycline présentait de faibles taux de sensibilité contre *A pleuropneumoniae* (0% à 10.6%), *P multocida* (23.2% à 38.2%), et *S suis* (0.8% à 2.1%). Aucune sensibilité de *B bronchiseptica* à l'ampicilline (0%) et de faibles taux de sensibilité au florfénicol (3.9% à 15.2%) ont également été observés.

Implications: Dans les conditions de cette étude, les agents pathogènes prédominants associés aux maladies respiratoires porcines aux États-Unis et au Canada, *A pleuropneumoniae*, *B bronchiseptica*, *P multocida*, et *S suis* recueillis de 2016 à 2020, affichent des taux élevés de sensibilité à la plupart des antimicrobiens.

Antimicrobials are critical to treat, control, and prevent disease in swine and other food animals. Responsible and timely antibiotic intervention is vital in controlling and mitigating disease incidence and spread, such as in swine respiratory disease (SRD) complex, which can endanger herd health and a sustainable food supply resulting in economic and commercial loss.[1] Of all the diseases that affect growing and finishing pigs, SRD is the most economically important as it is highly prevalent among indoor production facilities and can be difficult to treat and control. The treatment and control of SRD requires an understanding of the complexities and interaction between the organisms that are present as well as management of the environment in which the pigs are raised.[2] Primary pathogens for SRD complex may include *Mycoplasma hyopneumoniae*, *Actinobacillus pleuropneumoniae*, and *Bordetella bronchiseptica*, as well as viral agents. Common secondary pathogens include *Pasteurella multocida*, *Streptococcus suis*, *Glaesserella parasuis*, *Actinobacillus suis*, and *Salmonella* Choleraesuis. These primary and secondary multi-etiologic pathogens act together to increase the severity and duration of SRD.[3]

Antimicrobial surveillance among veterinary bacterial pathogens obtained from clinical specimens provides a platform from which to detect emergence of resistance in animal populations. While veterinary diagnostic laboratories throughout North America and Europe provide important antimicrobial susceptibility information for clinical isolates submitted by the attending veterinarian or animal caretaker, the susceptibility results are not typically examined. Few surveillance programs monitor susceptibility in swine pathogens nationally or internationally.[4-6] Portis et al[4] reported minimal inhibitory concentration (MIC) values for 7 antimicrobials against *A pleuropneumoniae*, *P multocida*, and *S suis* isolated from diseased swine in the United States and Canada over a 10-year period (2001-2010) and concluded that most isolates showed high rates of susceptibility to all antimicrobials tested. Additionally, Sweeney et al[5] reported MIC values for 10 antimicrobials against *A pleuropneumoniae*, *B bronchiseptica*, *P multocida*, and *S suis* isolated from diseased swine in the United States and Canada over a 5-year period (2011-2015) and concluded that most isolates showed high rates of susceptibility to all antimicrobials tested except tetracycline.

Continuing this surveillance program, we report the percentages of *A pleuropneumoniae*, *B bronchiseptica*, *P multocida*, and *S suis* pathogens isolated from swine in the United States and Canada that were susceptible to the veterinary antimicrobials ampicillin, ceftiofur, danofloxacin, enrofloxacin, florfenicol, penicillin, tetracycline, tilmicosin, trimethoprim-sulfamethoxazole (TMP-SMX), and tulathromycin. This paper presents the findings of the most contemporaneous 5-year surveillance period on SRD pathogens collected in North America from 2016 to 2020.

Animal care and use

Diagnostic submission data from clinical submissions were used in this study, therefore no animal use protocol was required.

Materials and methods

Laboratory participants and isolate characterization

Veterinary diagnostic laboratories from the United States and Canada participated in this surveillance study. The regions from which isolates were obtained are shown in Table 1.

Table 1: Origin and number of bacterial isolates per year by region for a 5-year study (2016-2020) of antimicrobial susceptibility of *Actinobacillus pleuropneumoniae*, *Bordetella bronchiseptica*, *Pasteurella multocida*, and *Streptococcus suis* from pigs in the United States and Canada*

Region and Year	2016	2017	2018	2019	2020	Total
A pleuropneumoniae						
Canada	22	10	6	2	0	40
Northeast	2	2	0	3	1	8
Midwest	30	28	30	27	32	147
South	8	5	6	7	4	30
West	1	6	5	9	4	25
Total	**63**	**51**	**47**	**48**	**41**	**250**
B bronchiseptica						
Canada	34	36	24	32	32	158
Northeast	2	3	4	5	7	21
Midwest	105	88	71	65	56	385
South	4	6	3	5	3	21
West	0	3	4	5	5	17
Total	**145**	**136**	**106**	**112**	**103**	**602**
P multocida						
Canada	53	66	32	59	49	259
Northeast	5	4	2	2	6	19
Midwest	119	124	100	98	78	519
South	9	8	8	3	7	35
West	8	13	5	12	4	42
Total	**194**	**215**	**147**	**174**	**144**	**874**
S suis						
Canada	86	87	56	74	83	386
Northeast	9	5	6	13	10	43
Midwest	155	155	138	132	130	710
South	8	9	13	8	6	44
West	6	11	7	11	5	40
Total	**264**	**267**	**220**	**238**	**234**	**1223**

* Provinces and states that submitted isolates originating from within the regions include Canada (Alberta, British Columbia, Manitoba, Nova Scotia, Ontario, Prince Edward Island, Quebec, and Saskatchewan); Northeast (Connecticut, Delaware, Maine, Maryland, Massachusetts, New Hampshire, New Jersey, New York, Pennsylvania, Rhode Island, and Vermont); Midwest (Illinois, Indiana, Iowa, Kansas, Michigan, Minnesota, Missouri, Nebraska, North Dakota, Ohio, South Dakota, and Wisconsin); South (Alabama, Arkansas, Florida, Georgia, Kentucky, Louisiana, Mississippi, North Carolina, Oklahoma, South Carolina, Tennessee, Texas, Virginia, and West Virginia); West (Arizona, California, Colorado, Hawaii, Idaho, Montana, Nevada, New Mexico, Oregon, Utah, Washington, and Wyoming).

All *A pleuropneumoniae*, *B bronchiseptica*, *P multocida*, and *S suis* isolates were recovered from diseased or dead pigs. Laboratories selected isolates based on their own protocols and were requested not to use antimicrobial susceptibility as a criterion for selection. Laboratories were also requested to submit no more than eight isolates per quarter year to prevent over-representation from any one geographic area. Each participating laboratory was also requested to send no more than one isolate of each bacterial species from a herd each quarter year to prevent the over-representation of bacterial clones from one region.[4,5]

Bacterial isolates were identified to the species level by each participating laboratory before shipment to a central laboratory for susceptibility testing and the species identifications were confirmed at Zoetis (Kalamazoo, Michigan) using Matrix Assisted Laser Desorption Ionization Time-of-Flight Mass Spectrometry (MALDI-TOF MS; Bruker). All isolates were stored in approximately 1.0 mL trypticase soy broth (BD Biosciences) supplemented with 10% glycerol and stored at approximately -70°C until tested.

Determination of MIC values

In vitro susceptibility data were generated annually by performing MIC testing at a central laboratory (Microbial Research Inc) and followed Clinical and Laboratory Standards Institute (CLSI) standardized methods and quality control guidelines during susceptibility testing.[7] The MIC values for all isolates were determined using a dehydrated broth microdilution system (Sensititre System; Thermo Fisher Scientific) which conforms to CLSI standards for testing of veterinary pathogens.[7] Additionally, the central laboratory followed all manufacturer instructions for quality assurance and quality control when using the Sensititre plates. Direct colony suspensions were used and prepared at a final bacterial concentration of approximately 5×10^5 colony forming units/mL. Custom-made 96-well microtiter panels included serial doubling dilutions of the antimicrobials ampicillin, ceftiofur, danofloxacin, enrofloxacin, florfenicol, penicillin, tetracycline, tilmicosin, TMP-SMX, and tulathromycin. All concentration ranges for antimicrobials were chosen to encompass appropriate quality control ranges and published clinical breakpoints, and appropriate quality-control organisms were included with each testing date.[8]

Results

Quality control

The quality control organisms used in this study included *Escherichia coli* ATCC 25922, *Pseudomonas aeruginosa* ATCC 27853, *Enterococcus faecalis* ATCC 29212, *Staphylococcus aureus* ATCC 29213, *Streptococcus pneumoniae* ATCC 49619, and *A pleuropneumoniae* ATCC 27090. Although not shown for this study, MIC values for all appropriate quality control organisms were acceptable when all study isolates were tested against antimicrobials on each date of testing.

A pleuropneumoniae

The MIC distributions, MIC_{50} values, and MIC_{90} values for 10 antimicrobials tested against *A pleuropneumoniae* (n = 250) are reported in Table 2. The CLSI has established clinical breakpoints for *A pleuropneumoniae* against ampicillin, ceftiofur, enrofloxacin, florfenicol, tetracycline, tilmicosin, and tulathromycin. *Actinobacillus pleuropneumoniae* susceptibility to ampicillin increased overall from 85.7% in 2016 (susceptible breakpoint ≤ 0.5 µg/mL) to 97.6% in 2020, but decreased to 83% in 2018. The percentage of isolates susceptible to ceftiofur over the 5-year study period was 100% (susceptible breakpoint ≤ 2 µg/mL) and the MIC_{90} values were ≤ 0.03 µg/mL. The percentage of susceptibility to enrofloxacin was very high (100% in 2016 and 2018-2020; breakpoint ≤ 0.25 µg/mL), and the MIC_{90} values over the study period were 0.06 to 1 µg/mL; florfenicol was 100% susceptible (breakpoint ≤ 2 µg/mL), with MIC_{90} values at 0.5 µg/mL. *Actinobacillus pleuropneumoniae* susceptibility to tetracycline (breakpoint ≤ 0.5 µg/mL) was very low, with a susceptibility range of 0% to 10.6%, while tilmicosin susceptibility (breakpoint ≤ 16 µg/mL) ranged from 96.8% in 2016 to 100% in 2020. There was 100% percent susceptibility of *A pleuropneumoniae* to tulathromycin (breakpoint ≤ 64 µg/mL) and MIC_{90} values ranged from 32 to 64 µg/mL. While CLSI-approved susceptible breakpoints have not been established for danofloxacin, penicillin, or TMP-SMX, the MIC_{90} values were determined as 0.06 to 1 µg/mL, 0.5 to ≥ 32 µg/mL, and ≤ 0.06 to 0.12 µg/mL, respectively, from 2016 to 2020.

B bronchiseptica

The MIC distributions, MIC_{50} values, and MIC_{90} values for 10 antimicrobials tested against *B bronchiseptica* (n = 602) are reported in Table 3. The CLSI has established clinical breakpoints for *B bronchiseptica* against ampicillin, florfenicol, and tulathromycin. *Bordetella bronchiseptica* isolates in this study had no *in vitro* activity to ampicillin (0% susceptibility; susceptible breakpoint ≤ 0.5 µg/mL) in which MIC_{90} values were 8 to ≥ 16 µg/mL. *Bordetella bronchiseptica* susceptibility to florfenicol (breakpoint ≤ 2 µg/mL) was low and ranged from 3.9% to 15.2% in which MIC_{90} values were 4 to 8 µg/mL over the 5-year study period. The percentage of *B bronchiseptica* susceptible to tulathromycin was 99.2% to 100% (breakpoint ≤ 16 µg/mL) and the MIC_{90} value was 8 µg/mL. While CLSI-approved susceptible breakpoints were not available, the MIC_{90} values were determined as ≥ 8 µg/mL for ceftiofur, 1 µg/mL for danofloxacin, 1 µg/mL for enrofloxacin, ≥ 32 µg/mL for penicillin, 1 to 2 µg/mL for tetracycline, 32 to ≥ 64 µg/mL for tilmicosin, and 8 to ≥ 16 µg/mL for TMP-SMX.

P multocida

The MIC distributions, MIC_{50} values, and MIC_{90} values for 10 antimicrobials tested against *P multocida* (n = 874) are reported in Table 4. The CLSI has established clinical breakpoints for *P multocida* against ampicillin, ceftiofur, enrofloxacin, florfenicol, penicillin, tetracycline, tilmicosin, and tulathromycin. *Pasteurella multocida* susceptibility to ampicillin was very high (95.5%-100%; susceptible breakpoint ≤ 0.5 µg/mL) from 2016 to 2020, while the percentage of susceptibility to ceftiofur was 100% (breakpoint ≤ 2 µg/mL), with MIC_{90} values at ≤ 0.03 µg/mL. *Pasteurella multocida* was 100% susceptible to enrofloxacin in 2016 and 2019 to 2020 (breakpoint ≤ 0.25 µg/mL) with MIC_{90} values at 0.03 µg/mL, and *P multocida* isolates were highly susceptible to florfenicol (> 98%; breakpoint ≤ 2 µg/mL), penicillin (97.7%-100%; breakpoint ≤ 0.25/per mL), tilmicosin (97.6%-100%; breakpoint ≤ 16 µg/mL), and tulathromycin (99.5%-100%; breakpoint ≤ 16 µg/mL) in which the tulathromycin MIC_{90} value ranged from 2 to 4 µg/mL. Clinical and Laboratory Standards Institute-approved susceptible clinical breakpoints have not been established for danofloxacin or TMP-SMX, but MIC_{90} values were determined as 0.03 µg/mL and 0.12 µg/mL, respectively.

S suis

The MIC distributions, MIC_{50} values, and MIC_{90} values for 10 antimicrobials tested against *S suis* (n = 1223) are reported in Table 5. The CLSI has established clinical breakpoints for *S suis* against ampicillin, ceftiofur, enrofloxacin, florfenicol, penicillin, and tetracycline.

Table 2: Summary of MIC values and frequency distributions for 10 antimicrobials tested with *Actinobacillus pleuropneumoniae* (n = 250) isolated from swine in the United States and Canada from 2016 to 2020*

Year	Isolates, No.	MIC_{50} (µg/mL)	MIC_{90} (µg/mL)	S, %	MIC frequency distribution (% of isolates)								
Ampicillin					**≤ 0.06**	**0.12**	**0.25**	**0.5**	**1**	**2**	**4**	**8**	**≥ 16**
2016	63	0.12	≥ 16	85.7	17.5	42.8	23.8	1.6	0	0	0	1.6	12.7
2017	51	0.25	0.25	92.1	3.9	35.3	51	1.9	0	0	0	0	7.8
2018	47	0.12	≥ 16	83	12.7	44.7	21.3	4.3	0	0	0	2.1	14.9
2019	48	0.25	0.25	97.9	2.1	43.7	52.1	0	0	0	0	0	2.1
2020	41	0.12	0.25	97.6	0	53.6	44	0	0	0	0	0	2.4
Ceftiofur					**≤ 0.03**	**0.06**	**0.12**	**0.25**	**0.5**	**1**	**2**	**4**	**≥ 8**
2016	63	≤ 0.03	≤ 0.03	100	95.2	4.8	0	0	0	0	0	0	0
2017	51	≤ 0.03	≤ 0.03	100	98	2	0	0	0	0	0	0	0
2018	47	≤ 0.03	≤ 0.03	100	97.8	2.8	0	0	0	0	0	0	0
2019	48	≤ 0.03	≤ 0.03	100	95.8	4.2	0	0	0	0	0	0	0
2020	41	≤ 0.03	≤ 0.03	100	100	0	0	0	0	0	0	0	0
Danofloxacin					**≤ 0.016**	**0.03**	**0.06**	**0.12**	**0.25**	**0.5**	**1**	**2**	**≥ 4**
2016	63	0.12	0.25	NA	0	0	36.6	50.7	7.9	3.2	1.6	0	0
2017	51	0.12	1	NA	0	0	29.4	56.9	0	0	13.7	0	0
2018	47	0.06	0.12	NA	0	2.1	74.6	17	2.1	4.2	0	0	0
2019	48	0.06	0.12	NA	0	2.1	60.4	37.5	0	0	0	0	0
2020	41	0.06	0.06	NA	0	24.4	70.7	4.9	0	0	0	0	0
Enrofloxacin					**≤ 0.008**	**0.016**	**0.03**	**0.06**	**0.12**	**0.25**	**0.5**	**1**	**≥ 2**
2016	63	0.06	0.12	100	0	15.9	71.4	6.3	4.8	1.6	0	0	0
2017	51	0.06	1	82.3	0	17.6	62.8	2	0	0	17.6	0	0
2018	47	0.03	0.06	100	6.3	51.3	36.1	2.1	2.1	2.1	0	0	0
2019	48	0.06	0.06	100	0	0	35.4	60.4	4.2	0	0	0	0
2020	41	0.03	0.06	100	0	7.4	56	36.6	0	0	0	0	0
Florfenicol					**≤ 0.06**	**0.12**	**0.25**	**0.5**	**1**	**2**	**4**	**8**	**≥ 16**
2016	63	0.5	0.5	100	0	1.6	47.6	49.2	1.6	0	0	0	0
2017	51	0.25	0.5	100	2	2	74.5	21.5	0	0	0	0	0
2018	47	0.25	0.5	100	0	4.3	74.4	21.3	0	0	0	0	0
2019	48	0.5	0.5	100	0	0	18.8	81.2	0	0	0	0	0
2020	41	0.5	0.5	100	0	0	22	75.6	2.4	0	0	0	0
Penicillin					**≤ 0.12**	**0.25**	**0.5**	**1**	**2**	**4**	**8**	**16**	**≥ 32**
2016	63	0.25	≥ 32	NA	14.3	44.4	25.4	1.6	0	0	0	0	14.3
2017	51	0.5	1	NA	9.8	15.6	51.2	15.6	0	0	0	0	7.8
2018	47	0.5	≥ 32	NA	12.8	31.9	34.1	4.2	0	0	0	4.2	12.8
2019	48	0.5	1	NA	2.1	25	60.4	10.4	0	0	0	0	2.1
2020	41	0.25	0.5	NA	7.2	51.2	36.8	2.4	0	0	0	0	2.4

Table 2: Continued

Year	Isolates, No.	MIC_{50} (µg/mL)	MIC_{90} (µg/mL)	S, %	MIC frequency distribution (% of isolates)								
Tetracycline					**≤ 0.25**	**0.5**	**1**	**2**	**4**	**8**	**≥ 16**		
2016	63	≥ 16	≥ 16	3.2	0	3.2	17.5	4.7	0	22.3	52.3		
2017	51	≥ 16	≥ 16	3.9	0	3.9	7.8	0	0	25.6	62.7		
2018	47	≥ 16	≥ 16	10.6	0	10.6	14.9	0	4.2	16.8	53.5		
2019	48	≥ 16	≥ 16	0	0	0	29.2	6.2	0	33.3	31.3		
2020	41	8	≥ 16	7.3	0	7.3	17.1	0	0	31.7	43.9		
Tilmicosin					**≤ 0.25**	**0.5**	**1**	**2**	**4**	**8**	**16**	**32**	**≥ 64**
2016	63	8	16	96.8	0	0	0	0	1.1	49.7	46	0	3.2
2017	51	16	16	98	0	0	0	4	0	43.1	50.9	0	2
2018	47	8	16	97.9	0	0	0	0	2.1	44.7	51.1	2.1	0
2019	48	16	16	97.9	0	0	0	0	6.3	29.1	62.5	0	2.1
2020	41	4	8	100	0	0	2.4	0	83	14.6	0	0	0
Trimethoprim-Sulfamethoxazole					**≤ 0.06**	**0.125**	**0.25**	**0.5**	**1**	**2**	**4**	**8**	**≥ 16**
2016	63	≤ 0.06	0.12	NA	80.1	18.3	0	1.6	0	0	0	0	0
2017	51	≤ 0.06	≤ 0.06	NA	90.2	9.8	0	0	0	0	0	0	0
2018	47	≤ 0.06	≤ 0.06	NA	97.8	2.2	0	0	0	0	0	0	0
2019	48	≤ 0.06	≤ 0.06	NA	95.8	4.2	0	0	0	0	0	0	0
2020	41	≤ 0.06	≤ 0.06	NA	92.7	7.3	0	0	0	0	0	0	0
Tulathromycin					**≤ 0.5**	**1**	**2**	**4**	**8**	**16**	**32**	**64**	**≥ 128**
2016	63	32	32	100	0	0	0	0	3.2	20.6	69.8	6.4	0
2017	51	32	32	100	0	0	0	1.9	1.9	17.9	74.5	3.8	0
2018	47	32	64	100	0	0	0	0	2.1	15	63.8	19.1	0
2019	48	32	64	100	0	0	0	0	4.2	20.8	54.2	20.8	0
2020	41	16	32	100	0	0	0	0	12.2	75.6	12.2	0	0

* Vertical red lines indicate the CLSI-approved breakpoint for susceptible, intermediate, and resistant in that swine respiratory disease pathogen; numbers in the lowest concentration of the tested antibacterial drug range represent the percentage of isolates that had MICs less than or equal to the lowest drug concentration tested per year, while numbers above the highest antibacterial drug concentration represent the percentage of isolates that had MICs greater than the highest drug concentration tested that year. Percent MIC frequency rows may not add to 100% due to rounding.

MIC = minimal inhibitory concentration; MIC_{50} = antibacterial drug concentration that inhibits 50% of the bacterial population; MIC_{90} = antibacterial drug concentration that inhibits 90% of the bacterial population; S = isolates that are susceptible to the antibacterial drug using CLSI criteria; NA = not applicable since there are no CLSI-approved clinical breakpoints for susceptibility in that swine respiratory disease pathogen; CLSI = Clinical and Laboratory Standards Institute.

Table 3: Summary of MIC values and frequency distributions for 10 antimicrobials tested with *Bordetella bronchiseptica* (n = 602) isolated from swine in the United States and Canada from 2016 to 2020*

Year	Isolates, No.	MIC_{50} (µg/mL)	MIC_{90} (µg/mL)	S, %	MIC frequency distribution (% of isolates)								
Ampicillin					**≤ 0.06**	**0.12**	**0.25**	**0.5**	**1**	**2**	**4**	**8**	**≥ 16**
2016	145	16	≥ 16	0	0	0	0	0	0	0	0.7	2.1	97.2
2017	136	≥ 16	≥ 16	0	0	0	0	0	0	0	2.2	0	97.8
2018	106	16	≥ 16	0	0	0	0	0	0	1.9	3.9	1.8	93.4
2019	112	16	≥ 16	0	0	0	0	0	0	0	10.7	0	89.3
2020	103	8	8	0	0	0	0	0	0	0.9	3.9	89.3	5.9
Ceftiofur					**≤ 0.03**	**0.06**	**0.12**	**0.25**	**0.5**	**1**	**2**	**4**	**≥ 8**
2016	145	≥ 8	≥ 8	NA	0	0	0	0	0	0	0	0	100
2017	136	≥ 8	≥ 8	NA	0	0	0	0	0	0	0	0	100
2018	106	≥ 8	≥ 8	NA	0	0	0	0	0	0	0	0	100
2019	112	≥ 8	≥ 8	NA	0	0	0	0	0	0	0	0	100
2020	103	≥ 8	≥ 8	NA	0	0	0	0	0	0	0	0	100
Danofloxacin					**≤ 0.016**	**0.03**	**0.06**	**0.12**	**0.25**	**0.5**	**1**	**2**	**≥ 4**
2016	145	1	1	NA	0	0	0	0	1.4	5.6	90.9	0.7	1.4
2017	136	1	1	NA	0	0	0	0	0.7	2.1	96.5	0.7	0
2018	106	1	1	NA	0	0	0	0.9	3.7	16.2	74.5	4.7	0
2019	112	1	1	NA	0	0	0	0.9	0.9	4.5	90.1	0	3.6
2020	103	1	1	NA	0	0	0	0	0.9	8.7	89.5	0	0.9
Enrofloxacin					**≤ 0.008**	**0.016**	**0.03**	**0.06**	**0.12**	**0.25**	**0.5**	**1**	**≥ 2**
2016	145	0.5	1	NA	0	0	0	0	0	2.7	63.6	31.7	2
2017	136	1	1	NA	0	0	0	0	0	2.2	30	67.8	0
2018	106	0.5	1	NA	0	0	0	0	4.7	0	59.4	35	0.9
2019	112	0.5	1	NA	0	0	0	0	1.8	0	56.2	38.4	3.6
2020	103	1	1	NA	0	0	0	0	0.9	0	88.5	9.7	0.9
Florfenicol					**≤ 0.06**	**0.12**	**0.25**	**0.5**	**1**	**2**	**4**	**8**	**≥ 16**
2016	145	4	4	6.9	0	0	0	0	0	6.9	87.6	5.5	0
2017	136	4	8	5.1	0	0	0	0	0.7	4.4	83.1	11.8	0
2018	106	4	8	9.4	0	0	0	0	2.8	6.6	75.5	15.1	0
2019	112	4	8	15.2	0	0	0	0	0.9	14.3	48.2	20.5	16.1
2020	103	4	4	3.9	0	0	0	0	0	3.9	92.2	3.9	0
Penicillin					**≤ 0.12**	**0.25**	**0.5**	**1**	**2**	**4**	**8**	**16**	**≥ 32**
2016	145	≥ 32	≥ 32	NA	0	0	0	0	0	0	0	0	100
2017	136	≥ 32	≥ 32	NA	0	0	0	0	0	0	0	0	100
2018	106	≥ 32	≥ 32	NA	0	0	0	0	0	0	0	0.9	99.1
2019	112	≥ 32	≥ 32	NA	0	0	0	0	0	0	0	0	100
2020	103	≥ 32	≥ 32	NA	0	0	0	0	0	0	0	0	100

Table 3: Continued

Year	Isolates, No.	MIC_{50} (µg/mL)	MIC_{90} (µg/mL)	S, %	MIC frequency distribution (% of isolates)								
Tetracycline					**≤ 0.25**	**0.5**	**1**	**2**	**4**	**8**	**≥ 16**		
2016	145	1	1	NA	0	45.5	44.8	6.3	3.4	0	0		
2017	136	1	2	NA	0	13.2	74.3	3.7	8.1	0	0.7		
2018	106	0.5	1	NA	0.9	49	40.6	3.8	3.8	0	1.9		
2019	112	0.5	2	NA	1.8	58	28.6	5.3	4.5	0	1.8		
2020	103	0.5	2	NA	0	73.8	11.7	4.8	2.9	0	6.8		
Tilmicosin					**≤ 0.25**	**0.5**	**1**	**2**	**4**	**8**	**16**	**32**	**≥ 64**
2016	145	32	≥ 64	NA	0	0	0	0	0	2.8	11	62.7	23.5
2017	136	32	≥ 64	NA	0	0	0	0	0.7	0.7	5.9	81.6	11.1
2018	106	32	≥ 64	NA	0	0	0.9	0	3.7	0	16	63.4	16
2019	112	32	32	NA	0	0	0	0	0.9	0.9	17	73.2	8
2020	103	16	32	NA	0	0	0	0.9	0	18.4	68	11.8	0.9
Trimethoprim-Sulfamethoxazole					**≤ 0.06**	**0.125**	**0.25**	**0.5**	**1**	**2**	**4**	**8**	**≥ 16**
2016	145	8	8	NA	6.2	1.4	0.7	0	0	5.5	18.6	65.5	2.1
2017	136	8	8	NA	5.9	0	0	0	0.7	0.7	8.9	77.9	5.9
2018	106	8	≥ 16	NA	4.7	0	0	0	2.8	1.9	10.4	64.1	16.1
2019	112	8	8	NA	5.4	0	0	0.9	0.9	1.8	33.8	54.5	2.7
2020	103	8	8	NA	6.8	0	0	0	0	0	32	57.3	3.9
Tulathromycin					**≤ 0.5**	**1**	**2**	**4**	**8**	**16**	**32**	**64**	**≥ 128**
2016	145	8	8	100	0	0	4.1	26.2	63.5	6.2	0	0	0
2017	136	8	8	99.2	0	0.8	1.6	19.5	76.5	0.8	0.8	0	0
2018	106	8	8	100	1.8	1.8	0.9	33.2	62.3	0	0	0	0
2019	112	8	8	100	0.9	0.9	0	32.1	63.4	2.7	0	0	0
2020	103	8	8	100	0	0.9	0	41.9	56.3	0.9	0	0	0

* Vertical red lines indicate the CLSI-approved breakpoint for susceptible, intermediate, and resistant in that swine respiratory disease pathogen; numbers in the lowest concentration of the tested antibacterial drug range represent the percentage of isolates that had MICs less than or equal to the lowest drug concentration tested per year, while numbers above the highest antibacterial drug concentration represent the percentage of isolates that had MICs greater than the highest drug concentration tested that year. Percent MIC frequency rows may not add to 100% due to rounding.

MIC = minimal inhibitory concentration; MIC_{50} = antibacterial drug concentration that inhibits 50% of the bacterial population; MIC_{90} = antibacterial drug concentration that inhibits 90% of the bacterial population; S = isolates that are susceptible to the antibacterial drug using CLSI criteria; NA = not applicable since there are no CLSI-approved clinical breakpoints for susceptibility in that swine respiratory disease pathogen; CLSI = Clinical and Laboratory Standards Institute.

Table 4: Summary of MIC values and frequency distributions for 10 antimicrobials tested with *Pasteurella multocida* (n = 874) isolated from swine in the United States and Canada from 2016 to 2020*

Year	Isolates, No.	MIC_{50} (µg/mL)	MIC_{90} (µg/mL)	S, %	MIC frequency distribution (% of isolates)								
Ampicillin					**≤ 0.06**	**0.12**	**0.25**	**0.5**	**1**	**2**	**4**	**8**	**≥ 16**
2016	194	0.12	0.12	99.5	36.1	61.3	2.1	0	0	0	0	0	0.5
2017	215	0.12	0.12	99.1	18.1	74.8	6.1	0	0	0	0.5	0	0.5
2018	147	0.12	0.12	100	42.8	55.8	1.4	0	0	0	0	0	0
2019	174	0.12	0.25	98.3	17.6	66.8	13.3	0.6	0	0	0	0	1.7
2020	144	0.12	0.12	97.9	49.3	45.8	2.8	0	0	0	0	0.7	1.4
Ceftiofur					**≤ 0.03**	**0.06**	**0.12**	**0.25**	**0.5**	**1**	**2**	**4**	**≥ 8**
2016	194	≤ 0.03	≤ 0.03	100	97.9	1.6	0.5	0	0	0	0	0	0
2017	215	≤ 0.03	≤ 0.03	100	100	0	0	0	0	0	0	0	0
2018	147	≤ 0.03	≤ 0.03	100	99.3	0.7	0	0	0	0	0	0	0
2019	174	≤ 0.03	≤ 0.03	100	96.6	2.2	0.6	0.6	0	0	0	0	0
2020	144	≤ 0.03	≤ 0.03	100	94.4	3.5	1.4	0.7	0	0	0	0	0
Danofloxacin					**≤ 0.016**	**0.03**	**0.06**	**0.12**	**0.25**	**0.5**	**1**	**2**	**≥ 4**
2016	194	0.03	0.03	NA	49	44.9	4.6	1	0.5	0	0	0	0
2017	215	0.03	0.03	NA	41.4	54.4	3.7	0	0	0.5	0	0	0
2018	147	≤ 0.016	0.03	NA	65.3	27.2	5.4	0.7	0.7	0.7	0	0	0
2019	174	≤ 0.016	0.03	NA	63.2	31	5.2	0.6	0	0	0	0	0
2020	144	≤ 0.016	0.03	NA	71.5	25.7	2.1	0.7	0	0	0	0	0
Enrofloxacin					**≤ 0.008**	**0.016**	**0.03**	**0.06**	**0.12**	**0.25**	**0.5**	**1**	**≥ 2**
2016	194	0.016	0.03	100	15.5	69	12.9	2.1	0.5	0	0	0	0
2017	215	0.016	0.03	99.5	11.6	65.6	21.5	1.4	0	0	0.5	0	0
2018	147	0.016	0.03	99.3	28.6	53.7	12.2	4.1	0	0.7	0.7	0	0
2019	174	0.016	0.03	100	16.1	63.2	16.7	4	0	0	0	0	0
2020	144	0.016	0.03	100	43	44.4	11.9	0	0.7	0	0	0	0
Florfenicol					**≤ 0.06**	**0.12**	**0.25**	**0.5**	**1**	**2**	**4**	**8**	**≥ 16**
2016	194	0.5	0.5	100	0	0	3	95.5	1.5	0	0	0	0
2017	215	0.5	0.5	100	0	0	0.9	94	5.1	0	0	0	0
2018	147	0.5	0.5	100	0	0	2.7	94.6	2.7	0	0	0	0
2019	174	0.5	0.5	98.9	0	0	2.9	93.7	2.3	0	0	1.1	0
2020	144	0.5	0.5	100	1.4	2.1	22.9	70.1	3.5	0	0	0	0
Penicillin					**≤ 0.12**	**0.25**	**0.5**	**1**	**2**	**4**	**8**	**16**	**≥ 32**
2016	194	≤ 0.12	≤ 0.12	98.9	97.9	1	0	0	0.5	0	0	0	0.5
2017	215	≤ 0.12	≤ 0.12	99.1	95.3	3.8	0	0	0	0.5	0	0	0.5
2018	147	≤ 0.12	≤ 0.12	100	100	0	0	0	0	0	0	0	0
2019	174	≤ 0.12	0.25	97.7	82.7	15	0.6	0	0	0	0	0	1.7
2020	144	≤ 0.12	≤ 0.12	97.9	96.5	1.4	0	0	0	0.7	0	0	1.4

Table 4: Continued

Year	Isolates, No.	MIC_{50} (µg/mL)	MIC_{90} (µg/mL)	S, %	MIC frequency distribution (% of isolates)								
Tetracycline					**≤ 0.25**	**0.5**	**1**	**2**	**4**	**8**	**≥ 16**		
2016	194	2	≥ 16	25.3	2.1	23.2	14.4	33.5	2.6	2.6	21.6		
2017	215	2	≥ 16	23.2	1.3	21.9	20.5	32.8	6.5	2.6	14.4		
2018	147	2	≥ 16	36.1	2.8	33.3	9.5	31.9	3.4	2.8	16.3		
2019	174	1	≥ 16	27	4.6	22.4	26.4	26.4	9.2	3	8		
2020	144	1	8	38.2	10.4	27.8	13.9	25.7	5.6	6.9	9.7		
Tilmicosin					**≤ 0.25**	**0.5**	**1**	**2**	**4**	**8**	**16**	**32**	**≥ 64**
2016	194	4	16	99	0	0.5	6.2	20	31.4	22.2	18.7	0.5	0.5
2017	215	4	16	98.5	0	0	1.5	18.6	30.7	25.6	22.1	0.5	1
2018	147	4	16	100	0.7	0	10.9	23.1	30.6	24.5	10.2	0	0
2019	174	4	16	97.6	0	0	4.4	20.7	29.9	30.4	12.2	1.2	1.2
2020	144	2	4	97.9	2.8	9	26.4	29.1	27.8	1.4	1.4	0.7	1.4
Trimethoprim-Sulfamethoxazole					**≤ 0.06**	**0.125**	**0.25**	**0.5**	**1**	**2**	**4**	**8**	**≥ 16**
2016	194	≤ 0.06	0.12	NA	67.5	25.8	4.6	0.5	0	0	0	0	1.6
2017	215	≤ 0.06	0.12	NA	76.3	20.1	1.3	0.5	0.9	0	0	0	0.9
2018	147	≤ 0.06	0.12	NA	78.9	17.7	2	0	0.7	0	0	0	0.7
2019	174	≤ 0.06	0.12	NA	89.1	8.6	2.3	0	0	0	0	0	0
2020	144	≤ 0.06	0.12	NA	81.2	11.8	4.2	0.7	0.7	0	0.7	0	0.7
Tulathromycin					**≤ 0.5**	**1**	**2**	**4**	**8**	**16**	**32**	**64**	**≥ 128**
2016	194	1	4	100	51.5	32	15.5	0.5	0.5	0	0	0	0
2017	215	1	4	99.5	21.4	30.7	37.7	9.2	0	0.5	0	0	0.5
2018	147	1	2	100	36	21.8	38.1	3.4	0.7	0	0	0	0
2019	174	2	2	100	47.1	47.1	5.8	0	0	0	0	0	0
2020	144	1	2	98.6	23.6	36.8	36.1	2.1	0	0	0	0	1.4

* Vertical red lines indicate the CLSI-approved breakpoint for susceptible, intermediate and resistant in that swine respiratory disease pathogen; numbers in the lowest concentration of the tested antibacterial drug range represent the percentage of isolates that had MICs less than or equal to the lowest drug concentration tested per year, while numbers above the highest antibacterial drug concentration represent the percentage of isolates that had MICs greater than the highest drug concentration tested that year. Percent MIC frequency rows may not add to 100% due to rounding.

MIC = minimal inhibitory concentration; MIC_{50} = antibacterial drug concentration that inhibits 50% of the bacterial population; MIC_{90} = antibacterial drug concentration that inhibits 90% of the bacterial population; S = isolates that are susceptible to the antibacterial drug using CLSI criteria; NA = not applicable since there are no CLSI-approved clinical breakpoints for susceptibility in that swine respiratory disease pathogen; CLSI = Clinical and Laboratory Standards Institute.

Table 5: Summary of MIC values and frequency distributions for 10 antimicrobials tested with *Streptococcus suis* (n = 1223) isolated from swine in the United States and Canada from 2016 to 2020*

Year	Isolates, No.	MIC_{50} (µg/mL)	MIC_{90} (µg/mL)	S, %	MIC frequency distribution (% of isolates)								
Ampicillin					**≤ 0.06**	**0.12**	**0.25**	**0.5**	**1**	**2**	**4**	**8**	**≥ 16**
2016	264	≤ 0.06	≤ 0.06	99.2	90.5	6	1.9	0.8	0.4	0	0	0.4	0
2017	267	≤ 0.06	0.12	97.8	87.6	6	3.4	0.8	0.4	1.2	0.4	0.4	0
2018	220	≤ 0.06	0.06	98.6	89.1	6.8	1.6	1.3	0.8	0	0.4	0	0
2019	238	≤ 0.06	≤ 0.06	99.2	83.6	10.5	3.8	1.3	0	0.8	0	0	0
2020	234	≤ 0.06	0.12	97.9	88	7.4	2.1	0.4	0.4	1.7	0	0	0
Ceftiofur					**≤ 0.03**	**0.06**	**0.12**	**0.25**	**0.5**	**1**	**2**	**4**	**≥ 8**
2016	264	0.12	2	95.5	5.3	33.3	29.5	5.7	7.6	8.4	5.7	1.5	3
2017	267	0.12	1	94.8	8.2	32.2	29.6	3.4	7.9	9.7	3.8	0.7	4.5
2018	220	0.12	1	97.7	2.3	34.5	27.3	8.6	12.3	8.6	4.1	0.9	1.4
2019	238	0.12	2	91.2	4.6	30.7	26.5	11.3	7.6	5.5	5	1.7	7.1
2020	234	0.06	2	93.2	5.1	44.9	13.3	10.7	7.7	7.7	3.8	1.7	5.1
Danofloxacin					**≤ 0.016**	**0.03**	**0.06**	**0.12**	**0.25**	**0.5**	**1**	**2**	**≥ 4**
2016	264	0.5	1	NA	0	0	0	3	13.3	47	34.1	1.5	1.1
2017	267	0.5	1	NA	0	0	0	0.4	12.4	43.8	39.3	1.9	2.2
2018	220	0.5	1	NA	0	0	0.8	2.3	16.4	51.4	26.8	0	2.3
2019	238	0.5	1	NA	0.4	0	0.4	2.4	18.9	53.4	22.9	0.4	1.2
2020	234	0.5	1	NA	0	0	0.4	0.8	15.4	48.7	31.1	1.6	2
Enrofloxacin					**≤ 0.008**	**0.016**	**0.03**	**0.06**	**0.12**	**0.25**	**0.5**	**1**	**≥ 2**
2016	264	0.5	1	89.4	0	0	0.4	0.4	5.3	25.7	57.6	8.7	1.9
2017	267	0.5	1	87.3	0	0	0	0	3	21	63.3	10.5	2.2
2018	220	0.5	0.5	92.7	0	0	0	0.9	5	28.6	58.2	5	2.3
2019	238	0.5	0.5	94.1	0	0.4	0.4	1.2	6.3	28.2	57.6	4.7	1.2
2020	234	0.5	1	89.3	0	0	0	0	3.8	32.9	52.6	7.7	3
Florfenicol					**≤ 0.06**	**0.12**	**0.25**	**0.5**	**1**	**2**	**4**	**8**	**≥ 16**
2016	264	2	2	97.7	0	0	0.4	1.5	23.5	72.3	1.1	0	1.1
2017	267	2	2	97.7	0	0	0	3.4	26.5	67.8	1.9	0	0.4
2018	220	2	2	96.4	0	0.4	1.2	6.4	25.2	63.2	3.6	0	0
2019	238	2	2	97.5	0	1.2	0.8	13	26.2	56.3	0.8	0	1.7
2020	234	1	2	100	0	0.4	0.8	6.5	42.7	49.6	0	0	0
Penicillin					**≤ 0.12**	**0.25**	**0.5**	**1**	**2**	**4**	**8**	**16**	**≥ 32**
2016	264	≤ 0.12	1	81.8	76.9	4.9	4.2	4.2	4.2	5.6	0	0	0
2017	267	≤ 0.12	2	79.4	74.2	5.2	4.9	1.9	4.5	5.2	2.6	1.5	0
2018	220	≤ 0.12	1	80	74.1	5.9	5.5	5.5	4.5	1.8	2.3	0.4	0
2019	238	≤ 0.12	2	78.6	70.2	8.4	2.5	5.5	5	6	1.6	0.8	0
2020	234	≤ 0.12	2	78.6	70.5	8.1	3.8	4.2	6.5	3	1.3	2.6	0

Table 5: Continued

Year	Isolates, No.	MIC_{50} (µg/mL)	MIC_{90} (µg/mL)	S, %	MIC frequency distribution (% of isolates)								
Tetracycline					**≤ 0.25**	**0.5**	**1**	**2**	**4**	**8**	**≥ 16**		
2016	264	≥ 16	≥ 16	0.8	0.4	0.4	0	0.4	1.9	1.9	95		
2017	267	≥ 16	≥ 16	1.1	0	1.1	0.7	1.9	4.2	0.7	91.4		
2018	220	≥ 16	≥ 16	0.9	0.4	0.4	1.6	1.6	3.8	0.8	91.4		
2019	238	≥ 16	≥ 16	1.7	1.3	0.4	0.8	2.4	4.3	3.8	87		
2020	234	≥ 16	≥ 16	2.1	1.3	0.8	0.8	0.4	5.2	1.3	90.2		
Tilmicosin					**≤ 0.25**	**0.5**	**1**	**2**	**4**	**8**	**16**	**32**	**≥64**
2016	264	≥ 64	≥ 64	NA	0	0.4	0	0	7.5	9.5	0.8	0.4	81.4
2017	267	≥ 64	≥ 64	NA	0.4	0	0.4	0	9.7	20.2	0	0	69.3
2018	220	≥ 64	≥ 64	NA	0	0	0	0.4	12.7	7	0.4	0	79.5
2019	238	≥ 64	≥ 64	NA	0	0	0.4	0.8	9.2	13.2	1.2	0.4	74.8
2020	234	≥ 64	≥ 64	NA	0	0	3.4	14.9	9.2	0.4	0.8	0.4	70.9
Trimethoprim-Sulfamethoxazole					**≤ 0.06**	**0.125**	**0.25**	**0.5**	**1**	**2**	**4**	**8**	**≥ 16**
2016	264	≤ 0.06	0.25	NA	62.9	25.3	4.2	2	0.8	1.2	0.4	0.4	2.8
2017	267	≤ 0.06	0.25	NA	64.4	21.9	4.5	2.4	0.4	1.6	1.2	0.8	2.8
2018	220	≤ 0.06	0.12	NA	70.9	21.5	0.8	1.2	0.8	0	1.2	1.2	2.4
2019	238	≤ 0.06	0.12	NA	76.9	14.7	0	0.8	1.2	1.6	0.8	1.6	2.4
2020	234	≤ 0.06	0.12	NA	76.1	15.5	2	1.2	0.8	1.2	1.6	0	1.6
Tulathromycin					**≤ 0.5**	**1**	**2**	**4**	**8**	**16**	**32**	**64**	**≥ 128**
2016	264	≥ 128	≥ 128	NA	0	1.1	9.1	7.7	0	0	1.5	3	77.6
2017	267	≥ 128	≥ 128	NA	0.8	2.8	7.1	17.5	2.4	0.4	0	2	67
2018	220	≥ 128	≥ 128	NA	0	1.2	10.9	9.9	0	0	1.6	3.2	73.2
2019	238	≥ 128	≥ 128	NA	0.4	1.2	7.1	13.9	2.4	0	1.2	2.8	71
2020	234	≥ 128	≥ 128	NA	0.4	5.1	10.2	10.7	2.6	2.6	1.3	3	64.1

* Vertical red lines indicate the CLSI-approved breakpoint for susceptible, intermediate and resistant in that swine respiratory disease pathogen; numbers in the lowest concentration of the tested antibacterial drug range represent the percentage of isolates that had MICs less than or equal to the lowest drug concentration tested per year, while numbers above the highest antibacterial drug concentration represent the percentage of isolates that had MICs greater than the highest drug concentration tested that year. Percent MIC frequency rows may not add to 100% due to rounding.

MIC = minimal inhibitory concentration; MIC_{50} = antibacterial drug concentration that inhibits 50% of the bacterial population; MIC_{90} = antibacterial drug concentration that inhibits 90% of the bacterial population; S = isolates that are susceptible to the antibacterial drug using CLSI criteria; NA = not applicable since there are no CLSI-approved clinical breakpoints for susceptibility in that swine respiratory disease pathogen; CLSI = Clinical and Laboratory Standards Institute.

Streptococcus suis susceptibility to ampicillin was very high (susceptible breakpoint ≤ 0.5 µg/mL) and ranged from 97.8% to 99.2%, while the percentage of susceptibility to ceftiofur was also high (91.2%-97.7%; breakpoint ≤ 2 µg/mL) over the 5-year study period in which MIC_{90} values ranged from 1 to 2 µg/mL. The percentage of *S suis* susceptible to enrofloxacin (breakpoint ≤ 0.5 µg/mL) ranged from 87.3% to 94.1% in which MIC_{90} values were 0.5 to 1 µg/mL. The percentage of *S suis* susceptibility to florfenicol was very high (breakpoint ≤ 2 µg/mL) and increased from 97.7% in 2016 to 100% in 2020, in which MIC_{90} values were 2 µg/mL. The percentage of *S suis* susceptibility to penicillin (breakpoint ≤ 0.25 µg/mL) decreased slightly from 81.8% in 2016 to 78.6% in 2020 in which MIC_{90} values ranged from 1 to 2 µg/mL. *Streptococcus suis* susceptibility to tetracycline was very low and ranged from 0.8% in 2016 to 2.1% in 2020. Susceptible breakpoints were not available for danofloxacin, tilmicosin, TMP-SMX, or tulathromycin, but MIC_{90} values were determined as 1 µg/mL, ≥ 64 µg/mL, 0.12 to 0.25 µg/mL, and ≥ 128 µg/mL, respectively.

Discussion

The prevalence of *A pleuropneumoniae, B bronchiseptica, P multocida,* and *S suis* pathogens associated with SRD emphasizes the importance of maintaining high levels of susceptibility to antimicrobials that are available to veterinarians for treatment of these pathogens.[9] Surveillance and monitoring studies for antimicrobial resistance in pathogenic bacteria of animal origin are necessary to understand any rates of change in the susceptibility of bacteria to antimicrobials, thereby serving as one component among many to help guide practitioners to select the most appropriate antimicrobial for treatment of disease.[10]

Antimicrobial resistance surveillance programs support antibiotic stewardship principles which require all antibiotic prescribers (for animals and humans) to assure good prescribing decisions that mitigate the emergence of resistance to preserve the effectiveness of antibiotics for veterinary and human medicine. Additionally, selecting the proper course of antimicrobial treatment for an animal, whether it is over-the-counter, prescribed, or through a Veterinary Feed Directive, should correlate with the Animal Medicinal Drug Use Clarification Act.

A limited number of surveillance studies have investigated *in vitro* susceptibilities of specific antimicrobials used to treat swine pathogens associated with respiratory disease on a national and international basis.[4-6,11-14] The SRD surveillance program reported herein has continuously obtained swine pathogens for over 20 years from North American veterinary diagnostic laboratories that have then been tested for antimicrobial susceptibility. The purpose for this ongoing surveillance study was to summarize the antimicrobial susceptibility profiles of 2949 isolates from 4 different pathogenic bacterial species associated with SRD collected from laboratories in the United States and Canada over a 5-year period from 2016 to 2020. To our knowledge, when coupled with our published SRD surveillance data from 2001 to 2010 and 2011 to 2015, this is the only surveillance program that has collected and published 20 years of SRD susceptibility data against a total of 11,992 isolates from the United States and Canada.[4,5]

Retrospective studies have been published that investigated the antimicrobial susceptibility of *A pleuropneumoniae* isolates from swine. Pangallo et al[15] showed high antimicrobial susceptibility for 354 isolates of *A pleuropneumoniae* from Italy to penicillins, fluoroquinolones, tetracyclines, and ceftiofur while low rates of susceptibility were observed for florfenicol. Holmer et al[16] reported the antimicrobial susceptibilities of *A pleuropneumoniae* from Danish pigs in which high susceptibility (> 95%) to ceftiofur, florfenicol, tulathromycin, tilmicosin, penicillin and tetracycline was observed for 135 isolates. Susceptibility data for *A pleuropneumoniae* from our 2001 to 2010 SRD surveillance program reported 100% susceptibility to ceftiofur, florfenicol, and tulathromycin and susceptibility data from our 2011 to 2015 SRD surveillance program reported 100% susceptibility to ceftiofur and florfenicol with high levels of susceptibility (> 90% to 100%) to enrofloxacin and tulathromycin.[4,5] This current report shows 100% susceptibility to ceftiofur, florfenicol, and tulathromycin along with high levels of susceptibility (> 95%) to tilmicosin, and low levels of susceptibility (0%-10.6%) to tetracycline for 250 *A pleuropneumoniae* isolates from 2016 to 2020. *Actinobacillus pleuropneumoniae* MIC values have remained high for tetracycline since 2001 and may be due to distribution of tetracycline resistance genes associated with plasmids which have been previously reported.[17,18]

For *B bronchiseptica*, El Garch et al[6] reported high susceptibility to amoxicillin-clavulanate (95.8%) and tulathromycin (99.2%) and lower susceptibility to florfenicol (52.5%). In our previous study we reported ≥ 99% susceptibility to tulathromycin, no susceptibility (0%) to ampicillin, and low susceptibility (5.4%-23.5%) to florfenicol against 572 *B bronchiseptica* isolates from 2011 to 2015.[5] This current report shows ≥ 99% susceptibility to tulathromycin, 0% susceptibility (100% resistance) to ampicillin, and low susceptibility (3.9%-15.2%) to florfenicol against 602 *B bronchiseptica* isolates from 2016 to 2020.

For *P multocida* isolated from swine, El Garch et al[6] reported 100% susceptibility to amoxicillin-clavulanate, ceftiofur, enrofloxacin, and tulathromycin and 65.8% susceptibility to tetracycline for 152 isolates. Susceptibility data from 2001 to 2010 for our SRD surveillance program reported 100% susceptibility to ceftiofur with high rates of susceptibility (> 90%-100%) to enrofloxacin, florfenicol, tilmicosin, and tulathromycin and data from our 2011 to 2015 SRD surveillance program reported 100% susceptibility to ceftiofur, enrofloxacin, and florfenicol and high levels of susceptibility (> 90%-100%) to ampicillin, penicillin, tilmicosin, and tulathromycin, with low levels of susceptibility (22.3%-35.3%) to tetracycline for 855 *P multocida* isolates.[4,5] This current report shows 100% susceptibility to ceftiofur along with high levels of susceptibility (> 95%) to ampicillin, enrofloxacin, florfenicol, penicillin, tilmicosin, and tulathromycin and low levels of susceptibility (23.2%-38.2%) to tetracycline for 874 *P multocida* isolates from 2016 to 2020.

For *S suis,* El Garch et al[6] reported high susceptibility (96%-100%) to amoxicillin-clavulanate, ceftiofur, enrofloxacin, and florfenicol and 4% susceptibility to tetracycline when tested against 151 isolates. Additionally, other studies have shown high rates of resistance among *S suis* isolates against tetracycline (75%-100% resistance) while the year 2 report from the US Department of Agriculture's Animal and Plant Health Inspection Service pilot project showed that of 167 *S suis* isolates, 2.4% were resistant to ceftiofur and enrofloxacin, 0.6% were resistant to ampicillin, 15.6% were resistant to penicillin, and 98% were resistant to tetracycline.[19,20] Susceptibility data from our 2001 to 2010 SRD surveillance program reported high rates of susceptibility (> 90%-100%) to ceftiofur and florfenicol and susceptibility data from our 2011 to 2015 report showed high levels of susceptibility (> 90%-100%) to ampicillin,

ceftiofur, and florfenicol, with low levels of susceptibility (0%-1.3%) to tetracycline against 1201 *S suis* isolates.[4,5] This current report shows > 90% susceptibility to ampicillin, ceftiofur, and florfenicol, low levels of susceptibility (0.8%-2.1%) to tetracycline, and moderate rates of resistance among *S suis* to penicillin (18.2%-21.4% resistance) for 1223 *S suis* isolates from 2016 to 2020. Due to the inability to genetically characterize these *S suis* isolates, some may belong to other bacterial species, and thus the resistance rates could be affected.

Numerous authors have highlighted the challenges of surveillance programs and the potential biases that may be encountered.[5,6,21,22] While there is no "gold standard" for evaluating the antimicrobial surveillance of animal pathogens, a report is available that offers guidance on areas in which harmonization can be achieved in veterinary antimicrobial surveillance programs with the intent of facilitating comparison of data among surveillance programs.[23] All surveillance studies still have certain biases and limitations to consider when interpreting susceptibility data. For this current study, 2949 clinical isolates were collected from 2016 to 2020 and analysed, but this number of clinical isolates is still small when considering the number of SRD cases in North America over the last 5 years. As the isolates in this current study originated from many veterinary diagnostic laboratories, the methods of sample selection, collection, and submission varied among laboratories. To help decrease regional sampling bias in this study, the number of isolates of a target species from any herd was restricted to one isolate during any quarter year period.[4,5] Biases reported in other programs, such as a passive surveillance design, no consideration in differences between livestock farm types and sizes, or prior treatment of animals with antibacterial agents, are acknowledged in this and other studies.[4-6] Furthermore, the lack of clinical breakpoints or interpretive criteria for certain antibacterial agents against pathogens to determine rates of susceptibility continue to be a limitation to veterinary surveillance. A greater collaborative effort among academic and industrial veterinary groups should be made to identify what gaps exist for available breakpoints and then establish CLSI-endorsed clinical breakpoints if a standardized approach is used.

The data presented from this current study, especially data that show a continued lack of susceptibility to certain antimicrobials such as tetracycline, should serve to underscore the importance of prudent use of these drugs when treating SRD. Although tetracycline has traditionally served as the class representative agent for *in vitro* susceptibility testing for veterinary tetracyclines, extrapolation of tetracycline susceptibility results may not necessarily be predictive of activity or clinical outcome for other tetracycline agents, such as oxytetracycline or chlortetracycline, due to differences in blood and lung-tissue concentrations and differences in bioavailability. Even though there are CLSI-established clinical breakpoints for tetracycline that were used in evaluating data in this study, these breakpoint values were derived partly from oxytetracycline pharmacokinetic data.[8]

Management practices used in modern pig farming such as manure management, age-segregation of pigs, and nutritional and metabolic awareness have profound influences on microbial interactions which may result in decreased disease among swine.[24] The high levels of antimicrobial susceptibility observed in this study and others may be attributed to specific health management practices within swine herds such as the all-in, all-out management practice system. Another management practice that may be contributing to overall high antimicrobial susceptibility rates is multi-site production where contained groups of pigs spend their production life in different facilities appropriately designed for each age group (site I: breeding herd; site II: nursery; site III: finishing, all of which are located at separate geographical locations to minimize disease transmission). Future studies may be able to determine if these management practices influence antibiotic resistance changes over time, and if resistance reduction can be achieved through alterations in further enhanced housing and cleaning practices.

The results of this surveillance study when using standardized susceptibility testing methods show high percentages of antimicrobial susceptibility among the major respiratory tract pathogens isolated from swine across the United States and Canada, except for tetracycline, and results from this 5-year SRD surveillance study are similar to those previously published.[4,5] This surveillance study continues to be useful in identifying the development of antimicrobial resistance among SRD target pathogens which is crucial for the prudent use of antimicrobials in veterinary medicine. Additionally, understanding the *in vitro* susceptibility of SRD pathogens isolated in the United States and Canada continues to be an important component of antimicrobial stewardship and One Health.

While this study shows high rates of susceptibility for antimicrobials against SRD pathogens, public perceptions and regulatory pressures continue to drive the need for newer, alternative treatment options which may include novel antibacterial classes, re-evaluation of older or discontinued antibacterial agents, posology, and alternative approaches such as bacteriophages and peptides.[25]

Implications

Under the conditions of this study:

- Susceptibility rates of SRD pathogens were high to key antimicrobials approved for SRD treatment.
- Antimicrobial stewardship benefits from susceptibility monitoring.

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Conflict of interest

Authors Sweeney, Gunnett, Kumar, Lunt, and Galina Pantoja were employed by Zoetis and authors Bade and Machin were employed by Microbial Research, Inc at the time this study was planned and performed.

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Peer reviewed **Brief communication**

Characterization of changes in productivity parameters as breeding herds transitioned through the 2021 PRRSV Breeding Herd Classification System

Onyekachukwu H. Osemeke, DVM; Tara Donovan, DVM; Kate Dion, DVM; Derald J. Holtkamp, DVM, MS; Daniel C. L. Linhares, DVM, MBA, PhD

Summary

Using retrospective data from 6 breed-to-wean herds over 4 years, porcine reproductive and respiratory syndrome virus (PRRSV) statuses were assigned by week according to the 2021 American Association of Swine Veterinarians PRRSV classification. Productivity changes were characterized as herds transitioned through status categories. Overall, productivity improved as farm status improved.

Keywords: swine, classification, American Association of Swine Veterinarians, productivity, monitoring

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Resumen - Caracterización de los cambios en los parámetros de productividad a medida que las piaras reproductoras hicieron la transición a través del sistema de clasificación de granjas reproductoras para el PRRSV 2021

Usando datos retrospectivos de 4 años de 6 hatos de gestación-maternidad, los estatus del virus del síndrome respiratorio y reproductivo porcino (PRRSV) se asignaron por semana de acuerdo con la clasificación del PRRSV de la Asociación Americana de Veterinarios de Cerdos de 2021. Los cambios de productividad se determinaron a medida que las piaras pasaron por las diferentes categorías de estatus. En general, la productividad mejoró a medida que mejoró el estatus de las granjas.

Résumé - Caractérisation des changements dans les paramètres de productivité lors de la transition des troupeaux reproducteurs dans le système de classification du PRRSV 2021 des troupeaux reproducteurs

À l'aide de données rétrospectives de six troupeaux de type saillie-au-sevrage sur une période de 4 ans, les statuts du virus du syndrome reproducteur et respiratoire porcin (PRRSV) ont été attribués par semaine selon la classification PRRSV 2021 de l'American Association of Swine Veterinarians. Les changements de productivité ont été caractérisés comme les troupeaux passaient d'une catégorie de statut à l'autre. Dans l'ensemble, la productivité s'est améliorée à mesure que le statut de l'exploitation s'améliorait.

The American Association of Swine Veterinarians (AASV) classification of breeding herds for the porcine reproductive and respiratory syndrome virus (PRRSV) helped facilitate PRRSV prevention, control, and elimination efforts. The standard terminology aided better information interchange between producers and veterinarians as to herd health status and intervention decisions, facilitated strategic biosecurity planning and execution, furnished researchers with standardized data, helped with assigning PRRSV infection status to herds, and helped to better understand market value of weaned pigs.[1]

Considering the emergence and widespread adoption of population-based sampling methods in the United States[2] and certain drawbacks associated with the classification scheme in use, for example, inconsistently weaning truly negative pigs from herds classified as PRRSV stable, the AASV proposed a modified PRRSV status classification scheme for breeding herds, hereafter defined as the AASV 2.0 PRRSV Classification System.[3]

The modified classification system relies solely on laboratory evidence. Therefore, there is no guarantee that there would be significant productivity differences between any 2 statuses, or how significant these differences would be. There has not been any study characterizing productivity differences between the PRRSV-positive unstable low-prevalence status just introduced (status 1B) and status 1A or 2vx.

The objective of this study was to characterize the changes in productivity of breeding herds as they transitioned between PRRSV status categories as defined by the AASV 2.0 PRRSV Classification System.

OHO, KD, DJH, DCLL: Veterinary Diagnostic and Production Animal Medicine, College of Veterinary Medicine, Iowa State University, Ames, Iowa.

TD: The Hanor Company, Spring Green, Wisconsin.

KD: The Hanor Company, Webster City, Iowa.

Corresponding author: Dr Daniel Linhares, 2221 Lloyd, 1809 S Riverside Dr, Ames, IA 50011-3619; Tel: 515-294-9358; Email: **linhares@iastate.edu**.

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Animal care and use

An animal use protocol was not required as this was a retrospective cohort study that used available laboratory diagnostic data, PRRSV outbreak information, and weekly productivity parameters.

Materials and methods

Overview

Six breed-to-wean farms belonging to a single production system in the southeastern United States were conveniently selected for the study. These sow farms were routinely exposed to PRRSV modified live virus (MLV) vaccines. Two of these six farms had no laboratory evidence of wild-type PRRSV shedding all through the study period (2017 to 2020). The remaining 4 farms had laboratory evidence of PRRSV shedding at one point or another, sufficient for herd placement into any of the AASV 2.0 PRRSV categories (1A, 1B, or 2vx). The reverse transcription polymerase chain reaction (RT-PCR) tests on samples to determine shedding status were carried out in an accredited veterinary diagnostic laboratory located in the United States. The following weekly productivity parameters were obtained from the system's production records:

- Total pigs born per litter (TBL)
- Pigs born alive per litter (BAL)
- Pigs weaned per sow (PWS)
- Preweaning mortality percentage (PWM)
- Neonatal losses per litter (NL; derived by subtracting BAL from TBL)

The farms used multiple sample types for RT-PCR testing to monitor PRRSV shedding including processing fluids, ear blood swabs, family oral fluids, fetal tissues, pig tissues, and sow tissues. The farms used these sample types individually or in combination.

Observational units and eligibility criteria

The observational unit was week, defined as a given calendar week for each study herd. To be eligible each week, the farm had to be void of perceived activity of other disease outbreaks that impact breeding herd productivity, including porcine epidemic diarrhea, transmissible gastroenteritis, and porcine delta coronavirus. Weeks without sufficient diagnostic information for assigning PRRSV status, according to the protocol described herein, were also excluded from the analysis.

AASV 2.0 PRRSV classification

The AASV 2.0 PRRSV Classification System was used to assign a status to each week based primarily on laboratory evidence of PRRSV activity over defined time periods for certain sample types and attenuated PRRSV vaccine use in the breeding herds. The full details of the AASV 2.0 PRRSV Classification System are described by Holtkamp et al.[3]

In summary:

Category 1A included PRRSV unstable, high prevalence herds evidenced by high viremia or viral shedding. A herd falls into this category if it does not meet conditions for any of the other categories.

Category 1B included PRRSV unstable, low prevalence herds evidenced by low viremia or viral shedding. To enter this category, herds required 3 of 4 tests in 90 days for sera or 10 of 13 weekly tests (using population-based aggregate samples) with zero detection of wild-type PRRSV RNA in weaning age pigs.

Category 2vx included PRRSV stable herds that were vaccinated. This is the best-case scenario for vaccinating herds. To enter this category, herds required all tests in a 90-day period have zero detection of wild-type PRRSV in weaning age pigs. Either 6 pools of 10 sera each or 6 pools of 5 sera each together with one pooled processing fluid sample is considered the minimum sample set to be tested for a herd to be promoted to this category.

This study was conducted on herds controlling PRRSV through MLV vaccine exposure. As such, no weeks were eligible for placement into AASV 2.0 PRRSV categories 2, 3 or 4, representing PRRSV stable, provisionally negative, and negative, respectively.

An additional analysis was implemented to characterize trends during the first 10 weeks of category 1A following diagnostic confirmation of a PRRSV outbreak as compared to the rest of the 1A weeks. This was based on a study where the median time to recover baseline productivity for herds using attenuated PRRSV vaccine was 10 weeks.[4]

For this study, any week where multiple samples were submitted, any positive result, regardless of sample type, was considered diagnostic evidence for a positive PRRSV herd test for that week.

Data analysis

A linear mixed regression analysis was performed with each productivity parameter as the response variable, the PRRSV status as a fixed effect, and farm ID and season of the year as random effects. The least-squares mean analysis was performed using the Kenward-Roger degrees of freedom method, 0.95 confidence level, Šidák method for confidence level adjustment, and Tukey method for *P*-value adjustment. These analyses were performed using the lme4 package[5] in R program.[6] Univariate analyses were chosen over multivariate as there was little to no correlation between most of the parameters measured.

Standardized residuals were plotted against fitted values for each model to assess heteroscedasticity and nonlinearity using the plot() function in base R.[6] The base R qqplot() function was used to evaluate the normality of residuals. There was a log transformation of the response variable to correct for violations in model assumptions wherever observed; this step sufficed. Outliers were assessed and confirmed to be valid data observations; no observations were removed.

Results

A total of 1125 weeks had sufficient information for category placement and data analysis. Overall, productivity improved as weeks improved PRRSV classification status (Table 1).

Discussion

This study aimed to investigate and describe the trends in selected productivity parameters as the study population changed AASV 2.0 PRRSV status categories. Data for 1125 weeks from 6 breed-to-wean farms in a single production system from 2017-2020 were included in the study. Each week was identified with productivity data and PRRSV status according to diagnostic test results, vaccination history, and PRRSV outbreak history. All study herds used attenuated PRRSV-vaccination as a control strategy during this time frame and, therefore, were classified as 1A, 1B, or 2vx. Routine PRRSV vaccination of the breeding female population is a common practice in some US swine herds and the results of this study will be informative to several other systems. There were no statistical differences across groups in the average TBL, which includes the total BAL and NL (mummified fetuses and still births).

Table 1: Least-squares means (SE) of productivity parameters for each AASV 2.0 PRRSV status classification*

	AASV 2.0 PRRSV classification			AASV 2.0 PRRSV classification - further categorization of 1A			
Parameter/wk	1A	1B	2vx	1A - first 10 weeks	1A - 11th week through promotion to 1B†	1B	2vx
Total born/litter, No. (SE)	14.3 (0.22)[a]	14.4 (0.21)[a]	14.4 (0.22)[a]	14.6 (0.24)[a]	14.3 (0.22)[b]	14.4 (0.23)[ab]	14.4 (0.21)[ab]
Born alive/litter, No. (SE)	12.6 (0.20)[a]	13.1(0.21)[b]	13.2 (0.20)[b]	12.1 (0.22)[a]	12.7 (0.20)[b]	13.1 (0.20)[c]	13.2 (0.19)[c]
Neonatal losses/ litter, No. (SE)	1.58 (0.12)[a]	1.23 (0.01)[b]	1.18 (0.10)[b]	2.46 (0.20)[a]	1.44 (0.11)[b]	1.23 (0.09)[c]	1.19 (0.09)[c]
Pigs weaned/sow, No. (SE)	10.7 (0.20)[a]	11.3 (0.21)[b]	11.5 (0.20)[c]	9.6 (0.21)[a]	10.9 (0.20)[b]	11.3 (0.20)[c]	11.5 (0.19)[c]
Preweaning mortality, % (SE)	14.0 (1.36)[a]	13.0 (1.29)[a]	12.1 (1.16)[b]	19.9 (2.08)[a]	12.9 (1.29)[b]	13.0 (1.32)[b]	12.2 (1.20)[b]

* The AASV 2.0 PRRSV status classification[3] categories assigned to herds in this study include 1A = positive unstable, high prevalence; 1B = positive unstable, low prevalence; 2vx = positive stable with vaccination.

† This period begins on the 11th week of a herd being classified as 1A status post-PRRSV outbreak and ends when the herd was promoted to 1B status.

[a,b,c] Different superscripts on compared statuses for each productivity parameter indicate statistical differences (α = .05).

PRRSV = porcine reproductive and respiratory syndrome virus

Provided there is not significant early gestation reproductive failures attributable to PRRSV, this parameter is expected to be about the same across categories. Differences between statuses would lie in the proportions of the component parameters that make up TBL. Records of other productivity parameters such as breeding repeats and number of aborts were not available for analyses; we therefore could not characterize reproductive disorders or prenatal losses attributable to PRRSV.

Neonatal losses per litter, BAL, PWS, and PWM improved as these herds improved PRRSV status. These results are similar to those observed in Torrents[7] where BAL and PWM had relatively better numbers when herds were PRRSV stable. Torrents[7] study was conducted in Spain with farms naturally exposed to PRRSV-1, while the farms in this study were naturally exposed to PRRSV-2.

As seen from the first few weeks following a PRRSV outbreak, the impact on productivity can be short lived relative to the time the virus is actively being shed and susceptible animals infected in herds. This demonstrates that productivity levels should not be used as a proxy of PRRSV circulation. It would also be economically beneficial for vaccinated herds to keep implementing best practices until their herds attain and maintain PRRSV stability; a low PRRSV-prevalence status should not be a comfortable destination for herds aiming to control PRRSV.

Considering that the parameters measured in this study are only a subset of those important for measuring productivity losses attributable to PRRSV, this study does not attempt to fully characterize the economic differences between PRRSV statuses, rather, to characterize differences in the averages of the mentioned parameters. Some liberty was taken in promoting herds from 1B to 2vx, in that, even though these herds demonstrated a lack of PRRSV shedding for several months using at least three sample types weekly, these samples were not exactly as described in the AASV 2.0 PRRSV classification scheme. To the best of our knowledge, this is the first study that has evaluated changes in productivity parameters as breeding herds transitioned through the AASV 2.0 PRRSV status categories. Therefore, there is a need for similar studies on PRRSV-negative herds and herds targeting elimination to characterize changes in productivity parameters for other AASV 2.0 PRRSV categories not included in this study (ie, categories 2, 3, and 4).

Complementary studies in this line will provide useful data for evaluating and choosing best intervention strategies (control versus elimination) at farm, production company, and regional levels.

Implications

Under the conditions of this study:

- Productivity improved as AASV 2.0 PRRSV classification status improved.
- Productivity can approach baseline even when a herd is actively shedding PRRSV.

Acknowledgments

Conflict of interest

None reported.

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