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Review

The Challenges in Vaccine Development and the Feasibility of a Vaccination Campaign against African Swine Fever Virus

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Abstract

African Swine Fever (ASF) was first described in Africa in 1921 and reached China in 2018. It eventually reached other Asian countries including the Philippines in 2019. Despite the efforts of the Philippine government to mitigate its spread, cases have been observed in 64 of the 81 provinces across 17 regions. Vaccine field trials done in the Philippines have promising results. Yet, until now, no vaccine has been made commercially available.

Efforts to develop a commercial vaccine against ASF have been hindered by the complex and genetically diverse nature of the ASF virus (ASFV). ASFV has evolved strategies to evade the host's immune response, inhibiting antigen presentation and infecting immune cells. The genetic variability among ASFV strains further complicates vaccine development, as different strains may require specific vaccine approaches. Despite challenges, progress has been made with live attenuated vaccines showing promise. However, concerns regarding safety, reversion to virulence, and limited efficacy against multiple genotypes persist. Strategies such as comprehensive safety evaluations, surveillance, combination control measures, and Public awareness is recommended to address the spread of ASF. A vaccination drive targeting prevalent strains in specific regions may provide partial protection but requires ongoing surveillance and complementation with other control measures.

Keywords

African swine fever; African swine fever virus; ASF vaccine; ASF in the Philippines

1. Introduction

African Swine Fever (ASF) is a highly contagious viral disease that affects both domestic and wild pigs. It is caused by the African swine fever virus (ASFV), a complex DNA virus that can survive in the environment for long periods of time. ASF is transmitted through direct contact between infected and susceptible pigs, or through the bite of infected ticks. It was first reported in Kenya in 1921, and since then it has spread to other African, European, and Asian territories [1–3]. It reached China in 2018[4, 5]. Subsequently, the disease spread to its neighboring countries including Mongolia, North Korea, South Korea, Vietnam, Cambodia, Laos, and Myanmar [6–11]. The Philippines confirmed its first outbreak in July 201912.

The economic impact on Asia is massive as China, Vietnam, South Korea, and the Philippines belong to the top global producers of pigs in 2019 [13]. It was estimated that China incurred losses of up to US$111.2 billion [14]. The Philippines is also losing at least $2 billion each year [15]. With these massive losses, it is rational for these governments to prioritize the elimination of ASFV in their territories. In the Philippines, movement restrictions, culling, strict biosecurity measures, and surveillance were implemented. A national zoning plan was developed to guide swine trading between

provinces (Figure 1). Sentinel animals were distributed to affected localities to confirm the presence of the disease and initiate repopulation [16–23].

Despite the progress in the understanding of the ASF virus biology and vaccine research, stakeholders are puzzled why a safe and effective vaccine is still not commercially available. The development of an effective vaccine against ASF would spark the pathway toward recovery and possible elimination of this disease. For countries with limited resources, having access to a vaccine is crucial because it is not feasible logistically or economically to depopulate affected swine herds. However, research focused on the development of an effective vaccine is ongoing. Experimental vaccines using live attenuated virus strains, which are created by removing specific genes associated with virulence, have shown effectiveness [24-29]. These include the deletion of I177L [30, 7] and multigene family (MGF) genes [31].

This paper aims to review the different factors hindering the successful development of an effective vaccine against ASFV. It discussed why creating a safe and effective vaccine against ASFV is an ongoing challenge. It identifies the unique characteristics of the virus that cause difficulty in vaccine development. It also provides updates on the status of the promising candidates. It also presented conditions required to ensure the positive impact of including vaccination drives in the campaign against ASF.

2. ASF in the Philippines

The first outbreak of ASF in the Philippines was confirmed in July 2019 in Rizal province. Subsequent outbreaks were reported in neighboring provinces in the following months [12]. As of May 2023, cases have been observed in 64 of the 81 provinces across 17 regions.

To address the spread of the virus, the Philippine government introduced the National Zoning and Movement (NZM) plan for African swine fever. This demarcates zones according to ASF risk levels and enforces movement restrictions between these regions. The Infected Zone includes provinces with confirmed ASF cases. The Surveillance Zone includes provinces that are high-risk areas because of the dense population of swine, and the volume of trade of pigs, pork, and pork products. The Buffer Zone includes cities/municipalities which are adjacent to the infected zones, as well as ASF-free localities in an infected province. The Protected Zone includes regions/provinces with no ASF cases but is contiguous with the yellow zone in terms of landmass [32]. Moreover, a 1-7-10 protocol is being implemented to contain the spread of ASF across neighboring farms. This protocol involves culling domestic pigs within a 1 km radius of ASF-infected farms, enforcing active surveillance activities and testing within a 7 km radius, and requiring swine farms within a 10 km radius to submit a report on the health status of their herd [33].

The analysis of outbreak data until July 2022 showed that there were 19,697 farm outbreaks. The highest number of outbreaks was observed in the second semester of 2020 (n = 5486). The top three regions that experienced ASF outbreaks were Regions III (n = 4857), I (n = 3404), and II (n =2664). A seasonal pattern was also observed. Most cases occurred between August and October. The lowest frequencies occurred between April and May [34].

2. Genetic Diversity of ASFV

African Swine Fever Virus (ASFV) is a complex and genetically diverse virus with a variety of strains and genotypes. The virus has evolved over time, with new strains and genotypes occurring through natural selection, genetic recombination, and adaptive mutations. Currently, there are 24 different genotypes of ASFV based on the B646L gene, with varying degrees of virulence and geographic distribution [35].

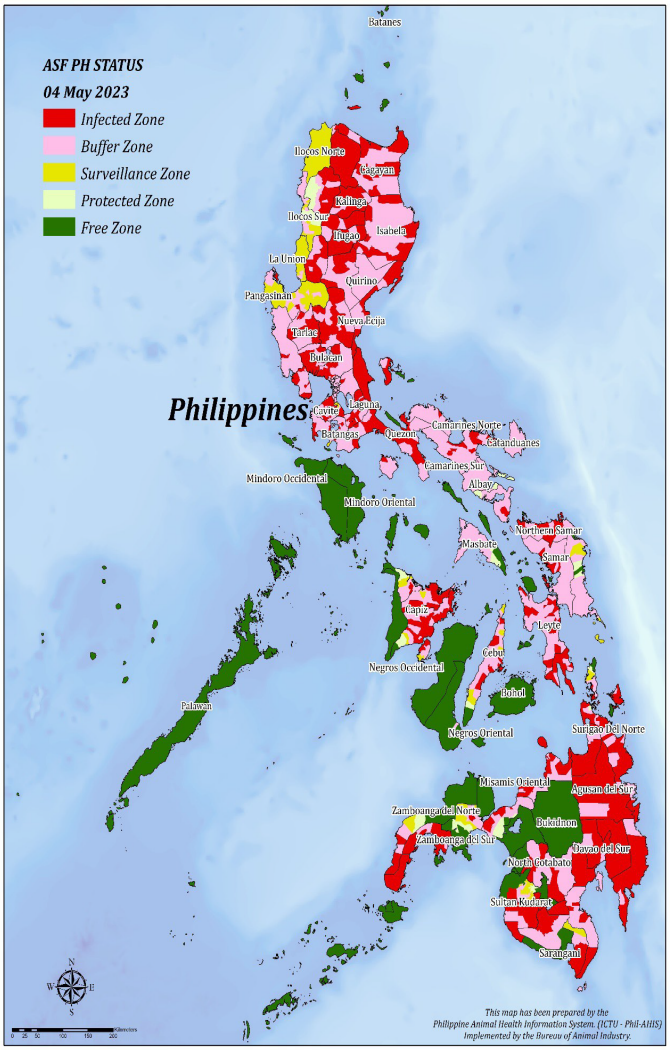

Figure 1. Provincial Classification Based on ASF Status as of May 4, 2023. Source: Philippine Animal Health Information System, Bureau of Animal Industry. Retrieved from the official National ASF Prevention and Control Program Facebook page

These genotypes are further divided into subgroups based on differences in their genetic sequences. They have been identified based on the analysis of the complete nucleotide sequence of the viral genome or specific genomic regions [35–37]. There may be more genotypes of ASFV than currently known and alternative genetic markers could potentially be utilized to classify within genotypes [38].

The blood samples taken from infected domestic pigs in Pangasinan, Philippines revealed that the isolated strain of ASFV was identified as Genotype II. This strain was classified in the same clade as PHL-1969, the 2019 Timor-Leste strain, Wuhan 2019, and other Genotype II strains found in countries such as China, Ukraine, Belgium, and Poland [39].

The ASFV has several unique characteristics that contribute to its genetic diversity. It has a (1) large genome size, (2) Multigenic families that can be subject to various forms of mutations, and (3) high selection pressure leading to the emergence of new genotypes and subgroups.

A larger genome size can potentially increase the genetic diversity of a virus. This is because a larger genome size allows for more genetic information to be stored. Some of these genetic materials may be beneficial for the virus in certain environments or conditions. It may also allow for the acquisition of new genetic elements or the recombination of existing ones. This can potentially lead to higher genetic diversity. This is because the virus has more genetic material to mutate and recombine,

leading to the generation of new variants. In the case of ASFV, its large genome size of approximately 170-193 kilobases provides ample opportunities for genetic diversity to arise, contributing to the high level of genetic variability observed among different ASFV strains [40–43].

Multigene Families (MGFs) are groups of genes sharing similar DNA sequences and encoding for proteins with related functions or structures [44,45]. Originating from a common ancestral gene through duplication and divergence, MGFs contribute significantly to immune response, cell signaling, and developmental regulation. ASFV has five MGFs, namely MGF100, MGF110, MGF300, MGF360, and MGF505/530. These MGFs can undergo several mutations, including insertions and deletions, leading to alterations in the amino acid sequences of the proteins they encode. Such alterations can bring about changes in protein function, antigenicity, and virulence, contributing significantly to the genetic diversity of ASFV [46,40, 47,48]

Moreover, selection pressure plays a vital role in shaping ASFV's genetic diversity. It refers to environmental factors or conditions that favor certain genetic traits or variants over others. As ASFV circulates in different regions or among different hosts, it encounters diverse selection pressures. For instance, the host immune system is a significant selection pressure, pushing ASFV to continuously adapt and evade the host's immune response. This leads to antigenic variation, where ASFV acquires mutations in genes encoding for surface proteins. Additionally, the movement of infected animals or animal products between different regions or countries can expose ASFV to new selection pressures, driving the emergence of new ASFV variants [35,49-52].

2. The Genome of the African Swine Fever Virus

The African Swine Fever virus (ASFV) has a large, complex, and highly structured genome. It is a double-stranded DNA virus with a genome size of approximately 170-193 kilobases [61–63]. Korea/YC1/2019, the ASFV strain from the first outbreak in Korea has 188 kilobases and 183 ORF64. Meanwhile, the ASFV strain from the first China outbreak has 189 kilobases [11]. The ASFV genome from an outbreak in the Philippines has 192.38 kilobases [39].

The genome is composed of linear, double-stranded DNA that contains at least 150 open reading frames (ORFs) [65–68]. Open reading frames (ORFs) are sequences of nucleotides in a viral genome that have the potential to encode proteins that play a critical role in the replication, assembly, and pathogenesis of viruses [69]. In the case of ASFV, the ORFs can encode structural proteins, enzymes, and factors involved in immune evasion [42, 66, 70, 71].

3. Evasion strategies of ASFV from the host's immune system

Pattern recognition receptors (PRRs) detect pathogen-associated molecular patterns (PAMPs) in viral infections, leading to signaling cascades that induce the production of pro-inflammatory cytokines, interferons (IFNs), and interferon-stimulated genes (ISGs), which impede the viral lifecycle. Cells like macrophages, Natural killer cells (NK), and dendritic cells are attracted to the infection site to eliminate virus-infected cells through processes like phagocytosis, complement-mediated lysis, and Cytotoxic T Lymphocytes (CTL) mediated killing [72,73].

However, ASFV manipulates IFN signaling cascades for its own replication. IFNs are produced via several signaling pathways such as Toll-like receptor (TLR), RIG-I-like receptor (RLR), and Cytosolic DNA sensing, which activate transcription factors like Nuclear Factor Kappa-light-chain-enhancer of activated B cells (NF-κB), Interferon Regulatory Factor 3 (IRF3), and Interferon Regulatory Factor 7 (IRF7), thereby inducing IFN gene expression [62]. ASFV gene products I329L and I267L suppress TLR3 signaling and RNA polymerase III-RIG-I-mediated responses, respectively, hindering type I IFN induction [74-76]. ASFV also suppresses the cGAS-STING pathway, inhibiting type I IFN production [77-81].

Interferon Regulatory Factors (IRFs), transcription factors activated by PAMPs via PRRs, regulate IFN and other immune response genes expression. IRF3 and IRF7 are key transcription factors for type I IFN gene expression [82-84]. NF-κB pathway,

activated by cytosolic DNA sensing, regulates immune cell functions and triggers the production of cytokines, chemokines, and other inflammatory mediators, but its suppression leads to inactivity [85-90]. Interferon absence also prevents the activation of the JAK-STAT pathway, a signaling mechanism aiding cell response to pathogens. This pathway involves the phosphorylation of signal transducers and activators of transcription (STATs) by activated Janus kinases (JAKs), stimulating the transcription of ISGs [91, 92].

ASFV proteins and genes help the virus evade host's immune response (Table 1), lengthening infected cell survival time and assisting the virus's persistence and replication. Likewise, ASFV primarily infects mononuclear phagocytes such as monocytes, macrophages, and dendritic cells, allowing it to evade detection and clearance by the host's immune system, and replicate throughout the body [66,43, 92-94].

Table 1. Proteins and Genes of ASFV that aid in evading its host's immune system

Proteins / Genes	Mechanism against Host's Immune System	References
A238L	Inhibits the activation of NF-κB by preventing the degradation of the NF-κB inhibitor protein IκB	[70,75,95–98]
A276R	Hinders the induction of IFN-β in an IRF3-dependent manner	[75,99]
I226R	Inhibits the activation of the IRF3 and NF-*Kb* pathway	[63,100]
E120R	Blocks the activation of the 1 TBK1-IRF3 pathway	[101,102]
EP402R	Inhibits the production of type I IFN by inhibiting the phosphorylation of IRF3 and NF-κB signaling pathways. It can also inhibit the activation of the cGAS-STING pathway by inhibiting the phosphorylation of TBK1 and IRF3	[103]
A137R	Inhibits the nuclear translocation of IRF3 stopping the production of type I IFN	[104]
MGF360-9L	Inhibits the activation of the interferon signaling pathway by inducing the degradation of the STAT proteins	[105,106]
I329L	Acts as a TLR3 antagonist and inhibits innate immune responses	[74,107,108]
MGF360-12L	Inhibits host type I IFN, NF-κB, and JAK/STAT pathways	[43,46]
MGF360-14L	Suppresses interferon-β (IFN-β) promoter activity driven by the cGAS-STING signaling pathway. It also interferes with the activation of the IRF3 signaling pathway	[99,109]
DP96R	Suppresses type I interferon production by interfering with the cGAS-STING-TBK1 signaling pathway	[62,78]
D345L	Suppresses cGAS/STING-mediated NF-κB signaling by inhibiting the activity of IKKα/β leading to reduced transcription of IFNβ and various proinflammatory cytokines, such as IL-1α, IL-6, IL-8, and TNFα	[62]
MGF 505-7R	Inhibits the production of type I interferon and the downstream JAK-STAT signaling of both type I and type II interferons	[110,111]
A224L	Disrupts apoptosis triggered by TNFα, cycloheximide, or staurosporine	[112–114]
A179L	Inhibits apoptosis by binding the (BH3) domain of the pro-apoptotic Bcl-2 family proteins by utilizing a conserved ligand-binding groove. It can also bind to caspases, a family of proteases that plays a critical role in apoptosis	[115–118]
DP71L	Blocks apoptosis by inhibiting the stress-induced induction and activation of the pro-apoptotic CHOP protein	[63,93,112,119]

NF-κB: Nuclear Factor kappa-light-chain-enhancer of activated B cells; IκB: Inhibitor of kappa B; IFN: Interferon; IRF: Interferon regulatory Factors; TBK: Tank-binding kinase; cGAS-STING: cyclic GMP-AMP synthase - Stimulator of Interferon Genes; STAT: signal transducer and activator of transcription; TLR3: Toll-like receptor 3; IKKα/β : IκB kinase alpha and beta,; IL: Interleukin; TNF: Tumor Necrosis factor; JAK-STAT: Janus Kinase - Signal Transducers and Activators of Transcription; BH3: Bcl-2 Homology 3; CHOP: C/EBP homologous protein

4. Updates in Vaccine Development against ASFV

Several approaches to vaccine development are currently under investigation. These include live attenuated vaccines, subunit vaccines, DNA vaccines, and viral vector vaccines. Live attenuated vaccines (LAVs) are created by reducing the virulence of a pathogen but keeping it alive to stimulate a robust immune response [124]. In the case of ASF, attenuated strains have been obtained through serial passages of the virus in cell culture or deletion of virulence-associated genes [125]. Subunit vaccines contain only specific parts of the virus, such as proteins or sugars, instead of the entire microorganism. These parts are carefully selected for their ability to trigger a strong immune response, effectively teaching the immune system to recognize and combat ASFV without causing the disease itself [126, 127]. A DNA vaccine involves the direct introduction of genetically engineered DNA into the recipient to produce an immune response [128]. Viral vector vaccines use a different, harmless virus as a delivery system, or vector, to introduce antigens into the cells of the host to trigger an immune response and develop immunity against the targeted pathogen [129].

One of the promising vaccine candidates is classified as LAVs. In 2022, Vietnam granted a license for the commercial use of ASFV-G-ΔI177L [130]. This was developed by removing the I177L gene from the genome of the Georgia strain (ASF-G). The deletion of this gene weakens the Georgia isolate. The first clinical trials demonstrated the ability of this experimental vaccine to protect subjects against the highly virulent ASFV Georgia strain [30]. It was also proven that it can be administered through the oronasal route and yield comparable efficacy to intramuscular administration [26]. A modified strain of the ASFV-G-ΔI177L vaccine, called ASFV-G-ΔI177L/ΔLVR, was created by deleting the left variable region (LVR). This deletion enables the modified strain to grow in stable cell cultures while retaining the potency and effectiveness of the original vaccine strain. This allows the production of this vaccine on a commercial scale [131]. Moreover, ASFV-I177L can protect pigs against the virulent ASFV isolate currently circulating and producing disease in Vietnam with similar efficacy as reported against the Georgia strain [132]. This vaccine was likewise proven to be safe. No residual virulence was observed among the subjects observed daily for 180 days post-vaccination [133].

LAVs were also developed by deleting MGF genes. The vaccine ASFV-G-ΔMGF was constructed from ASFV Georgia 2007 isolate (ASFV-G). Six genes from the MGF360 or MGF505 families including MGF505-1R, MGF360-12L, MGF360-13L, MGF360-14L, MGF505-2R, and MGF505-3R were removed. Upon exposure to the ASFV-G virus, inoculated pigs remained healthy. Some of these animals harbored the challenge virus. The vaccine also exhibited equivalent replication efficiency as the parental virus in primary pig macrophage cell cultures [133]. Likewise, ASFV-Δ9L/Δ7R was constructed by deleting MGF360-9L and MGF505-7R from ASFV CN/GS/2018, a highly virulent ASFV strain circulating in China. This vaccine was able to establish a sterile immunity among the inoculated pigs [134]. Another study develops a new ASFV-specific LAV called ASFV-Δ110-9L/505-7R by deleting interferon inhibitors MGF110-9L and MGF505-7R of the ASFV CN/GS/2018. This vaccine also resulted in sterile immunity and full protection in a virulent challenge [135].

Several concerns are associated with the use of LAVs. These include safety, as there is a risk that the attenuated virus could revert to virulence136,137. Moreover, differentiating infected from vaccinated animals (DIVA) is difficult with this strategy, complicating disease control efforts [124]. These concerns can be addressed through the use of subunit, DNA, and virus-vectored ASFV vaccines. These vaccine types have strong safety profiles, as they cannot revert to a virulent form and cause disease because they do not contain whole virus particles [126,127].

Subunit vaccines for African Swine Fever Virus (ASFV) incorporate proteins like p54, p30, pp220, pp62, p72, and CD2v that participate in virus attachment and internalization [138–141]. Baculovirus-expressed ASFV proteins stimulated neutralizing antibodies and partial protection [139,142], though results varied due to interfering antibodies or experimental setups [143]. Appreciating the vital role of antibody-mediated immune response and CD8+ T cells, DNA vaccines have been tried as an alternative

ASF vaccine platform [145,146]. To enhance efficacy, a DNA–protein vaccination strategy has been proposed. Yet, DNA vaccines or vector-based vaccine platforms, though safer and potentially inducing broad immune responses, haven't provided full protection [146,147].

5. Discussion

Vaccination has been instrumental in managing infectious diseases. It provides protection among susceptible animals and limits the spread of diseases. Despite being identified since 2021 and the improvement in biotechnology, there is no commercial vaccine against African swine fever made available to the public yet. Efforts to generate an effective vaccine have been limited by several challenges.

The fundamental problem lies in the complexity of the ASFV. ASFV is a large, enveloped, double-stranded DNA virus with a genome size of approximately 170-193 kilobases [61]. This makes it one of the largest viruses known, and its genetic complexity is a significant hurdle in vaccine development. The total number of proteins encoded by the ASFV genome complicates the identification of appropriate antigens for inclusion in a vaccine. While researchers have identified certain proteins that may be important for the immune response, like the p30 and p54 proteins [139], it is still difficult to understand the roles and interactions of all ASFV proteins.

As discussed above, ASFV has evolved numerous strategies to evade the immune response. One key issue is that ASFV inhibits antigen presentation, preventing infected cells from signaling their infection to the immune system. Additionally, ASFV can infect various types of immune cells, including macrophages, and use them to spread throughout the body. The ability of ASFV to evade the immune system presents a substantial challenge in the development of effective vaccines. To be effective, a vaccine needs to stimulate a robust immune response that will protect the host against future infections [120, 121]. ASFV's inhibition of interferon production and antigen presentation can prevent the activation of immune cells and the development of an effective immune memory [122, 123].

Moreover, there is high genetic variability among different ASFV isolates. This diversity could potentially render a vaccine effective against only a subset of ASFV strains.

Nonetheless, research is ongoing towards the development of an effective vaccine. One of the most advanced vaccines is the ASFV-G-ΔI177L, a live attenuated vaccine. This has been licensed in Vietnam. It was also proven to be effective against the ASFV Georgia strain and the Vietnamese strain TTKN/ASFV/DN/2019 [148]. A derivative strain of this vaccine, the ASFV-G-ΔI177L/ΔLVR has been constructed to facilitate mass production as it can replicate efficiently in a stable porcine epithelial cell line. Despite these breakthroughs, a commercial vaccine based on the ASFV-G-ΔI177L prototype is not yet made available in the market. The Vietnamese Dabaco group and the Navetco National Veterinary JSC, laboratories working on ASF vaccine development failed to meet their claim of making the vaccine available no later than the second quarter of 2022 [149].

The observed delay may be attributed to the risks associated with live attenuated vaccines. One is the possible reversion to virulence. This possibility has been observed for the experimental vaccine strain HLJ/18-6GD where the virus became more virulent during replication in pigs [150]. The risk of vaccine virus shedding under field conditions is another concern. This has been realized in a vaccine challenge using the E75 and E75CV1 strains [151].

Another issue is the duration of the protection. Attenuated viruses have demonstrated protective effects when administered through short immunization protocols, wherein pigs were exposed to a viral challenge a few weeks after the initial immunization. It was reported that pigs did not exhibit protection against the virulent Benin 97/1 ASFV genotype I isolate when challenged at day 130 post-vaccination [152].

Moreover, ASF LAVs have limited efficacy against multiple genotypes of ASFV strains circulating in Eurasia. Developing vaccines with cross-protective efficacy against different ASFV strains is a considerable challenge. Genetic diversity contributes to the complexity of vaccine development and

hinders the creation of a universal vaccine that can provide broad protection against all ASFV strains. It can lead to differences in the virulence, pathogenicity, and antigenic properties of various strains. This means that a vaccine developed using one strain may not necessarily confer protection against other strains with different genetic characteristics [24 53, 54]. There are currently at least 24 known genotypes. Developing a vaccine that can effectively protect against all genotypes becomes extremely challenging due to this diversity. For instance, molecular studies showed that there are many different ASFV strains across China [55–58]. At least three variants of genotype II have been detected in Vietnam [59]. Some of the pigs inoculated with an ASF vaccine in Vietnam tested positive for a field strain of ASFV [60]

Nonetheless, the ASFV-G-ΔI177L was also proven to be effective against the ASFV Georgia strain and the Vietnamese strain TTKN/ASFV/ DN/2019 [148]. Both strains belong to genotype II. Though the Philippine strain likewise falls under this genotype, evaluation of the efficacy of this vaccine candidate is still needed.

Field trials have been done in the Philippines. Stakeholders claimed encouraging results [153,154]. Nonetheless, vaccine manufacturers still have to address the discussed risks related to bringing the vaccine to the Philippine market. This may take some time. Guidelines recommend conducting comprehensive safety evaluations of LAVs which should involve long-term studies with a substantial number of animals. These studies aim to assess the degree and stability of attenuation. Moreover, assays should be implemented to differentiate between attenuated strains, fully virulent strains, and partially virulent strains to evaluate the potential for reversion. Due to the significant financial incentives involved, there is a concern regarding the potential for illicit sales of promising vaccine candidates prior to obtaining official approval from regulatory authorities. This is a biosecurity threat. The illegal vaccine may introduce new strains or recombine with future licensed vaccines. This may eventually lead to reversion to virulence [149].

If the vaccines evaluated under the Philippine condition were approved for commercial use without demonstrating cross-protection, they can still provide benefits in regions where those specific strains are prevalent [30]. However, the drawback is that it leaves the swine population vulnerable to other strains. If the virus mutates or if other strains are introduced into the region, a large portion of the swine population could still be at risk. Moreover, using a strain-specific vaccine could potentially create selective pressure on the virus. This could lead to an increase in the prevalence of the strains not covered by the vaccine, which could then become the dominant strains.

A vaccination drive that provides protection against some, but not all, strains of the ASF virus would be feasible under the following conditions: 1) limited strain diversity; 2) regular surveillance; 3) combination with other control measures; and 4) public awareness and collaboration. To be effective, the vaccine to be used should match the most common strain in a region. The surveillance must not only cover disease frequency. It should include monitoring of the circulating ASF strains. Complementing the vaccination drive with other control measures such as early detection, rapid response, and strict biosecurity can help mitigate the impact of ASF involving strains not covered by the vaccine. Public awareness campaigns and education on the other hand can help ensure compliance with vaccination programs and other control measures.

Laboratories must also be equipped to differentiate infected from vaccinated animals (DIVA). This distinction is crucial for disease control and surveillance purposes. LAVs contain weakened forms of the virus, which can stimulate an immune response in vaccinated animals without causing the disease. However, these vaccinated animals may still test positive for ASFV if they are subjected to diagnostic tests that detect the presence of the virus. Therefore, laboratories need to employ specific diagnostic methods capable of DIVA. This differentiation is necessary to accurately assess the disease status and to ensure the effectiveness of control measures in combating ASF.

6. Conclusion

Despite being discovered in 1921, there is no vaccine made available for commercial use against African swine fever in the market. The complexity of the ASF virus poses significant

challenges for vaccine development, including its large size, genetic complexity, and ability to evade the immune response. Efforts to develop an effective vaccine are ongoing, with some promising live attenuated vaccine candidates showing efficacy against specific ASF strains. However, there are concerns about vaccine safety, duration of protection, and the diversity of ASF virus strains. Field trials have shown encouraging results, but comprehensive safety evaluations are necessary before commercial use.

Availability of Data and Materials

This is a review article and did not use data.

Author Contributions

RS was responsible for all the aspects of this research project

Ethics Approval and Consent to Participate

Not applicable

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Conflict of Interest

The authors declare no conflict of interest.

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