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ASFV Proteins as Drug Targets: Insights from Genomic and Proteomic Studies

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Abstract The study characterizes African swine fever virus (ASFV) proteins that can serve as potential drug targets, leveraging insights from genomic and proteomic analyses. Through high-throughput proteomic analysis, several ASFV proteins, including P34, E199L, MGF360-15R, and E248R, were found to interact with key cellular pathways such as intracellular and Golgi vesicle transport, endoplasmic reticulum organization, lipid biosynthesis, and cholesterol metabolism. Notably, Rab proteins, crucial regulators of the endocytic pathway, were identified as significant interactors of P34 and E199L, suggesting their role in ASFV infection. Additionally, proteins like MGF-505-7R, MGF-360-10L, and MGF360-9L were shown to inhibit the JAK-STAT signaling pathway, thereby evading the host immune response and promoting viral virulence. The I73R protein was identified as a Z-DNA binding protein, providing structural insights that could aid in the design of targeted inhibitors. The findings highlight several ASFV proteins as critical players in the virus's ability to hijack host cellular mechanisms and evade immune responses. These proteins represent promising targets for the development of antiviral drugs and vaccines, offering new avenues for combating ASFV infections.

Keywords African swine fever virus (ASFV); Drug targets; Proteomics; Genomic analysis; JAK-STAT signaling; Rab proteins; Z-DNA binding protein; Viral virulence; Antiviral strategies

1 Introduction

African Swine Fever Virus (ASFV) is a highly contagious and lethal virus affecting domestic and wild pigs, causing African Swine Fever (ASF). ASF is characterized by severe hemorrhagic fever, leading to high mortality rates, often reaching 100% in affected herds (Bisimwa et al., 2021; Gallardo et al., 2021). The virus belongs to the Asfarviridae family and is the only known DNA virus that can infect pigs. Since its first identification in the early 20th century, ASF has spread across various continents, including Africa, Europe, and Asia, causing significant economic losses in the swine industry (Njau et al., 2021).

The control of ASF is challenging due to the absence of effective vaccines and antiviral treatments. Current control measures primarily rely on the culling of infected animals and strict biosecurity protocols (Hạnh et al., 2021). Identifying drug targets within ASFV is crucial for developing therapeutic strategies to mitigate the impact of the virus. Targeting specific viral proteins can inhibit the virus's ability to replicate and spread, providing a means to control outbreaks and reduce economic losses (Minoungou et al., 2021; Senthilkumar et al., 2022).

Genomic and proteomic studies play a pivotal role in understanding the molecular mechanisms of ASFV infection and identifying potential drug targets. Complete genome analyses of ASFV isolates have revealed genetic variations and mutations that can be exploited for therapeutic interventions (Rajukumar et al., 2021; Senthilkumar et al., 2022). Proteomic studies help in identifying viral proteins that are essential for the virus's life cycle, providing insights into potential targets for antiviral drugs. These studies also aid in understanding the virus's interaction with the host's immune system, which is critical for developing effective treatments (Gallardo et al., 2021; Njau et al., 2021).

This research aims to provide a comprehensive overview of ASFV proteins as potential drug targets, leveraging insights from genomic and proteomic studies. The objectives are to summarize the current understanding of ASFV biology and its impact on the swine industry, highlight the importance of identifying drug targets within ASFV, discuss the role of genomic and proteomic studies in uncovering potential drug targets, and present a detailed

analysis of specific ASFV proteins that could serve as targets for antiviral drug development. By achieving these objectives, this research seeks to contribute to the ongoing efforts to develop effective therapeutic strategies against ASFV, ultimately aiding in the control and prevention of ASF outbreaks.

2 ASFV Genome: Structure and Function

2.1 Detailed description of ASFV genome organization

The African Swine Fever Virus (ASFV) genome is a large double-stranded DNA molecule ranging from approximately 170 to 193 kilobase pairs (kbp) in length, depending on the isolate. The genome is characterized by closely spaced open reading frames (ORFs) that are read from both DNA strands. The termini of the ASFV genome are covalently closed by imperfectly base-paired hairpin loops, which exist in two complementary and inverted forms. Adjacent to these termini are inverted arrays of tandem repeats (Dixon et al., 2013). The ASFV genome encodes a variety of structural and non-structural proteins, with 68 structural proteins and over 100 non-structural proteins identified (Wang et al., 2021). The genome is organized into several multigene families (MGFs), including MGFs 100, 110, 300, 360, and 505/530, which are primarily located within the left terminal 40 kbp and right terminal 20 kbp of the genome (Dixon et al., 2013).

2.2 Key genes involved in viral replication and infection

ASFV encodes numerous genes essential for its replication and infection processes. Key genes include those involved in DNA replication, transcription, and repair, such as the viral DNA polymerase, RNA polymerase, and various transcription factors (Dixon et al., 2013). The pA104R gene, encoding a histone-like protein, plays a crucial role in viral genome packaging and replication by binding to DNA and facilitating genome condensation (Liu et al., 2020; Urbano and Ferreira, 2020). Additionally, genes like A238L, which modulates NFκB and NFAT pathways, and A224L, an apoptosis inhibitor, are involved in immune evasion and virulence (Gallardo et al., 2018). The virus also encodes enzymes for base excision repair, which may help it replicate in the oxidative environment of macrophage cytoplasm (Dixon et al., 2013).

2.3 Genomic variations across ASFV strains

ASFV exhibits significant genomic diversity, with variations primarily arising from the gain or loss of members of its multigene families (Dixon et al., 2013). Comparative genomic analyses have revealed an "open" pan-genome for ASFV, indicating a high level of natural diversity in its genomic composition and regulation. Of the 151-174 genes found in various ASFV strains, only 86 are considered core genes, while the rest are flexible accessory genes (Wang et al., 2020). This diversity is further highlighted by the presence of numerous single-nucleotide variations (SNVs) and structural variations, such as G-quadruplexes (G4s), which can impact gene expression and viral pathogenicity (Gong et al., 2021; Muturi et al., 2021).

2.4 Potential drug targets identified through genomic analysis

Several potential drug targets have been identified through genomic and proteomic analyses of ASFV. G-quadruplexes (G4s) within the ASFV genome have been shown to be stabilizable by G4 ligands, such as N-Methyl Mesoporphyrin (NMM) and pyridostatin (PDS), which can inhibit viral replication (Muturi et al., 2021). The pA104R protein, essential for viral genome packaging, has been identified as a target for stilbene derivatives, which can disrupt its DNA binding and inhibit ASFV replication (Liu et al., 2020). Additionally, proteins involved in the endocytic pathway, such as Rab proteins, have been identified as potential targets due to their role in ASFV infection (García-Dorival et al., 2023). These findings highlight the potential of targeting specific genomic and proteomic elements of ASFV for antiviral drug development.

3 Proteomic Analysis of ASFV

3.1 Overview of ASFV proteome

African swine fever virus (ASFV) encodes more than 150 proteins, many of which have unknown functions. Proteomic studies have been instrumental in identifying and characterizing these proteins, providing insights into their roles in the viral lifecycle and host interactions (Figure 1). For instance, high-throughput proteomic analysis has been used to elucidate the interactome of key ASFV proteins involved in critical infection steps, such as

fusion and endosomal exit of virions (García-Dorival et al., 2023). Additionally, proteomic technology has been employed to examine ASFV-infected cells, identifying infection-associated proteins and their potential roles in pathogenesis (Alfonso et al., 2004).

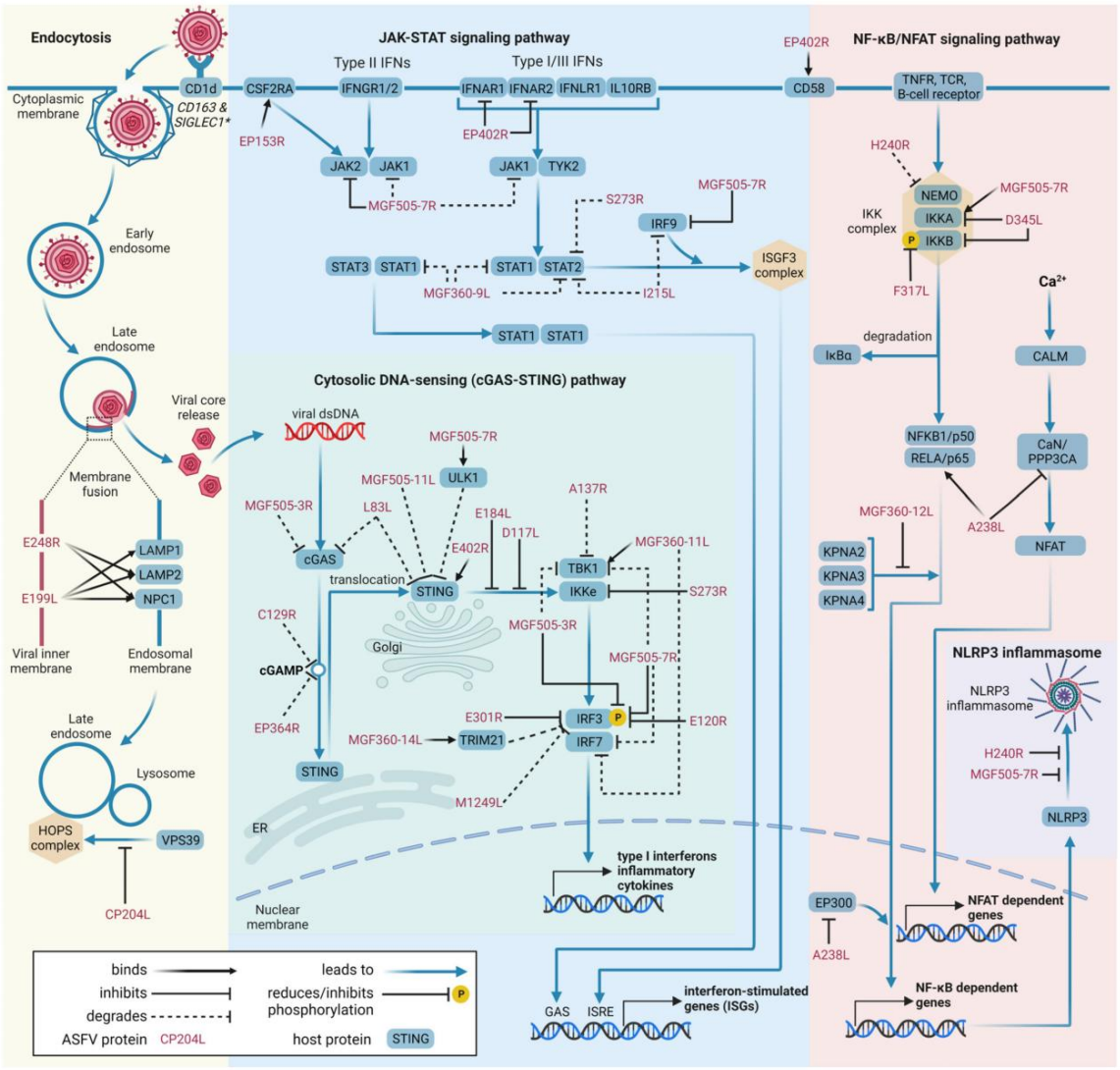

Figure 1 Schematic overview of cellular pathways modulated by ASFV (Adopted from Dolata et al., 2023)
Image caption: The pathways have been reproduced and simplified from KEGG pathway maps for endocytosis (hsa04144), cytosolic DNA-sensing (cGAS-STING) pathway (hsa04623), JAK-STAT signaling pathway (hsa04630), and NF-κB (hsa04064) and NFAT (hsa04660) signaling pathways. Viral proteins are marked in red font, and host proteins are in blue boxes. The effects caused by the interactions between proteins are represented by the edges and explained in the legend. Created with BioRender.com. * CD163 and SIGLEC1 are considered to act together as potential receptors for ASFV entry (Adopted from Dolata et al., 2023)

3.2 Techniques used in proteomic studies

Proteomic studies of ASFV have utilized various advanced techniques to analyze the viral proteome. Key methods include:

Mass Spectrometry (MS): This technique is widely used for the identification and quantification of proteins. It has been employed to study the interactome of ASFV proteins and to identify cellular proteins modified in response to ASFV infection (Alfonso et al., 2004; García-Dorival et al., 2023).

Affinity Purification: This method is used in conjunction with MS to isolate and identify protein-protein interactions, providing insights into the molecular pathways involved in ASFV infection (García-Dorival et al., 2023).

Two-Dimensional Electrophoresis: This technique separates proteins based on their isoelectric point and molecular weight, allowing for the identification of differentially expressed proteins in ASFV-infected cells (Alfonso et al., 2004).

Matrix-Assisted Laser Desorption/Ionization (MALDI) Peptide Mass Fingerprinting: This method is used to identify proteins by matching the mass of peptide fragments to known protein databases (Alfonso et al., 2004).

3.3 Functional classification of ASFV proteins

ASFV proteins have been functionally classified based on their roles in various molecular pathways and cellular processes. For example:

Membrane Trafficking and Lipid Metabolism: ASFV proteins such as P34 and E199L interact with Rab proteins, which are crucial regulators of the endocytic pathway, necessary for ASFV infection (García-Dorival et al., 2023).

Intracellular and Golgi Vesicle Transport: Proteins involved in these pathways have been identified as interacting partners of ASFV fusion proteins, suggesting their role in the viral lifecycle (García-Dorival et al., 2023).

Redox-Related Proteins and Heat Shock Proteins: These proteins are significantly altered in ASFV-infected cells, indicating their involvement in the cellular response to infection (Alfonso et al., 2004).

3.4 Identification of essential proteins involved in viral lifecycle

Proteomic studies have identified several essential ASFV proteins that play critical roles in the viral lifecycle. For instance:

Fusion Proteins (P34, E199L, MGF360-15R, E248R): These proteins are involved in the fusion and endosomal exit of virions, a critical step in the ASFV infection cycle. Their interacting partners include proteins involved in membrane trafficking and lipid metabolism, which are essential for viral entry and replication (García-Dorival et al., 2023).

Proteins Involved in Apoptosis and Transcriptional Modulation: Cellular proteins such as nucleoside diphosphate kinases and members of the Ran-Gppnhp-Ranbd1 complex are modified in response to ASFV infection, suggesting their roles in viral pathogenesis and host cell manipulation (Alfonso et al., 2004).

By leveraging these proteomic techniques and analyses, researchers have gained valuable insights into the ASFV proteome, identifying potential therapeutic targets and advancing our understanding of the virus's interaction with host cells.

4 ASFV Proteins as Drug Targets

4.1 Criteria for selecting ASFV proteins as drug targets

The selection of African Swine Fever Virus (ASFV) proteins as drug targets is guided by several critical criteria. Firstly, the protein must play a pivotal role in the virus's life cycle, such as being essential for viral replication, assembly, or evasion of the host immune response. For instance, the pS273R protease is crucial for the proteolysis of viral polyproteins, making it a prime target for antiviral drugs (Lu et al., 2023). Additionally, proteins involved in the virus's ability to evade the host's immune system, such as those interfering with the interferon (IFN) response, are also considered valuable targets. The ASFV A276R, A528R, and I329L genes have been identified to inhibit various aspects of the IFN response, highlighting their potential as drug targets (Correia et al., 2013; Correia et al., 2023).

Another criterion is the protein's structural and functional uniqueness, which reduces the likelihood of off-target effects on host proteins. For example, the identification of G-Quadruplexes (G4s) in the ASFV genome, which can be stabilized by specific ligands, offers a novel target that is distinct from host cellular mechanisms (Muturi et al., 2021). Furthermore, the protein's amenability to high-throughput screening and drug design, such as the ability to perform virtual screening and molecular dynamics simulations, is also a key consideration. This approach has been successfully applied to identify potential inhibitors of the pS273R protease (Lu et al., 2023).

4.2 Mechanisms of action and inhibition strategies

The mechanisms of action and inhibition strategies for targeting ASFV proteins are diverse and tailored to the specific functions of the proteins. One common strategy is the inhibition of viral entry and replication. For example, targeting endosomal membrane proteins involved in the virus's entry pathway has shown significant inhibition of ASFV, as well as other viruses like Ebola and SARS-CoV-2 (Galindo et al., 2020). This approach leverages the commonalities in the entry mechanisms of different viruses to develop broad-spectrum antivirals.

Another strategy involves the direct inhibition of viral enzymes essential for replication. The pS273R protease, for instance, can be inhibited by compounds identified through virtual screening and molecular dynamics simulations, which disrupt the enzyme's active site and prevent the proteolysis of viral polyproteins (Lu et al., 2023). Similarly, the stabilization of G-Quadruplexes in the ASFV genome by ligands such as N-Methyl Mesoporphyrin (NMM) and pyridostatin (PDS) can inhibit the expression of essential viral genes, thereby reducing viral replication (Muturi et al., 2021).

Inhibition of immune evasion mechanisms is also a critical strategy. ASFV proteins that interfere with the host's IFN response, such as A276R, A528R, and I329L, can be targeted to enhance the host's antiviral defenses. For example, the deletion of these genes from the virus can lead to a stronger IFN response, potentially resulting in an attenuated virus that could be used as a vaccine (Correia et al., 2013; Correia et al., 2023). Additionally, the dual action of the I329L protein in inhibiting multiple Toll-like receptor (TLR) pathways presents an opportunity to develop inhibitors that can restore the host's innate immune response (Correia et al., 2023).

5 Case Studies

5.1 Case study 1: DNA polymerase X

DNA Polymerase X is a crucial enzyme in the replication machinery of African swine fever virus (ASFV). It plays a significant role in the virus's ability to replicate its DNA within the host cells. The structural analysis of ASFV DNA Polymerase X has revealed unique features that differentiate it from other polymerases, making it a potential target for antiviral drug development. The enzyme's active site and its interaction with DNA substrates have been characterized, providing insights into its mechanism of action and potential inhibition strategies (Wang et al., 2021).

5.2 Case study 2: p72 major capsid protein

The p72 major capsid protein is the most abundant structural protein in ASFV, forming the outermost icosahedral capsid of the virion. Recent studies have identified nanobodies against the p72 protein, which were screened from a camelid immune VHH library using phage display techniques. Among the identified nanobodies, Nb25 showed the highest affinity to both recombinant and native p72 protein. Nb25's long CDR3 region allows it to access hidden epitopes, making it a valuable tool for diagnostic and therapeutic applications. The specificity and high affinity of Nb25 to p72 suggest its potential use in biosensors and immunoassays for ASFV detection (Yang et al., 2020).

5.3 Case study 3: dUTPase

Deoxyuridine 5′-triphosphate nucleotidohydrolase (dUTPase) is an essential enzyme for ASFV replication, catalyzing the hydrolysis of dUTP to dUMP. Structural studies of ASFV dUTPase (E165R) have provided detailed insights into its active site configuration, which is highly similar to dUTPases from other pathogens like Plasmodium falciparum and Mycobacterium tuberculosis (Figure 2). This similarity suggests that existing inhibitors for these pathogens could be repurposed for ASFV. Additionally, monoclonal antibodies targeting specific antigenic regions of ASFV dUTPase have been developed, showing inhibitory effects on the enzyme's activity. These findings highlight dUTPase as a promising target for antiviral drug development against ASFV (Li et al., 2019; Zhang et al., 2021).

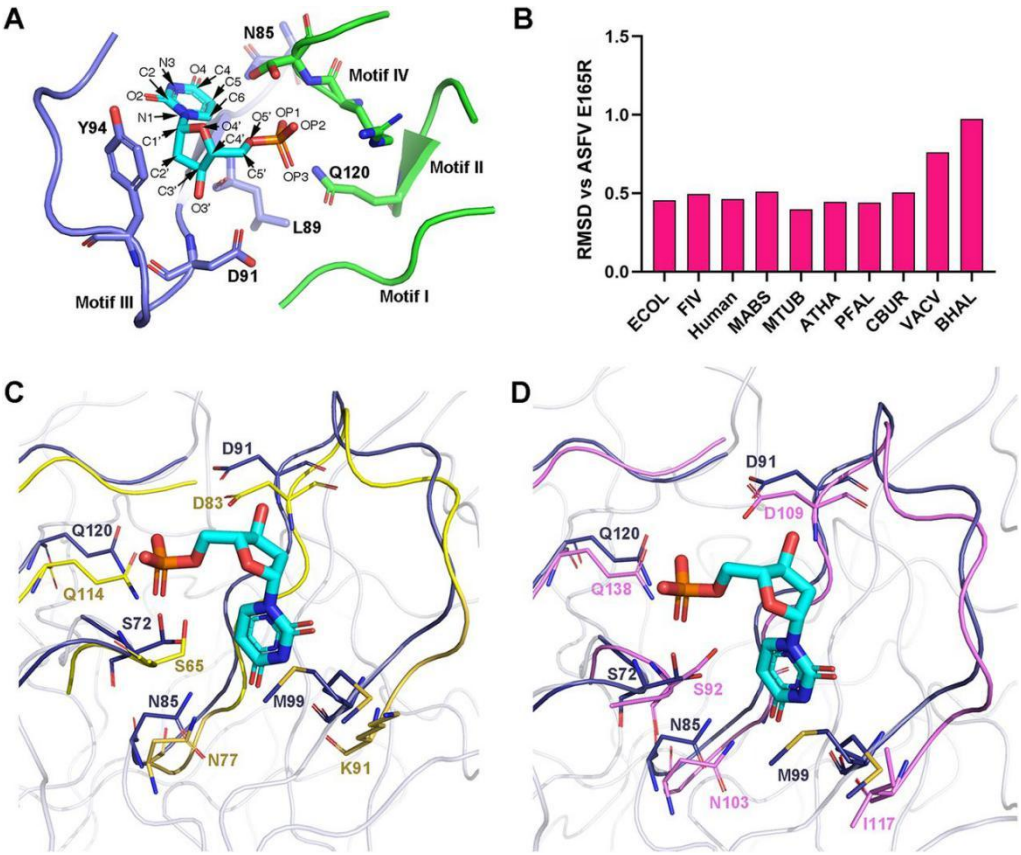

Figure 2 FIG 4 Comparison of the structures of active center motifs of different trimeric dUTPases (Adopted from Li et al., 2019)

Image caption: (A) The four enzyme active center motifs (I, II, III, and IV) of E165R. The atom names of the dUMP are indicated and side chains of the residues that form atom contacts with the dUMP are shown as sticks. (B). The RMSD values between motifs I, II, III, and IV from ASFV E165R and from other trimeric dUTPases. (C) Superimposition of the active center motifs (I, II, III, and IV) from ASFV E165R (blue) with those of *M. tuberculosis* dUTPase (yellow). The side chains of the residues that form hydrogen bonds with dUMP in ASFV E165R (please refer to Fig. S1B in the supplemental material) and those of their corresponding aligned residues in *M. tuberculosis* are shown as sticks. (D) Superimposition of the active center motifs (I, II, III, and IV) from ASFV E165R (blue) with those of *P. falciparum* dUTPase (pink). The side chains of the residues that form hydrogen bonds with dUMP in ASFV E165R (please refer to Fig. 2) and those of their corresponding aligned residues in *P. falciparum* are shown as sticks. ECOL, *Escherichia coli*; MABS, *Mycobacterium abscessus*; MTUB, *Mycobacterium tuberculosis*; ATHA, *Arabidopsis thaliana*; PFAL: *Plasmodium falciparum*; CBUR, *Coxiella burnetii*; VACV, *Vaccinia virus*; BHAL, *Bacillus halodurans* (Adopted from Li et al., 2019)

6 Genomic and Proteomic Integration

6.1 Integration of genomic and proteomic data for comprehensive target identification

The integration of genomic and proteomic data is crucial for the comprehensive identification of drug targets in African swine fever virus (ASFV). By combining these two data types, researchers can gain a more holistic view of the virus's biology and its interaction with host cells. For instance, high-throughput proteomic analyses have been used to elucidate the interactome of ASFV proteins, identifying potential interacting partners and molecular pathways involved in the infection cycle (García-Dorival et al., 2023). This approach allows for the identification of proteins that are not only encoded by the virus but also those that are significantly altered in the host cells upon infection (Alfonso et al., 2004). Such integrative studies have revealed critical insights into the roles of various proteins in processes like membrane trafficking and lipid metabolism, which are essential for ASFV infection and replication (García-Dorival et al., 2023).

6.2 Use of bioinformatics tools to predict protein-drug interactions

Bioinformatics tools play a pivotal role in predicting protein-drug interactions, especially when integrating genomic and proteomic data. These tools can analyze large datasets to identify potential drug targets and predict their interactions with small molecules. For example, proteogenomic mapping has been employed to create

detailed maps of gene-protein-disease connections, which can be used to prioritize candidate drug targets (Pietzner et al., 2021). Additionally, computational pipelines can identify synthetic lethality and prioritize tumor-associated antigens for immunotherapy targets, as demonstrated in cancer research (Lei et al., 2023). These methodologies can be adapted to ASFV research to predict interactions between viral proteins and potential antiviral compounds, thereby facilitating the development of targeted therapies.

6.3 Challenges in correlating genomic data with proteomic findings

Despite the advantages of integrating genomic and proteomic data, several challenges remain. One significant challenge is the poor correlation between mRNA and protein levels, which complicates the interpretation of data and the identification of true drug targets (Lei et al., 2023). Proteins can exist in multiple forms and locations within the cell, and their functions can vary depending on their cellular context (Butler and Overall, 2009). This pleiotropy necessitates careful interpretation of proteomic data to avoid misidentification of drug targets. Additionally, the dynamic nature of protein expression and modification during viral infection adds another layer of complexity. For instance, ASFV infection leads to significant changes in the host cell proteome, including the overexpression of redox-related proteins and heat shock proteins, which may play distinct roles in the infection process (Alfonso et al., 2004). These challenges highlight the need for robust bioinformatics tools and experimental validation to accurately correlate genomic data with proteomic findings and identify viable drug targets.

By addressing these challenges and leveraging the strengths of both genomic and proteomic data, researchers can enhance the identification and validation of ASFV drug targets, ultimately contributing to the development of effective antiviral therapies.

7 Current Advances in ASFV Drug Development

7.1 Overview of current therapeutic strategies against ASFV

African swine fever virus (ASFV) is a highly contagious and deadly virus affecting domestic and wild pigs, with no available vaccine or effective therapy. Current therapeutic strategies primarily focus on antiviral drugs that target various stages of the viral life cycle. One promising approach involves targeting endosomal membrane proteins, which are crucial for viral entry into host cells. Experimental and FDA-approved compounds targeting these proteins have shown significant inhibition of ASFV replication, suggesting that cellular proteins related to the endocytic pathway can serve as suitable targets for broad-spectrum antiviral compounds (Galindo et al., 2020).

7.2 Small molecules and peptide inhibitors targeting ASFV proteins

Small molecules and peptide inhibitors have emerged as potent tools in the fight against ASFV. Recent studies have highlighted the potential of small molecules to inhibit RNA-binding proteins, which play crucial roles in various cellular activities and viral replication. These inhibitors can disrupt the interaction between RNA-binding proteins and RNA, thereby impeding viral replication (Wu, 2020). Additionally, peptide-based ligands have shown promise in the affinity purification of biotherapeutics, including those targeting viral proteins. These ligands offer high binding affinity and selectivity, making them excellent candidates for developing next-generation antiviral drugs (Chu et al., 2020).

7.3 Potential for RNA interference and CRISPR/Cas9 technologies

RNA interference (RNAi) and CRISPR/Cas9 technologies represent cutting-edge approaches for targeting ASFV at the genetic level. CRISPR/Cas9, in particular, has shown remarkable efficacy in inhibiting ASFV replication by targeting the viral p30 gene (CP204L). This gene-editing technology can abrogate plaque formation and significantly reduce virus yields, demonstrating its potential as a robust antiviral strategy (Hübner et al., 2018). Furthermore, RNA-based therapeutics, including small-interfering RNAs (siRNAs) and microRNAs (miRNAs), have the potential to target undruggable genes and gene products, offering new therapeutic paradigms for ASFV and other viral diseases (Dowdy, 2017). Recent advances in the recruitment of RNAi and CRISPR/Cas pathways in mammalian cells have further underscored their potential as specific and efficient antiviral therapeutics with minimal off-target effects (Chin et al., 2017).

8 Future Directions

8.1 Emerging technologies in ASFV drug target identification

The identification of drug targets for African Swine Fever Virus (ASFV) has significantly advanced with the advent of high-throughput proteomic and genomic technologies. Techniques such as affinity purification coupled with mass spectrometry have been instrumental in elucidating the interactome of ASFV proteins, revealing critical interactions with host cellular machinery. For instance, the identification of Rab proteins as key interactors of ASFV proteins P34 and E199L highlights the importance of the endocytic pathway in ASFV infection, suggesting potential therapeutic targets (García-Dorival et al., 2023). Additionally, the comprehensive mapping of virus-host and virus-virus protein interactions provides a systematic overview of the ASFV interactome, identifying crucial molecular mechanisms and potential antiviral targets (Dolata et al., 2023). These emerging technologies not only enhance our understanding of ASFV biology but also pave the way for the development of novel antiviral strategies.

8.2 Prospects of personalized medicine in treating ASFV

Personalized medicine, which tailors treatment based on individual genetic and proteomic profiles, holds promise for ASFV treatment. The integration of proteomic data with genomic information can identify specific biomarkers and therapeutic targets unique to different ASFV strains or host responses. For example, the identification of conserved epitopes in ASFV proteins, such as the CD2v protein, can inform the development of targeted vaccines and diagnostic tools (Liu et al., 2022). Moreover, the use of monoclonal antibodies against specific ASFV proteins, like p54, demonstrates the potential for personalized therapeutic approaches that can enhance the efficacy of treatment and control measures (Petrovan et al., 2020). As our understanding of ASFV-host interactions deepens, personalized medicine approaches could significantly improve the management and outcome of ASFV infections.

8.3 Importance of continued research in ASFV genomics and proteomics

Continued research in ASFV genomics and proteomics is crucial for the ongoing battle against this devastating virus. The dynamic nature of ASFV and its ability to evade host immune responses necessitate a thorough understanding of its genetic and proteomic landscape. Studies focusing on the modulation of host antiviral innate immunity by ASFV proteins provide insights into potential vaccine targets and antiviral drugs (He et al., 2022). Furthermore, the identification of novel therapeutic targets through proteomic analyses underscores the importance of sustained research efforts (Henry et al., 2022). By expanding our knowledge of ASFV genomics and proteomics, we can develop more effective diagnostic tools, vaccines, and treatments, ultimately leading to better control and eradication of African Swine Fever.

9 Concluding Remarks

Recent genomic and proteomic studies have significantly advanced our understanding of African Swine Fever Virus (ASFV) and its potential as a target for therapeutic intervention. High-throughput proteomic analyses have elucidated the interactome of several ASFV proteins, identifying critical molecular pathways involved in the virus's life cycle, such as intracellular and Golgi vesicle transport, endoplasmic reticulum organization, lipid biosynthesis, and cholesterol metabolism. Additionally, bioinformatics analysis has revealed numerous G-Quadruplex-forming sequences within the ASFV genome, which can be stabilized by specific ligands, thereby inhibiting viral replication. These findings underscore the importance of targeting viral proteins and genomic structures to develop effective antiviral strategies.

The identification of ASFV proteins and genomic structures as drug targets holds significant promise for the development of novel antiviral therapies. For instance, the discovery of Rab proteins as crucial regulators of the endocytic pathway necessary for ASFV infection suggests that targeting these proteins could disrupt the virus's ability to enter and exit host cells. Furthermore, the stabilization of G-Quadruplexes in the ASFV genome by ligands such as N-Methyl Mesoporphyrin and pyridostatin has demonstrated potential in inhibiting viral replication in vitro. These targeted approaches could lead to the development of broad-spectrum antiviral compounds that are effective against ASFV and other pathogenic viruses.

The future of ASFV research lies in the continued integration of genomic and proteomic data to uncover novel therapeutic targets and develop effective antiviral strategies. The use of multi-omics approaches, combining proteomics, genomics, and transcriptomics, will be crucial in identifying mechanisms of resistance and potential drug targets. Additionally, the exploration of cross-cancer effects of circulating proteins and their modulation by lifestyle changes could provide new insights into the prevention and treatment of ASFV infections. As research progresses, the development of targeted therapies and vaccines will be essential in mitigating the impact of ASFV on the global swine population and preventing future outbreaks.

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Conflict of Interest Disclosure

The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

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