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African Swine Fever

Vienna R. Brown
USDA APHIS Wildlife Services

Julianna B. Lenoch
USDA APHIS Wildlife Services

Courtney F. Bowden
USDA APHIS Wildlife Services

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12 African Swine Fever

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Introduction

At the time of writing this chapter, a global pandemic of African swine fever (ASF) is ongoing with the virus having moved from Eastern Europe, Asia, and into the Caribbean—leaving swine production in devastation along the way. Due to the global spread of African swine fever virus (ASFV), the persistence of the virus, and the increasing number of endemic countries, this disease poses an imminent threat of introduction into North America and other countries that are currently ASF free.

Throughout the chapter, we reference Eurasian wild boar (*Sus scrofa*) which are charismatic megafauna that are native to Europe and Asia. Wild boar were introduced into numerous areas in the southeastern United States and California by early settlers and they subsequently augmented and hybridized with established feral domestic swine (*Sus scrofa*) to give rise to contemporary populations of feral swine, a highly invasive species that are present across much of the United States. Feral swine are referred to by various terms, including wild hogs, feral pigs, wild boar, wild swine, razorbacks, and other regional names in North America. African swine fever has never been introduced into the United States; as such, we do not discuss feral swine in specific within

Illustration by Laura Donohue.

the chapter. However, experimental inoculations demonstrate that feral swine are acutely susceptible to ASFV and given its current rapid global movement we anticipate similar patterns of exposure, infection, and risk amongst these populations.

History and Global Distribution

In 1909, ASF was first detected following the importation of European domestic swine into Kenya when nearly 100% of the animals succumbed to a hemorrhagic disease (Gallardo et al. 2015, Sánchez-Cordón et al. 2018). The disease was also detected in central and western Africa but confined to sub-Saharan Africa until it was reported in Portugal in 1957. In 1960, ASF spread to the Iberian Peninsula and other countries in Europe such as France (1964), Italy (1967, 1969, and 1983), Malta (1978), Belgium (1985), and the Netherlands (1986). Various countries in the Americas were also affected by ASF during this period including Cuba (1971, 1980), Brazil (1978), the Dominican Republic (1978), and Haiti (1979). By the 1990s, the disease had been successfully eradicated from these countries, with the exception being the island of Sardinia off the coast of Italy.

Transcontinental spread of ASF occurred for a second time in 2007 with the disease reaching Georgia within the Caucasus region and subsequently spreading further into eastern Europe (Figure 12.1; Revilla et al. 2018, Sánchez-Cordón et al. 2018). Specifically, ASF outbreaks were reported in Armenia, Russia, Belarus, Ukraine, Estonia, Lithuania, Latvia, Romania, Moldova, the Czech Republic, and Poland (Revilla et al. 2018). In August 2018, ASF was reported on a small-scale pig farm in China and has since spread throughout the country as well as through much of Asia and Southeast Asia including Mongolia, Korea, Vietnam, Laos, Cambodia,

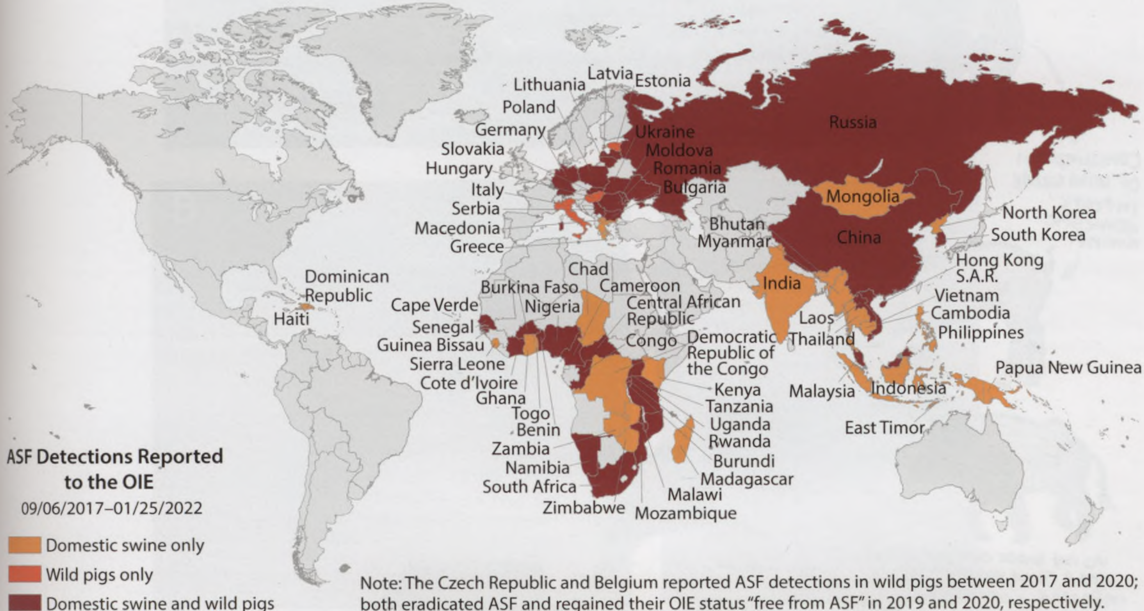

Fig. 12.1. Global African swine fever (ASF) detections reported to the World Animal Health Organization (OIE) by immediate notifications, follow-up reports, and biannual reports occurring in domestic swine and wild pigs from 6 September 2017 to 25 January 2022. Data and map sources: OIE WAHIS, USDA APHIS.

Myanmar, the Philippines, Hong Kong, Indonesia, Timor-Leste, Papua New Guinea, and India (Ge et al. 2018, Zhao et al. 2019, Li et al. 2020, Mighell and Ward 2021). Hungary, Bulgaria, and Belgium reported their first ASF outbreaks in 2018 (Martinez-Aviles et al. 2020), and Germany experienced their first outbreak in 2020 (Sauter-Louis et al. 2021*b*). In the Americas, African swine fever was detected in the Dominican Republic in July 2021 (USDA APHIS 2021*a*) and in Haiti in September 2021 (USDA APHIS 2021*b*).

Etiology

African swine fever is a hemorrhagic disease caused by ASFV, which is a large, linear double-stranded DNA virus (Sanchez-Vizcaino et al. 2019). African swine fever virus is the only member of the family *Asfarviridae* (Alonso et al. 2018) and the only known DNA arbovirus (Gaudreault et al. 2020). Whole-genome sequencing and subtyping has revealed that ASF viruses demonstrate considerable variation in virulence and significant genomic diversity (de Villiers et al. 2010). Wild and domestic members of the Suidae family (see picture on page 198) are the only natural, vertebrate hosts of ASF (Gallardo et al. 2015, Golnar et al. 2019), and soft ticks of the genus *Ornithodoros* are natural, arthropod vectors that play a significant role in pathogen maintenance and transmission.

Epidemiology and Transmission

African swine fever virus transmission dynamics are especially complex: there are three epidemiological cycles, and a fourth has been proposed, that exist independent of one another (Figure 12.2).

Fig. 12.2. Cycles of transmission for African swine fever virus (ASFV). Illustration by Laura Donohue.

Sylvatic Cycle

African swine fever virus evolved in eastern and southern Africa in the burrows of common warthogs (*Phacochoerus africanus*) with the *Ornithodoros moubata* soft ticks that inhabit these dwellings (Penrith et al. 2019). Warthogs are believed to be the original vertebrate host of ASFV, and transmission within the warthog population occurs exclusively between infected ticks and the neonatal warthogs that they feed upon (Figure 12.3; Costard et al. 2013). Newly infected juvenile warthogs exhibit viremia for a short duration, which can serve to infect naïve ticks and allows pathogen maintenance in the absence of vertical and horizonal transmission amongst warthogs. Infected warthogs are asymptomatic carriers, although

Fig. 12.3. Components of the sylvatic epidemiological cycle of African swine fever virus: (A) a mother and juvenile warthog, (B) a warthog burrow, and (C) *Ornithodoros spp.* ticks removed from a warthog burrow. Photograph courtesy of Dr. Charles Masembe and the African swine fever research consortium, Makerere University, Kampala, Uganda.

they often maintain the virus for the duration of their lives in infected lymph nodes (Costard et al. 2013).

Similar to warthogs, bushpigs (*Potamochoerus larvatus*) exhibit moderate viremia when infected with ASFV via the bite of an infected tick but do not develop clinical signs (Anderson et al. 1998, Oura et al. 1998). The contribution of bushpigs to ASFV maintenance and transmission is relatively unknown as they do not inhabit burrows (Netherton et al. 2019); however, bushpigs are thought to play a minor role in ASFV epidemiology as their populations are less dense and they appear to have lower infection rates (Jori and Bastos 2009). Very little is known about red river hogs (*Potamochoerus porcus*) in relation to the epidemiology of ASF; however, ASFV genomic DNA was detected in a single free-ranging red river hog in Nigeria (Luther et al. 2007). Similarly, reports of ASFV infections have been limited for giant forest hogs (*Hylochoerus meinertzhageni*), and the contribution of giant forest hogs to the sylvatic cycle is believed to be negligible.

Tick–Pig Cycle

The soft tick–pig cycle is characterized by ASFV-infected ticks transmitting the pathogen to domestic swine (Costard et al. 2013). Competent tick vectors of the genus *Ornithodoros* (Table 12.1) become infected after feeding on viremic animals and are then capable of transmitting the virus during blood meals (Costard et al. 2013). In the absence of viremic hosts, transstadial, transovarial, and sexual transmission has been documented in *O. moubata* ticks, which contributes to ASFV persistence (Plowright et al. 1970, 1974; Rennie et al. 2001). This cycle is particularly prevalent in sub-Saharan Africa with *Ornithodoros moubata* ticks infecting domestic swine; however, it also played an important role in the outbreak on the Iberian Peninsula with *O. erraticus* ticks transmitting ASFV to domestic swine (Gaudreault *et al.* 2020). The tick–pig epidemiologic cycle is particularly important in outdoor swine production areas that have endemic disease in soft ticks in nearby areas (Sanchez-Vizcaino *et al.* 2012).

Table 12.1. Tick vectors from the genus *Ornithodoros* capable of transmitting African swine fever virus to pigs

Ornithodoros species	Global distribution
O. coriaceus (O. marocanus)	North America
O. erraticus	Africa, Asia, Europe
O. moubata complex	Africa, Madagascar
O. puertoricensis	Caribbean, North America
O. savignyi	Africa, Asia
O. turicata	North America

Domestic (Pig–Pig) Cycle

Once ASFV is introduced into domestic pig or Eurasian wild boar populations, virus can be efficiently transmitted between swine hosts and does not require a vector (Costard et al. 2013, Dixon et al. 2020, Blome et al. 2021). ASFV spreads systemically within infected swine, and all secretions and excretions contain virus (Guinat et al. 2016). Direct and indirect contact as well as the consumption of contaminated meat products (e.g., swill feeding practices), allow for the ready transmission of ASFV between pigs (Costard et al. 2013). As an example, interactions between free-ranging domestic swine and wild boar are believed to have contributed to ASFV endemicity in some parts of Europe (Cadenas-Fernandez et al. 2019).

Wild Boar–Habitat

The wild boar–habitat cycle consists of direct transmission through contact with infected wild boar as well as indirect transmission from dead conspecifics or contaminated environments (e.g., soil, drinking water, crops, or feed; Chenais et al. 2018, O'Neill et al. 2020, Sauter-Louis et al. 2021*a*, Viltrop et al. 2021). Direct transmission may occur within or between herds of wild boar (i.e., sounders; O'Neill et al. 2020) and is particularly troublesome in areas with high wild boar density (Guberti et al. 2019). Reports of wild boar scavenging on carcasses are common (Cukor et al. 2019, Probst et al. 2020); in wild boar populations in Europe, carcass-based transmission is the primary route of infection (EFSA 2014, Cukor et al. 2019, Fischer et al. 2020). Carcass-based transmission is estimated to account for 53–66% of transmission events in the ASF outbreak that took place in eastern Poland in 2014 and 2015 (Pepin et al. 2020). Failure to remove carcasses from the landscape provides ample opportunity for ASFV transmission via direct interactions between live and dead conspecifics. Additionally, ASFV is highly stable in a proteinaceous environment, and as such, indirect transmission can occur through environmental contamination during carcass decomposition (Dixon et al. 2020; O'Neill et al. 2020).

Clinical Signs and Gross Lesions

With highly virulent strains of ASFV, death occurs very quickly in nearly 100% of affected domestic swine or wild boar (OIE 2019). Clinical disease associated with peracute and acute cases typically manifests as fever, increased pulse and respiratory rate, reddening of the skin (especially of the extremities; Figure 12.4), anorexia, vomiting, and diarrhea (sometimes bloody). Moderate- and low-virulence strains of ASFV cause weight loss, intermittent fever, and general malaise and result in subacute and chronic forms of the disease, respectively. In swine that succumb to ASFV, gastrohepatic and renal lymph node hemorrhage as well as enlarged, friable spleens can often be observed (Figure 12.4).

Pathogenesis and Pathology

Infection with ASFV in domestic swine and wild boar is associated with severe lymphoid depletion and hemorrhages (Salguero 2020). Once the virus

Fig. 12.4. Clinical signs and gross lesions associated with African swine fever virus infection in swine: (A) reddening of the skin on the ear; (B) red–purple skin discoloration of the skin on the leg; (C) hemorrhagic gastrohepatic lymph nodes; and (D) enlarged, friable spleen. Photograph courtesy of Plum Island Animal Disease Center, Plum Island, New York, USA.

enters the body, tonsils are the primary site of replication (Heuschele 1967; Greig 1972) before spreading to local lymph nodes, disseminating to the secondary organs of replication, and ultimately spreading systemically via the lymphatic system. The lymphoid depletion characterized by ASF results from massive destruction of lymphoid organs, tissues, and cell types. Experimental infection of domestic swine with ASFV has demonstrated that tissues abundant in reticuloendothelial cells, including the lymph nodes, spleen, bone marrow, and liver, commonly have the highest virus titers and serve as secondary sites of viral replication (Heuschele 1967).

The pathogenesis of ASFV is largely mediated by the host immune response and the corresponding cytokine storm (Zhu et al. 2019). Monocytes and macrophages are the main target for ASFV (Howey et al. 2013), and virus replication induces an intense upregulation in proinflammatory cytokines that ultimately results in significant apoptosis in both infected cells and uninfected lymphocytes (Howey et al. 2013; Wozniakowski et al. 2016). The vascular changes are those of a disseminated intravascular coagulopathy leading to petechial and ecchymotic hemorrhages in multiple organs, hyperemic splenomegaly, and pulmonary edema (Salguero 2020).

Diagnostics

Given that there is no effective vaccine or treatment, early detection of ASFV is paramount in managing the disease and limiting outbreak size. Validated diagnostic tests are classified into two primary types: antigen and antibody-based assays (OIE 2019). Polymerase chain reaction (PCR) is the gold standard antigen-based test as it is highly sensitive and specific, allows for high throughput, and generates rapid results (Gallardo et al. 2019). Virus isolation can be used to detect ASFV and direct immunofluorescence and antigen-based enzyme-linked immunosorbent assays (ELISA) can detect ASFV antigens (Gallardo et al. 2019, OIE 2019).

Whole blood captured in EDTA tubes is the best suited sample for ASFV detection (Pikalo et al. 2021); however, serological assays can be useful for low to moderately virulent strains of ASF, when clinical signs are not significant enough to trigger an ASF investigation (OIE 2019). It is worth noting that antibody testing is suboptimal for screening apparently healthy animals (Pikalo et al. 2021). A number of diagnostic tests are available for detecting ASFV antibodies, including ELISAs, indirect fluorescent antibody test (IFAT), indirect immunoperoxidase test (IPT), and immunoblotting test (IBT; OIE, 2019). The recommendation for ASF antibody testing is screening via ELISA with nonnegatives being confirmed with IB, IFAT, or IPT (Beltran-Alcrudo et al. 2019).

Treatment and Vaccination

To date, there are no efficacious treatments to reduce the severity of the disease. Infected animals will either die rather quickly, especially with virulent strains of ASFV, or become convalescent (Costard et al. 2009). Natural infection with a low to moderately virulent strain of ASFV confers a high degree of protection against infection with a highly virulent homologous strain of ASFV however (Sang et al. 2020).

The quest to develop a safe, efficacious vaccine for ASFV has proven to be extremely challenging, and there is not a licensed vaccine available to date (Das et al. 2021). This is driven in large part by gaps in knowledge related to ASFV entry and replication within host cells, virus immune evasion and modulation, and the primary antigens responsible for triggering immune activity (Arias et al. 2017, Rock 2017, Sang et al. 2020, Wang et al. 2020). Several vaccine platforms have been evaluated and are showing varying degrees of promise. For example, inactivated ASFV vaccines are often nonprotective as they fail to induce a cellular immune response, even when administered with adjuvant (Teklue et al. 2019; Gavier-Widén et al. 2020). Subunit vaccines, recombinant proteins, and DNA vaccines have demonstrated partial protection against wild-type ASFV (Teklue et al. 2019; Gavier-Widén et al. 2020; Sang et al. 2020). Several live attenuated vaccines have been developed, and this is currently the most promising vaccine candidate (Bosch-Camos et al. 2020; Wu et al. 2020; Muñoz -Pérez et al. 2021), as the host responds to the vaccine as if it were naturally encountering ASFV (Sang et al. 2020).

In live attenuated vaccines, the virus can be modified naturally, through multiple passages in a laboratory setting, or by intentional alterations (Liu et al. 2021). The genes deleted in live attenuated vaccines are typically associated with a reduction in virulence, a decrease in viral replication rate and dissemination, and a dampening of the proinflammatory immune response (Sang et al. 2020). One live attenuated vaccine strain, developed by the United States Department of Agriculture, has been shown to provide protection against homologous virulent strains of ASFV in pigs with varying backgrounds (Tran et al. 2022), although testing is still ongoing. The significant limitation with live attenuated vaccines is that unpredictable, strain-specific virus phenotypes are created following genetic alteration of ASFV (Turlewicz-Podbielska et al. 2021). Some animals can develop clinical disease following vaccination, or vaccinated animals can contribute to virus transmission via shedding patterns (Bosch-Camos et al. 2020, Gavier-Widén et al. 2020). In addition to safety concerns in vaccinated animals, developing these vaccines is challenging due to the need for high-level biocontainment facilities for production, stable and suitable cell lines, and cell culture optimization (Sang et al. 2020). However, efficacious, attenuated live vaccine strains have been cultivated and can be produced (Borca et al. 2021*a*).

An important consideration for vaccine development is the ability to differentiate between infected and vaccinated animals (DIVA). DIVA-compatible vaccines are typically generated by the inclusion of a marker within the vaccine that can induce an immune response in the host that is distinct from that of a natural infection with a wild-type pathogen (Hardham et al. 2020). This differentiation is paramount for understanding pathogen epidemiology on the landscape, for informing management practices and policies, and for demonstrating disease elimination following an outbreak.

Developing vaccines for wild pigs presents significant ecological, logistical, and moral considerations that make it challenging to reach desired vaccine efficacy and herd-level immunity (Maki et al. 2017, Barnett and Civitello 2020, Edwards et al. 2021). Vaccines for wild pigs are especially challenging in that they probably need to be delivered orally necessitating that they are both attractive and palatable to the swine species of interest (Balseiro et al. 2020). Additionally, a sufficient quantity of immunogen must be present and available at the induction site to stimulate a protective response requiring a biocompatible encapsulation process (Cross et al. 2007). A DIVA-compatible, oral vaccine for classical swine fever (CSF) was successfully engineered and delivered to wild boar in Europe (Blome et al. 2011; Rossi et al. 2015), and this achievement could be used as a foundation for the successful implementation of an oral ASF vaccine in wild boar (Teklue et al. 2019).

Given the nature of the global ASFV pandemic, vaccine development for wild boar has been an international research priority, and studies may indicate that oral vaccination is plausible. An experimental ASF vaccine that was originally developed using domestic swine and delivered via intramuscular injection (Tran et al. 2022; Borca et al. 2020, 2021*a*) was found to confer high levels of protection against challenges with a virulent strain of ASFV when the vaccine was administered via the oronasal route (Borca et al. 2021*b*). Additionally, vaccination of wild boar with an attenuated strain of ASFV from Latvia was found to be protective against a virulent strain of ASFV (Barasona et al. 2019), and studying shedding patterns of this vaccination strain demonstrated it to be safe for wild boar and contact animals (Kosowska et al. 2020). Further work is necessary to ensure safety and efficacy for use in free-roaming wild boar.

ASFV Introduction Routes Into Disease-free Countries

Given the lack of a vaccine or treatment for ASF and the devastating consequence of the disease for pork production, preventing viral spread into previously unaffected geographical areas is paramount. Introduction pathways vary by country; however, the primary routes identified for ASFV include legal and illegal importation of live swine, swine products, and swine byproducts for commercial use or personal consumption (Figure 12.5; Brown and Bevins 2018,

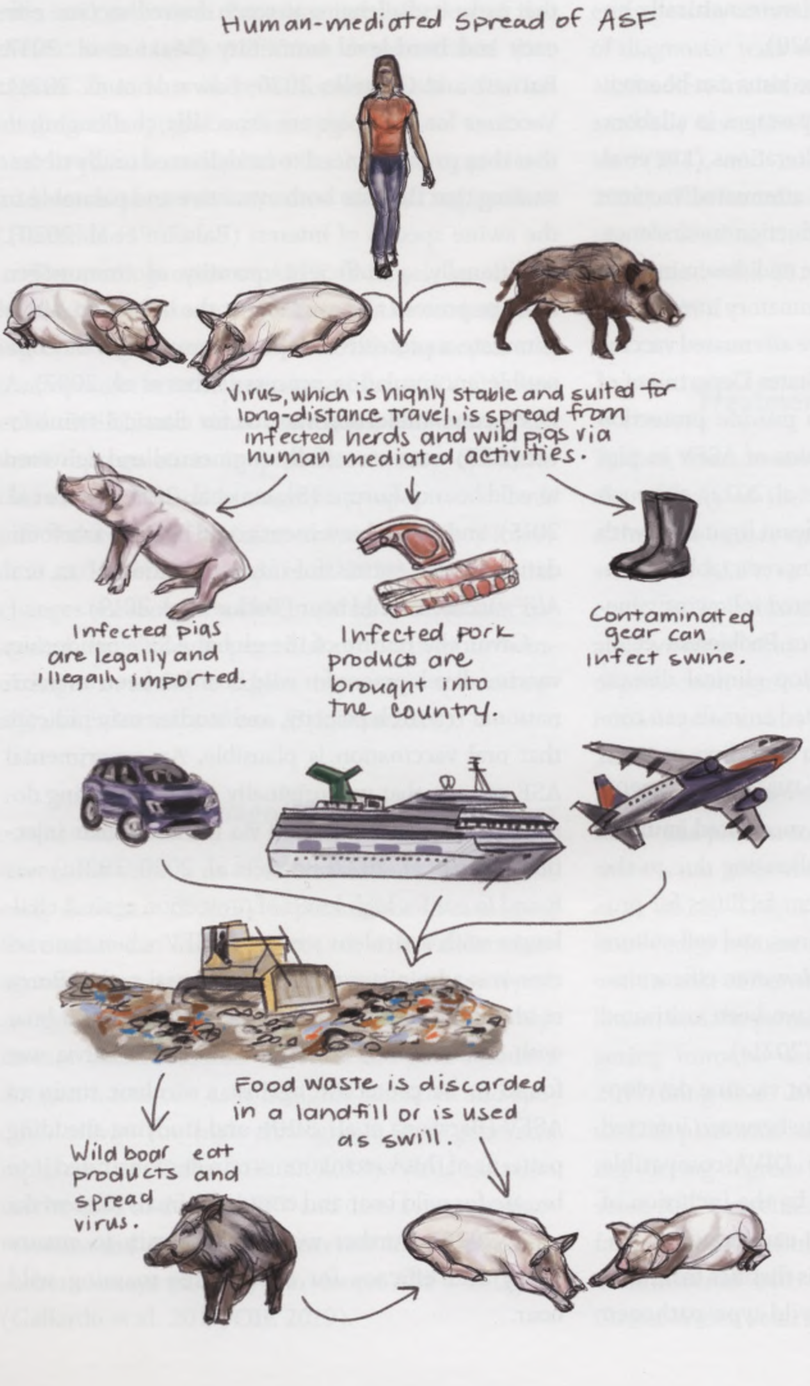

Fig. 12.5. Human-mediated routes of introduction of African swine fever (ASF) from infected to disease-free areas. Illustration by Laura Donohue.

Jurado et al. 2019). Another introduction pathway that must be considered is food waste from airlines, trains, or ships that originated in ASF-infected regions. Human food waste may be discarded in landfills that can be accessed by wild boar, improperly disposed of through meat composting or littering, or illegally sold for swill (Figure 12.5; Vergne et al. 2017, Beltran-Alcrudo et al. 2019, Taylor et al. 2020).

Legal importation of live swine poses a risk for ASFV introduction as the virus can go undetected during the incubation period, in which there is an absence of clinical disease (Vergne et al. 2017; Beltran-Alcrudo et al. 2019; Gao et al. 2020; Taylor et al. 2020). This latent stage following infection is problematic for countries that are historically ASF free and do not have any trade barriers in place for live animals or their products. As an example, classical swine fever (CSF) spread to Italy and Spain from the Netherlands in 1997 when infected piglets were shipped prior to a transportation moratorium (Beltran-Alcrudo et al. 2019). In ASF-endemic countries, swine, their products, and their byproducts are often banned for trade and importation; however, at a local level, "emergency sales" of swine can occur during ASF outbreaks to minimize economic impacts. If ASF is undetected in the herd, then these sales are silently contributing to the spread of ASFV into the production system (Costard et al. 2015).

The illegal movement of swine and their products presents a greater risk of ASFV entry than legal activities (Beltran-Alcrudo et al. 2019; Fanelli et al. 2021). Unregulated movement of live swine within or between countries for personal or commercial use creates opportunities for direct transmission via infected animals or swill as well as indirect transmission via fomites. Due to the difficulty of smuggling live animals, this introduction pathway presents a lower risk of ASFV transmission than illegal movement of products or byproducts (Beltran-Alcrudo et al. 2019). Although most countries have systems in place to confiscate and destroy illegally imported animal products, numerous transboundary animal disease outbreaks have been attributed to illegal imports (Costard et al. 2013). Quantifying the magnitude of illegal imports is difficult and reliant on extrapolation from products that have been detected and confiscated, and data are widely variable. Between 2012 and 2016, approximately 68,000 domestic swine products and specimens were confiscated from travelers entering the United States, and many confiscated products originated from countries known to have ASF (Brown and Bevins 2018). Similarly, in August of 2018 custom officials in South Korea identified 4,064 illegal pork products originating from China, and 4 of the 52 submitted for ASFV testing were positive (Kim et al. 2019).

Management Practices

Current management strategies for new ASFV introductions include quarantining infected swine, increased biosecurity practices, epidemiological investigations, restricted swine movement, disposal of infected and exposed swine, and multiple forms of surveillance (i.e., passive, active, and targeted; Sánchez-Cordón et al. 2018; Danzetta et al. 2020). Given that ASFV is highly stable and easily spread, biosecurity is critical for preventing exposure via fomites or a contaminated environment (Nurmoja et al. 2020). Biosecurity, defined as practices to prevent pathogens both coming onto a farm or commercial property or spreading within the premises, is critical. (Mutua and Dione 2021). Producers should minimize the introduction of animals from outside sources, and a quarantine period should be implemented if outsourcing. Access to production areas should be limited for people, birds, and other small mammals, site-specific equipment and supplies need to be maintained, and materials entering and exiting the property need to be thoroughly cleaned and disinfected (Mutua and Dione 2021). Proper disinfection, which includes both mechanical cleaning and the application of an effective disinfectant, is necessary (Juszkiewicz et al. 2019). Swill feeding is widely considered to be a risky practice (EFSA 2014), and the majority of outbreaks in ASFV-free zones have occurred as a result of feeding food waste products from infected pigs to susceptible hosts (Bellini et al. 2016). Although strongly discouraged, swill should be heated to a minimum of 70°C if it is to be fed to swine.

Human-mediated activities are important drivers for the spread of ASFV, and baiting and hunting wild boar present challenges in managing the disease (Guberti et al. 2019). Supplemental feeding increases the carrying capacity of wild boar on the landscape, amplifies the opportunities for direct and indirect contact between animals, and changes movement patterns—all of which contribute to the maintenance and persistence of ASFV in wild boar. Regulations for hunters aimed at minimizing the risk of ASFV spread include safe storage of the carcass until laboratory results are completed, a prohibition of leaving offal piles in the forest, and washing and disinfecting vehicles, boot, knives, and other equipment used during hunting that has been in contact with blood or tissues of excreta (Bellini et al. 2016; Guberti et al. 2019).

Controlling ASFV has proven especially challenging once it is introduced into wild boar populations, and eradication is nearly impossible, although it has been accomplished on a couple of occasions. Early detection, a prompt and coordinated approach to prohibit movement of infected wild boar, and restricted public access have been demonstrated to be effective in stopping the spread of ASFV. Identifying and disposing of carcasses on the landscape, the use of strategic fencing, and culling operations to reduce densities can also help slow or halt the spread of ASFV (Danzetta et al. 2020; Gavier-Widén et al. 2020).

In addition to field activities to manage an ASFV outbreak, disease-dynamic models can be helpful to guide ASFV preparedness efforts or response and management activities (Miller and Pepin 2019). Given ASFV's multiple routes of transmission and stability, transboundary management is extremely challenging. Extensive collaboration and cooperation between governments and industry are paramount (Shi et al. 2021), and science-based policies and approaches must engage stakeholders across many disciplines (Tucker et al. 2021).

Human Dimensions of ASF

The financial, social, and political implications of ASF are potentially tremendous and can simultaneously impact multiple economic sectors. A systematic literature review on the country-level economic impact of ASFV outbreaks found the range from $649,000 (USD 2019) for annual production loss in Nigeria to $94,539,870,064 for the total economic impact of an outbreak in Spain (Brown et al. 2020). This meta-analysis also found that there is a paucity of data that allows estimation of costs and losses from ASF on national or global scales.

In addition to the short-term direct macroeconomic impacts related to outbreak management, production losses and exclusion from international export markets are secondary impacts for associated products. For example, with an ASF outbreak causing greatly reduced pork production, the demand for animal feed would likely decrease drastically in the United States, causing decreased prices and revenue in the feed market (Stancu 2018). The magnitude of a foreign animal disease introduction event ripples through the economy with direct and indirect costs that have short- and long-term impacts.

A significant reduction in live hog prices can be expected in countries where ASF is reported, as the market clears out surplus pork that would otherwise be exported (Carriquiry et al. 2020), as well as increases to pork products with demand exceeding supply in other markets and regions (Mason-D'Croz et al. 2020). Both scenarios are likely to drive-up costs for alternative sources of animal-based protein, including beef and poultry, impacting the most vulnerable communities globally, and negatively impacting food and financial security (Abworo et al. 2017; Plavšić et al. 2019; Matsumoto et al. 2021; Paulino-Ramirez et al. 2021). Pork supply–demand patterns are believed to have played a significant role in ASFV dissemination within China (Yang et al. 2021).

When ASF outbreaks occur, pig trader networks rush to sell their pigs to ensure that their animals do not succumb to infection (Lichoti et al. 2017; Penrith et al. 2019). This has social implications and been linked to rapid viral dissemination. As an interesting aside and a compelling tale on the interconnectedness of human and animal health, it has been postulated that the ASFV outbreak in China reached its worst impacts around December 2019, near the time when SARS-CoV-2 emerged (Xia *et al.* 2021). The authors suggest that the dramatic pork shortage led to an increase in the risk of transmission of a zoonotic disease as human–wildlife interactions were more frequent.

Summary

African swine fever outbreaks in ASF-free countries have become commonplace in the last several years, and the global ASF pandemic is an example of the tremendous implications of diseases shared by livestock and wildlife. In addition to morbidity and mortality events, production losses, and barriers to international trade, an outbreak of ASF has political ramifications. Measures to reduce the risk of ASFV introduction in ASF-free countries should be of the utmost priority as control and eradication is time consuming, costly, and often out of reach.

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