Infectious agents in feral swine in Ohio, USA (2009-2015): A low but evolving risk to agriculture and public health

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\textbf{ABSTRACT}

As highly mobile and prolific animals, feral swine threaten public and livestock health. To quantify these threats, we analyzed disease surveillance samples to estimate the prevalence of key pathogens and parasites in feral swine captured in Ohio. Between 2009 and 2015, samples from 205 feral swine were tested for up to 13 pathogens. Methicillin susceptible \textit{Staphylococcus aureus} was cultured from 29 of 138 (21\%) individuals and antibodies to \textit{Leptospira} spp. (16/69; 23\%), \textit{Toxoplasma gondii} (11/76; 15\%), \textit{Trichinella spiralis} (4/69; 6\%), hepatitis E virus (1/32; 3\%), \textit{Brucella} spp. (2/138; 1\%), and influenza A virus (2/176; 1\%) were also detected. Lungworms (\textit{Metastrongylus} spp.) were frequently identified (46/55; 84\%). Evidence of infection or exposure was not detected to \textit{Mycobacterium bovis}, classical swine fever, pseudorabies, and porcine reproductive and respiratory syndrome. All positive \textit{Brucella} and hepatitis E virus samples and 63\% (10/16) of the positive \textit{Leptospira} spp. samples came from individuals identified as illegal out-of-state feral swine introductions. Results indicated an overall low prevalence of pathogens in feral swine in Ohio; however, the importation of live feral swine from other states remains an important concern for pathogen introduction and spread.

1. Introduction

The United States of America feral swine (\textit{Sus scrofa}) population is estimated at over 6 million individuals (USDA-APHIS-WS, 2015a). The population in Ohio state is comparably low, estimated at fewer than 2,000 individuals. These swine likely originated from hunting preserve escapees or from illegal interstate transportation, with continued population growth through breeding and on-going illegal importation. As of 2015, established breeding populations of feral swine were present in at least nine Ohio counties and sporadic reports of feral swine sightings recorded in an additional eight counties across the state (Fig. 1).

Feral swine are potential carriers of over 60 viral, bacterial and parasitic pathogens, many of which are transmissible to other animals including livestock, domestic pets, wildlife and humans (Davidson, 2006). Additionally, they are carriers of external parasites such as ticks and lice, many of which are vectors for numerous pathogens (Davidson, 2006). Despite their low numbers, the ability of feral swine to carry a variety of pathogens and their potential interactions with wildlife, domestic animals, and people make them potentially important infectious vectors in the state.

Since 2009, Ohio Wildlife Services (OHWS), a program of the United States Department of Agriculture's Animal and Plant Health Inspection Service, has performed disease surveillance in feral swine in conjunction with a population elimination program. Known feral swine populations are carefully monitored with an end goal of elimination. New populations are identified through reports by the public and partnerships with local and regional government agencies. New populations are investigated by wildlife personnel to determine the likely source (e.g., local release, inter-state importation) and monitored, again with an end goal of elimination. The present study analyzed the results of biological samples collected from feral swine taken during elimination efforts by OHWS from April 2009 to September 2015.

2. Material and methods

All procedures for sample collection and processing were performed in accordance with standard guidelines set forth by the USDA Wildlife Services National Wildlife Disease Program in the annual “Wildlife Services’ Comprehensive Feral Swine Disease Surveillance Procedures Manual” for the years 2009-2015 (USDA-APHIS-WS, 2015b). During
that time, there was some variation in sample type, sample processing, and specific laboratories due to funding changes and specific disease interest at the national level. Between 2009-2012, sample collection occurred irrespective of animal age and was based on availability of captured individuals. This approach was replaced in 2013 by targeted sampling of adults, when available, to maximize pathogen detection as seroprevalence of some pathogens has been shown to be increased in older feral swine (Hill et al., 2014).

During necropsy, the heart, liver, lungs, and trachea were grossly examined and the presence of lung worms (Metastrongylus spp.) was noted. Samples (n = 1244; serum, axilla and nasal swabs, feces, bronchial alveolar lavage samples) were shipped to collaborating laboratories for pathogen testing. A combination of serological, polymerase chain reaction (PCR) and culture techniques were used to detect...
A total of 205 feral swine were tested for one or more of 13 pathogens and examined for the presence of *M. bovis* (Pedersen et al., 2018), *Brucella* spp. (Pedersen et al., 2013), *hepatitis E virus* (HeV), *IAV*, and *Brucella* spp. (Table 1). Multiple pathogens were identified in eight individuals: *T. gondii* and *T. spiralis* (n = 1), *T. spiralis* and *Leptospira* spp. (n = 1), *T. gondii* and *Leptospira* spp. (n = 1), and *Leptospira* spp. and MSSA (n = 5).

Antibodies to *Leptospira* spp. were identified in 16 feral swine (16/69; 23%), with some individuals having elevated titers to multiple serovars. The most common serovars detected were *L. Bratislava* (9/69; 13%), followed by *Icterohaemorrhagiae* (6/69; 9%), *Grippotyphosa* (5/69; 7%) and *Canicola* (2/69; 3%). Serovars Pomona and Hardjo were not detected. *Staphylococcus aureus* was detected in 21% (29/138) of the samples; all were MSSA. Antibodies to *T. gondii* were identified in 15% of samples (11/76), while antibodies to *T. spiralis* were found in 6% of samples (4/69). Two samples tested positive for brucellosis (2/138; 1%). One sample was positive for HEV (1/32; 3%) and two samples were positive for IAV antibodies (2/136; 1%).

Presence of (or antibodies to) *M. bovis*, *CSF*, PRV, and PRRSV were not detected. One of the 45 pigs tested for PEDV had test results interpreted as suspect positive (i.e., result between negative and positive ranges). *M. avium* spp. were noted in 84% (46/55) of the pigs examined.

During the study period, legal investigations into new feral swine populations indicated some of the pathogen-positive samples had come from individuals illegally imported into the state and intentionally released (Table 2). Specifically, all positive *Brucella* spp. and HEV samples and 63% (10/16) of the positive *Leptospira* spp. samples were from feral swine populations determined to be illegally imported from other states (reportedly Georgia and Louisiana). Previous studies have documented an elevated prevalence of *Brucella* spp. in feral swine from the southern US (Pedersen et al., 2012).

Feral swine are a potential reservoir of zoonotic and non-zoonotic pathogens and parasites, and as long as they are present in a region, the risk of infectious disease transmission and/or re-emergence of diseases should not be ignored. From a public health standpoint, our results indicate feral swine pose a risk, albeit overall low, for zoonotic pathogen transmission in Ohio. The risk to the public is perhaps greatest for hunters, biologists and other professionals who have close contact with these animals or those who consume their meat. Based on our results, the southern counties of Ohio had the greatest chance of contact with these animals or those who consume their meat.
between infected/exposed feral swine, livestock, domestic swine and humans (Fig. 1, Table 2); the presence of backyard livestock and facilities with limited biosecurity systems likely elevated this risk.

Our results are similar to the estimated national prevalence of pathogens in feral swine (e.g., 13% positive for *Leptospira spp.*; Pedersen et al., 2015) yet considerably lower than some regional studies (e.g., 49% positive for *Leptospira spp.* in a Texas study; Pedersen, Bauer, Rodgers et al., 2017). It is interesting to note that MSSA was recovered from 21% of individuals, suggesting this human and animal pathogen was circulating in the feral swine population. The high prevalence of *Metastrongyulus spp.* we noted is consistent with the limited previous reports of this parasite in feral swine (*Shender, Botzler, & George, 2002*) and poses an important concern for the domestic swine industry.

Given that pork production is a USD 15 billion industry in the United States and as Ohio is the eighth highest US state for swine inventory (NPB, 2016), introduction of one or more of these pathogens into an Ohio swine facility could result in significant economic impact. Fortunately, most of the commercial swine production in Ohio is located to the northwestern region of the state, and most established feral swine populations remain in the southeastern reaches of the state. The cases of *Brucella spp.* and *Leptospira spp.* found in Lorain County (north central Ohio) came from the same intentional release; this Lorain County population was completely eliminated in 2015.

This study had several limitations. The number of samples available for testing was low and opportunistic, which may have affected prevalence estimates and precluded analysis by subgroups (e.g., age). As this work was part of a larger elimination and surveillance program, sample numbers (including number of feral swine tested) was based on availability and national program priorities. However, the total number of feral swine tested (*n* = 205) provided an adequate sample size to ensure reasonable pathogen testing breadth and depth. Specifically, all individuals were tested for one or more of 13 pathogens with most samples per pathogen exceeding 50 (number needed to detect a pathogen with a low (i.e. 5%) prevalence with 95% confidence, as well as provide a reasonable estimate for a relatively common pathogen (i.e. 15% prevalence ± 10% with 95% confidence)). Additionally, some testing modalities have been shown to underestimate true prevalence in feral swine (e.g., antibody testing for *B. suis*), therefore actual prevalence may be greater than what estimated (Pedersen, Bauer, Olsen et al., 2017). Although samples were tested for 13 pathogens, many were not included, such as pathogens carried by ectoparasites. The tick vector *Ixodes scapularis*, along with associated disease-causing pathogens (e.g., *Borreliaburgdorferi*), are emerging in Ohio (Wang et al., 2014). Ticks are frequently found on feral swine, potentially increasing risk of tick-borne-associated diseases for humans with feral swine contact. Future studies are encouraged to improve our understanding of feral swine population dynamics and pathogen presence in Ohio.

This study serves as an important step in recognizing feral swine risks in Ohio and assisting in prioritizing future surveillance, pathogen testing, and control strategies. Illegal introductions of animals carrying pathogens remain a critical threat to Ohio's swine industry.

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**Conflict of interest statement**

None of the authors has any financial or personal relationships that could inappropriately influence or bias the content of the paper.

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