STAR-IDAZ
International Research
Consortium on Animal Health

2022 African Swine Fever Virus Research Review

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2022 African Swine Fever Virus

Research Review

Full Report: https://www.star-idaz.net/reports/irc/

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INSIGHT EDITING LONDON

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GARA

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Commissioning Body

This report was commissioned by the STAR-IDAZ International Research Consortium in collaboration with the Agricultural Research Service, United States Department of Agriculture, and the Global African Swine Fever Research Alliance.

The STAR-IDAZ International Research Consortium

The STAR-IDAZ International Research Consortium (IRC) is a global initiative aiming to coordinate research programmes at the international level and to contribute to the development of new and improved animal health strategies for priority diseases/infections/issues. The partners, research funders and programme owners, together form the Executive Committee which is supported by a Scientific Committee of 16 experts and an EU-funded Secretariat (SIRCAH – Horizon Europe Grant Agreement Number 727494).

The target deliverables of the STAR-IDAZ IRC include candidate vaccines, diagnostics, therapeutics, other animal health products and procedures, and key scientific information/ tools to support risk analysis and disease control. To achieve these goals, the IRC partners agree to coordinate/align their research programmes to address identified research needs relating to the priority topics and to share results. Research gaps identified by expert Working Groups are organised into research roadmaps for the development of (i) candidate vaccines, (ii) diagnostics, (iii) therapeutics and (iv) disease control strategies, providing a structure to plot the identified research gaps and focus future investment (Entrican et al. 2021).

Agricultural Research Service, United States Department of Agriculture

The Agricultural Research Service (ARS) is the principal in-house research agency of the United States Department of Agriculture (USDA). ARS is one of four agencies in the Research, Education, and Economics (REE) mission and is charged with extending the nation's scientific knowledge with research projects in agriculture, human nutrition, food safety, natural resources, and the environment. ARS supports more than 2,000 scientists organized into approximately 660 permanent research projects at over 90 locations across the country and five laboratories overseas.

ARS conducts innovative research to find solutions to problems of high national priority that impact the American people daily. ARS often undertakes high-risk research endeavours to make significant breakthroughs in important problem areas, including biodefence initiatives to detect, prevent, and mitigate the impact of especially dangerous infectious diseases that pose a threat to animals and public health.

Global African Swine Fever Research Alliance

The Global African Swine Fever Research Alliance (GARA) was founded in 2013 at the Plum Island Animal Disease Center in New York, US. Bringing together an international group of partners, collaborators, and stakeholders, the mission of GARA is to expand and maintain global research partnerships that will generate scientific data critical for the progressive prevention, control, and potential eradication of African swine fever. This mission is articulated through six strategic goals:

1. Identify research opportunities and facilitate collaborations within the Alliance
2. Conduct strategic and multi-disciplinary research to better understand ASF
3. Determine social and economic drivers and impact of ASF
4. Develop novel and improved tools to support the prevention and control of ASF
5. Determine the impact of ASF prevention and control tools
6. Serve as a communication and technology-sharing gateway for the global ASF research community and stakeholders

Purpose of the Report

African swine fever is currently the greatest single threat to global pork production, and our options for controlling and eradicating this disease remain highly limited. Stopping the current outbreak will require coordinated international research and biosecurity efforts. These efforts should be focused on the areas of greatest potential, and this requires regular updates and analyses to inform researchers, policymakers, and stakeholders of the current state of the field.

The primary background for this update is the African Swine Fever Gap Analysis Report published by the Global African Swine Fever Research Alliance (GARA) in November 2018 (GARA 2018), supplemented by the proceedings of the 3rd annual GARA Scientific Workshop in 2016 (GARA 2016). The purpose of this report is to revisit the research areas discussed in these resources, report relevant progress, and provide a general overview of the research that has been conducted across the major fields of African swine fever research since 2015. This report also incorporates research updates and input from leading scientists in the field, thereby providing an up-to-date picture of research around the world, enriched by the first-hand knowledge of researchers working at the cutting edge.

The findings of this report will be used to support future detailed gap analyses that will also incorporate expert opinion and review of current research and control measures, alongside knowledge of on-the-ground countermeasures (both in use and under development) and their efficacy. Importantly, this literature review does not attempt to rank the knowledge gaps identified, and this will therefore form a key part of future analyses.

About the Author

Dr Daniel Ackerman completed his Ph.D. in biological sciences and his subsequent post-doctoral studies at Carnegie Mellon University, Pittsburgh, USA. Since then, he has developed advanced communication and editing skills, and joined Insight Editing London in 2020. Daniel has assisted with the publication of diverse research articles during his time with IEL, rapidly building his reputation for writing and editing excellence across fields. He also recently co-authored the well-received and widely read Animal Influenza Research Review and Gap Analysis 2021.

Daniel Ackerman

About the Editor

Lucy Robinson

Dr Lucy Robinson gained her D.Phil. in veterinary immunology from the University of Oxford, UK, and continued her post-doctoral research into exotic infections at the Singapore Immunology Network. Following her editorial training and freelance experience, Lucy founded Insight in 2009 and has since successfully assisted with the publication of hundreds of articles and the construction of successful grant applications across diverse scientific fields. She has spoken at international conferences and delivered effective writing training to scientists from around the globe. Alongside Daniel Ackerman, she recently co-authored the Animal Influenza Research Review and Gap Analysis 2021.

Executive Summary

This report combines a comprehensive literature review with input from leading scientists across the field (for details of contributors, see here) to describe progress made in African swine fever virus research globally since 2015. By reference to previously identified knowledge gaps and expert consultation, we provide a literature-based update that identifies some of the areas in which future research and research funding should be targeted for maximum impact. The gap analysis presented here is intended to be used as a tool to supplement future in-depth gap analyses that include additional factors.

African swine fever has posed the greatest global threat to pig farming and pork production since its introduction to Georgia in 2007. The disease spread rapidly across Eastern and Central Europe, where it remained until 2015. Since then, it has spread into Western Europe, and in 2018, it was introduced into China. The pandemic has not slowed over the past 3 years, with further spread through Europe and East/Southeast Asia. In 2021, African swine fever reached the Dominican Republic and Haiti. The fight against this disease is in an urgent phase, and this report will summarize the substantial research progress that has been made in the face of this pandemic.

Research priorities by area:

Understanding African Swine Fever Virus

Epidemiology

African swine fever virus (ASFV) is a difficult pathogen to track and control due to its abilities to survive in the environment (e.g. within wild boar carcasses) and to be transmitted and maintained even within very low-density populations of swine. The transmission characteristics of ASFV also vary depending on geography – forest coverage, mountain ranges, number of water bodies, etc. – and local farm management systems, with smallholder/backyard farms more likely to facilitate untracked spread of the virus within domestic herds and to wild boar. One of the biggest challenges to ASFV epidemiology is the wide range of environments covered by the ongoing African swine fever (ASF) pandemic – many different ecological, geographical, and socioeconomic systems are currently dealing with ASF outbreaks, including Europe, Southeast Asia, Russia, Africa, and even island nations like Timor-Leste. This situation does not lend itself to one-size-fits-all solutions. Meanwhile, questions and controversies remain in many areas of ASFV epidemiology, and lack of standardization between study designs often makes direct comparisons difficult.

In Europe, the past 6 years have seen introductions of ASF to the Czech Republic, Romania, Belgium, Bulgaria, Hungary, Moldova, Serbia, Slovakia, Greece, Germany, North Macedonia, and Italy. Only two countries – the Czech Republic and Belgium, in which no domestic pigs were infected – now appear to have eradicated ASF via swift disease identification and biosecurity measures. Elsewhere (including Bulgaria, Hungary, Poland, Romania, and Slovakia in particular) the virus generally appears to be gaining ground, with numerous outbreaks especially on smallholder farms. Epidemiological investigations have revealed some details of the ASFV transmission patterns unique to these countries (e.g. Poland, where wild boar infections are dominant, vs. Romania, where domestic outbreaks are more common) and have also identified the apparent evolution of lower-virulence ASFV strains in Estonia and Latvia.

In Asia, the introduction of ASFV to China had dramatic socioeconomic consequences, and the country's pork production now appears to be stabilizing/increasing due to a shift in economic focus from smallholder farms to large, consolidated commercial producers. However, the virus has continued to cross international borders at a brisk pace, with subsequent introductions into Mongolia, Vietnam, Cambodia, Hong Kong, North Korea, Laos, the Philippines, Myanmar, Indonesia, Timor-Leste, South Korea, India, Papua New Guinea, Malaysia, Bhutan, and Thailand. Rural pig farms and smallholder operations dominate in many of these countries, and the resulting outbreaks have proven especially difficult to track. Epidemiological data on farm management and wild boar populations in Southeast Asia is lacking, and many lessons learned in Eurasia are unlikely to be applicable here.

Throughout the current pandemic, wild boar have played an important role in the transmission and maintenance of the disease, though the parameters involved (e.g. transmission speed, environmental contamination and spread to domestic pigs, the importance of boar population density, etc.) remain mostly unclear and may vary between geographical regions. Numerous risk factor assessments have been published for various European countries, with differing findings on the spatiotemporal correlation between wild boar infections and domestic outbreaks. Meanwhile, no conclusive role for carrier animals (wild boar that survive ASF and continue to shed the virus asymptomatically) has been demonstrated in the current pandemic, though this remains an active area of research. Environmental transmission (from infected wild boar carcasses to other boar or to domestic pigs) is also under intense study and may play a more significant role in colder climates.

Arthropods, the vectors responsible for half of ASFV's native sylvatic cycle in Africa, have also come under scrutiny in Europe. To date, no definitive link has been shown between Eurasian ticks and ASFV transmission in the current pandemic, but these studies continue to fill an important knowledge gap (particularly in Asia, where our understanding of tick populations is very limited).

The one factor that has proven relatively constant across the many environments of the current pandemic is human activity – anthropogenic factors have conclusively played a major role in the propagation and maintenance of ASF, with many recent reports describing routes of human-mediated transmission in Europe, Asia, Africa, and elsewhere. Within national borders, these routes include the transport and sale of infected domestic animals, feeding of untreated swill and food waste to pigs, inadequate biosecurity on farms, and uncontrolled hunting of infected boar leading to population dispersal and wider transmission patterns. Internationally, both legal and illegal transport of pigs can carry ASFV across great distances, with the recent introductions to Timor-Leste, the Dominican Republic, and Haiti proving that oceans are no barrier to anthropogenic transmission.

Virology/Molecular Biology

ASFV is a highly complicated virus, with a complex physical structure and large, G:C-rich genome that make virological studies inherently difficult. Sequencing of new ASFV isolates historically focused on specific regions of interest (e.g. the p72/B646L gene), but concentrating exclusively on such limited sequences may miss substantial genetic diversity. Since 2015, the continuing development and validation of next- and third-generation sequencing technologies has brought a dramatic uptick in the number of fully sequenced ASFV genomes. Many complete ASFV genome sequences have now been published, and the information in these papers is useful also for comparing the circumstance-specific efficacy and usability of the various new sequencing technologies now available on the market. The strengths and weaknesses of various instruments (e.g. for short-read vs. long-read sequencing) must be kept in mind when sequencing new isolates and resequencing old ones. Other recent studies have focused on the transcriptomics of ASFV infection (both from viral and host perspectives) and the potential roles of small non-coding RNAs in the infection process.

Understanding the functions of viral proteins is also critical for many areas of ASF research, including the study of viral evolution, the identification of the determinants of virulence and host immune response, and the development of new vaccine candidates. From a proteomic standpoint, approximately 50% of ASFV's genome remains functionally unresolved, with many protein products that are essentially uncharacterized. Though the picture is still not fully resolved, recent studies focusing on individual viral proteins have begun to narrow this deficit, using structural biology and in vitro approaches to determine the functions of poorly understood proteins. Computational resources also continue to grow in both power and accessibility, allowing complicated protein modelling and interaction studies that explore the molecular-scale activities of virally encoded enzymes and transcription factors.

Pathogenesis

Different strains of ASFV can vary widely in virulence, but the determinants of these differences are not well-understood. High-resolution genomic assays are required to tease apart the often-subtle genetic differences between different ASFV isolates, and detailed in vitro studies can begin to identify the functions and interacting partners of viral proteins. Particularly critical functions for virulent strains are efficient entry and infection, manipulation of infected cells to avoid immune detection, and release of factors that lead to widespread lymphocyte death and general immunodeficiency. Our ability to generate new vaccine candidates is also dependent on understanding how individual proteins are used by ASFV to alter host cell immune responses.

Recent advances in sequencing and proteomic technologies, and in in vitro models, have allowed researchers to identify specific viral proteins that are required for infection, host immune evasion, and virulence - though many questions still remain. Over the past 6 years, studies have identified roles for viral proteins in regulating autophagy, host cell metabolism, and immune-related signalling pathways like the cGAS/STING and JAK/STAT1 pathways. Meanwhile, *in vitro* studies in primary porcine cells have begun to clarify the functions of particularly important proteins like CD2v and the MGF family proteins.

Another important area of ASF pathogenesis research is the African warthog, the second half of ASFV's native sylvatic cycle, which displays remarkable resistance to virulent ASFV infection. Several recent studies have addressed different potential sources (both environmental and genetic) of this resistance and the ways in which they may be applicable to domestic pigs.

Immunology

The most critical host-virus interactions occur at the interface between infected cells and the host immune system. ASFV preferentially infects porcine cells of the monocyte/macrophage lineage, and acute ASF is associated with massive apoptosis of lymphocytes leading to systemic immunodeficiency.

Knowledge of the immune response to ASFV infection, and the various proteins used by the virus to evade this response, is critical for developing an effective treatment and/or vaccine against ASFV. The nature of the anti-ASFV immune response remains unclear and occasionally controversial, with **in vivo** experimental infection studies giving different results regarding the importance of neutralizing antibodies, $CD8^+$ T cell responses, and other immunological factors in the effectiveness of the host immune response.

Since 2015, researchers have identified roles for viral proteins in a wide array of immunomodulatory activities including inhibition of type I interferons, and regulation of

autophagy, apoptosis, and MHC protein expression. Inflammatory cytokine release is another important area of research, and several viral proteins are involved in the control of this process. Viral immune evasion is a complex process involving potential redundancy and/or combinatorial activity within the ASFV proteome – host- and strain-specific factors can combine to produce unpredictable outcomes, making it difficult to generalize specific experimental results. Increased standardization of ASFV gene characterization, and evaluation in multiple strains of varying virulence, will continue to be critical in the future to build our understanding of viral immunomodulation.

Meanwhile, transcriptomic studies have allowed high-resolution mapping of the response of porcine macrophages to ASFV infection, and in vivo analyses of infections with specific ASFV isolates have enabled us to begin to characterize strain-specific immune responses (including the importance of both humoral and cellular activity).

The historical system of genotyping new ASFV isolates based on *p72/B646L* gene sequence has also recently been called into question, and determinants of immunologically homologous vs. heterologous strains have been studied to guide vaccine development and boost our understanding of the requirements for immune protection against ASFV.

Controlling African Swine Fever

Biosecurity

With no commercially available vaccine or antiviral drug active against ASFV, biosecurity and depopulation remain our only lines of defence against the introduction of the virus and spread of the current pandemic. ASF has proven itself a very difficult disease to contain and eradicate, and strict control measures are necessary to provide the best possible chance of managing regional outbreaks.

It is critical that current biosecurity programmes are analysed and validated to determine their efficacy. However, it is also increasingly acknowledged that such measures should be tuned to the specific cultural and socioeconomic circumstances of individual nations and populations in order to be effective. Control measures that are successful in one region/country may not be successful in another.

During the last 6 years, many risk assessments, expert opinion studies, and reviews have been conducted to determine the effectiveness of the different ASF biosecurity measures applied across Eurasia. Studies on the practical effects of wild boar-focused biosecurity measures are critically important, potentially allowing location-specific planning by currently ASF-free countries and opening new avenues for disease control in epidemic regions. Epidemiological

and surveillance data have been used to model the efficacy of wild boar containment measures including culling, feeding bans, hunting restrictions, and the construction of barriers to block wild herd movements. In domestic pigs, scientists have described the various risks present at the farm/environment boundary and the strategies that can be used to mitigate them. Meanwhile, key factors in human-mediated transmission have been identified, including inter-farm movements of people and animals and cross-contamination from wild boar habitats.

Participatory epidemiology has also begun to play an increasing role in ASF biosecurity research, with a growing understanding that smallholder pig farmers and other actors in the pork production chain are far more likely to comply with biosecurity regulations that do not place their cultural and economic livelihoods at risk. Studies of the knowledge, attitudes, and practices of farmers in resource-poor regions have expanded our understanding of the factors underlying biosecurity failure and the measures that can be taken to minimize these risks in different countries.

Surveillance

Unnoticed or unreported ASFV infections are an ever-present danger – once entrenched in regional wild and domestic pig populations, the disease is extremely difficult to eradicate, as demonstrated by the current epidemiological situation in Eurasia. Surveillance programmes allow us to monitor the spread of ASFV, facilitating the rapid identification of infected animals and efficient deployment of biosecurity resources in the event of an outbreak. Recent studies have described new approaches for ASF surveillance, including automated on-farm detection systems, novel sampling methods, and data collection techniques.

From an international standpoint, new computational models have been developed to simplify the collection and analysis of large surveillance datasets, thereby simplifying large-scale epidemiological research and potentially allowing faster governmental and regulatory responses to developing outbreaks. Meanwhile, web databases have been developed to make it easier for pork producers, academics, and regulatory officials to access publicly available surveillance data and design region- specific surveillance strategies.

Diagnostics

Rapid diagnosis of ASF in domestic pigs or wild boar is the first step in effective biosecurity, allowing farmers and regulators to react quickly to developing outbreaks and impose controls before the virus begins to spread unchecked. Today, several effective diagnostics are available to check for the presence of ASFV in various sample types. However, these tests are critically

limited by their requirements for laboratory instrumentation and experienced users – this includes the current “gold standard”, OIE-approved assays like qPCR, ELISA, and immunoperoxidase tests. Since 2015, substantial research effort has focused on the development of diagnostic tests with fewer laboratory requirements, variously detecting ASFV DNA, viral antigens, or anti-ASFV antibodies. New DNA tests include isothermal amplification methods, which gain field applicability by not requiring thermocyclers, and CRISPR/Cas-based assays that allow highly sensitive ASF diagnosis from even limited starting samples. Immunofluorescence and lateral flow assays for ASFV antigens or antibodies continue to be developed and refined to increase their sensitivity. Meanwhile, new sample collection techniques have also been described, aiming to reduce the difficulty of gathering samples (e.g. from wild boar carcasses) in the field and transporting them to diagnostic sites.

Isolation of infectious ASFV is also necessary for confirming a qPCR-positive sample. Currently, this process relies on the use of primary porcine cells, which necessarily reduces standardization due to the inherently donor-specific nature of primary cells. These cells are also generally difficult to culture, increasing labour requirements and introducing potential time delays into diagnostic processes. Stable cell lines have recently been validated for use in in vitro ASFV isolation techniques, avoiding these issues and increasing the reproducibility of standard diagnostic tests.

Vaccines

There is currently no ASF vaccine commercially available. This greatly limits our ability to control the ongoing pandemic, placing extreme pressure on biosecurity and control measures and necessitating the costly depopulation of entire pig herds to prevent the spread of disease. Therefore, vaccine development has remained an active and dynamic field of research over the last 6 years, with studies on the design and testing of live attenuated vaccines (LAVs) somewhat dominating since 2015. However, there are many difficulties involved in developing a live attenuated vaccine (LAV) for ASFV, including the combinatorial nature of ASFV’s complex gene program, the unpredictable effects of multiple gene deletions, and the differences between in vitro and in vivo viral characteristics. Nevertheless, substantial progress has been made since 2015, leading to the identification of several LAV candidates with great potential. ASFV strains with deletions to specific genes have been validated for attenuation *in vitro* and *in vivo*, expanding our knowledge of ASFV protein functions while also demonstrating homologous (and sometimes heterologous) protection against challenge with virulent viruses.

Limited advances have also been made toward different approaches to subunit vaccinations, which may avoid potential biosafety issues associated with LAVs. Elsewhere, researchers

have begun to identify genes potentially useable as markers for DIVA (differentiating infected from vaccinated animals) tests, which will be critical in future vaccine deployment strategies. Several stable cell lines have also been proposed for the production of LAV candidates, removing the necessity of using primary porcine cells for this purpose. However, significant research challenges remain in all of these areas, and current ASFV vaccine candidates have yet to go through a full vaccine development plan subject to a robust regulatory process.

Drugs and Therapeutic Approaches

There are no commercially available antiviral drugs marketed for the treatment of ASF. This lack of antivirals for ASF control limits our options in outbreak response and control. As with vaccines, development of new anti-ASFV drugs (or validation of existing ones for anti-ASFV activity) is hampered by our incomplete understanding of the functional ASFV proteome. Since 2015, studies have begun to address this gap by characterizing the structural biology of important virally encoded enzymes and other factors that may be susceptible to small molecule treatment. Recent studies have tested antivirals both in vitro and in vivo for their ability to reduce ASFV replication, limit viral gene transcription, or otherwise interfere with the ASFV infection pathway.

Disinfectants

ASFV is a tenacious virus, capable of surviving on various surfaces (or within biological matrices like blood, urine, and faeces) for a considerable amount of time depending on environmental circumstances such as temperature and pH level. Disinfection is therefore a critical part of biosecurity, particularly on pig farms where thorough decontamination of affected premises is essential for halting an outbreak. There are many commercial products capable of inactivating ASFV, but their applicability to specific surfaces or contaminated environments is often untested, limiting the ability of farmers and pork producers to make informed decisions during disinfection. Numerous studies have been conducted over the past 6 years to close this gap by testing the efficacy of various disinfectants on relevant surfaces (e.g. steel and concrete) and in the presence of common biological contaminants.

Conclusions

The studies described in this report were selected based on practical parameters (excluding papers not published or available in English) and the degree to which they directly addressed previously identified research gaps in ASFV research (GARA 2018; 2016). The ongoing threat posed by African swine fever has galvanized the ASFV research field, leading to a massive upswing in associated publications. A search of the PubMed database for “African swine fever”, for instance, shows that 45 relevant papers were published in 2014 compared to 398 in 2021. At the time of writing this report (early February 2022), 59 relevant papers had already been published this year. ASFV research is very active and fast-moving. Even this breakneck pace, however, has had trouble matching the speed at which the ongoing pandemic has moved through Eurasia and beyond. Many valuable research papers and reviews were published between 2015 and 2018, but this timeframe accounts for only ~25% of the total papers cited in this report. Far from reflecting a lack of quality or importance in these papers, this is simply attributable to many of them being superseded by recent events. Genomic studies, for instance, have been transformed by new techniques like third-generation sequencing and CRISPR/Cas; novel vaccine candidates have been validated and refined; and previously cutting-edge reviews and risk assessments have been rendered outdated by the introduction of ASF to China and its subsequent spread through Asia. At the time of writing, it is still too early for published risk assessments to have incorporated the recent outbreaks in the Dominican Republic and Haiti, and if ASF reaches the American mainland, it will bring another significant shift in the epidemiological outlook of the current pandemic. The next ASFV research review/gap analysis may look very different from this one.

Meanwhile, the enduring COVID-19 pandemic continues to strain national resources and place additional burdens on international collaboration and research efforts. In this situation, increased research harmonization and international collaboration are a necessity to allow the fastest possible responses to new ASF developments. This includes standardization of viral genome sequencing techniques and diagnostic tests, streamlining of pipelines for reporting ASF detections and accessing these data, and increased integration of research, policy, and resource implementation. For the time being, biosecurity and surveillance remain our only means of preventing and controlling the spread of ASFV. At the local level, particularly in the many resource-poor regions currently suffering with endemic ASF, biosecurity solutions cannot be disentangled from the socioeconomic needs of pig farmers and smallholders – any control measures or strategies that do not take this reality into account are likely doomed to failure. An effective response to this disease will therefore require sustained coordination between researchers, regulators/policymakers, and stakeholders at all levels of the pig production chain.

With this situation in mind, the substantial progress reported here encourages optimism about the future of the ASFV research field. In particular, we are nearer than ever before to the deployment of an effective live attenuated vaccine, and essential studies of biosafety and long-term efficacy are proceeding apace. Rapid advances in sequencing technology, genomics, transcriptomics, and proteomics are rapidly closing knowledge gaps in the ASFV genome and viral protein functions. Computational modelling will continue to open new doors in epidemiology, structural biology, surveillance and risk assessment, and other critical fields of ASFV research. Meanwhile, increasing integration of social sciences into the fields of participatory biosecurity and epidemiology are beginning to address the foundational socioeconomic factors underpinning poor biosecurity.

Altogether, we hope that this report will provide a useful resource for increasing understanding of the advances made between 2015-2021 and for focusing ASF research on areas of critical need. ASFV is a complex and mysterious virus at every level, but the progress made since 2015 has answered many questions relating to the virus itself, the host response to infection, and the interactions between the two. The pace of ASFV research holds great promise for the future, and effective measures for the control and eradication of this disease appear closer now than ever before.

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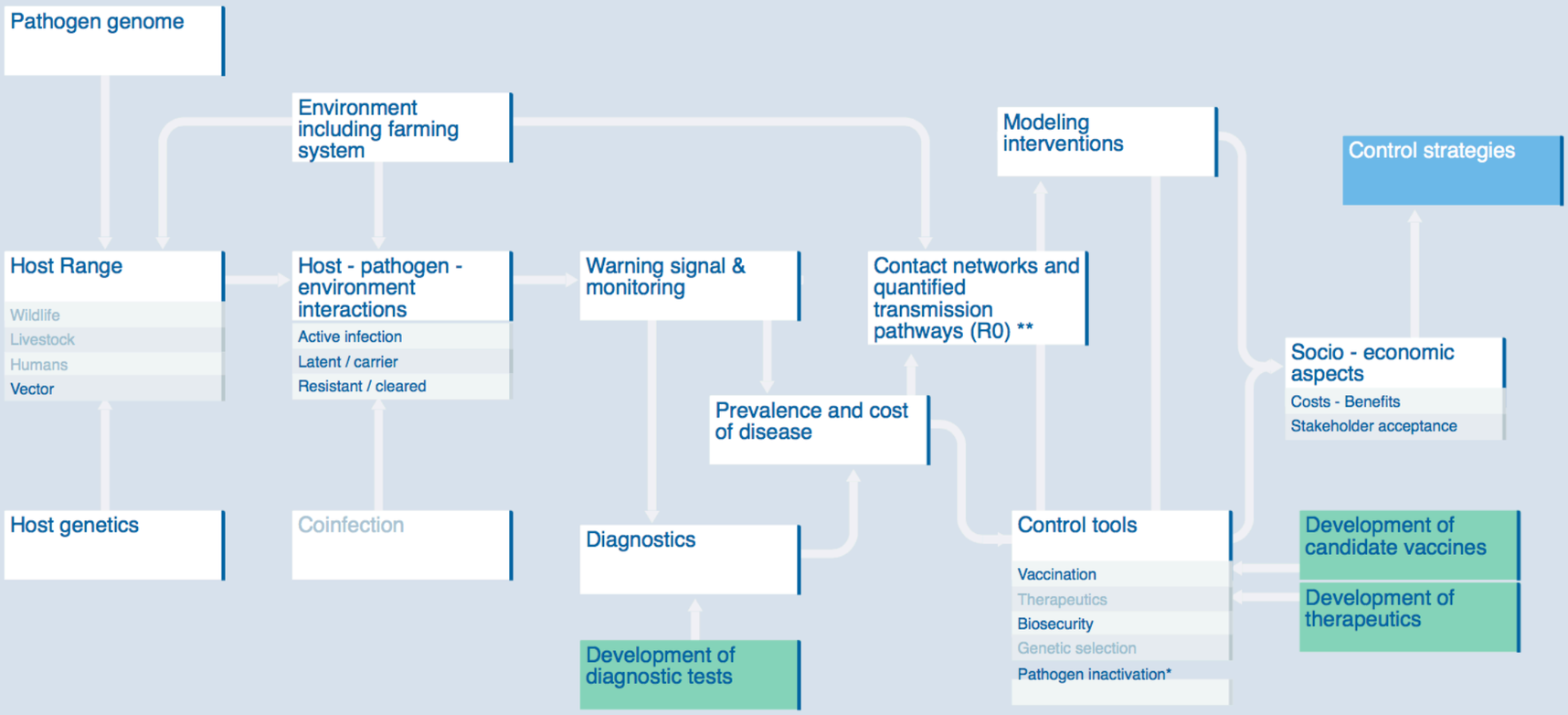
Conflict of Interest Statement: The authors declare no conflict of interest.

Additional Resources: Please see the following websites for additional information and/or resources around the content and aims of this report:

OIE-WAHIS GARA STAR-IDAZ ASFVdb

ASF: DEVELOPMENT OF DISEASE CONTROL STRATEGIES



https://roadmaps-public.star-idaz.net

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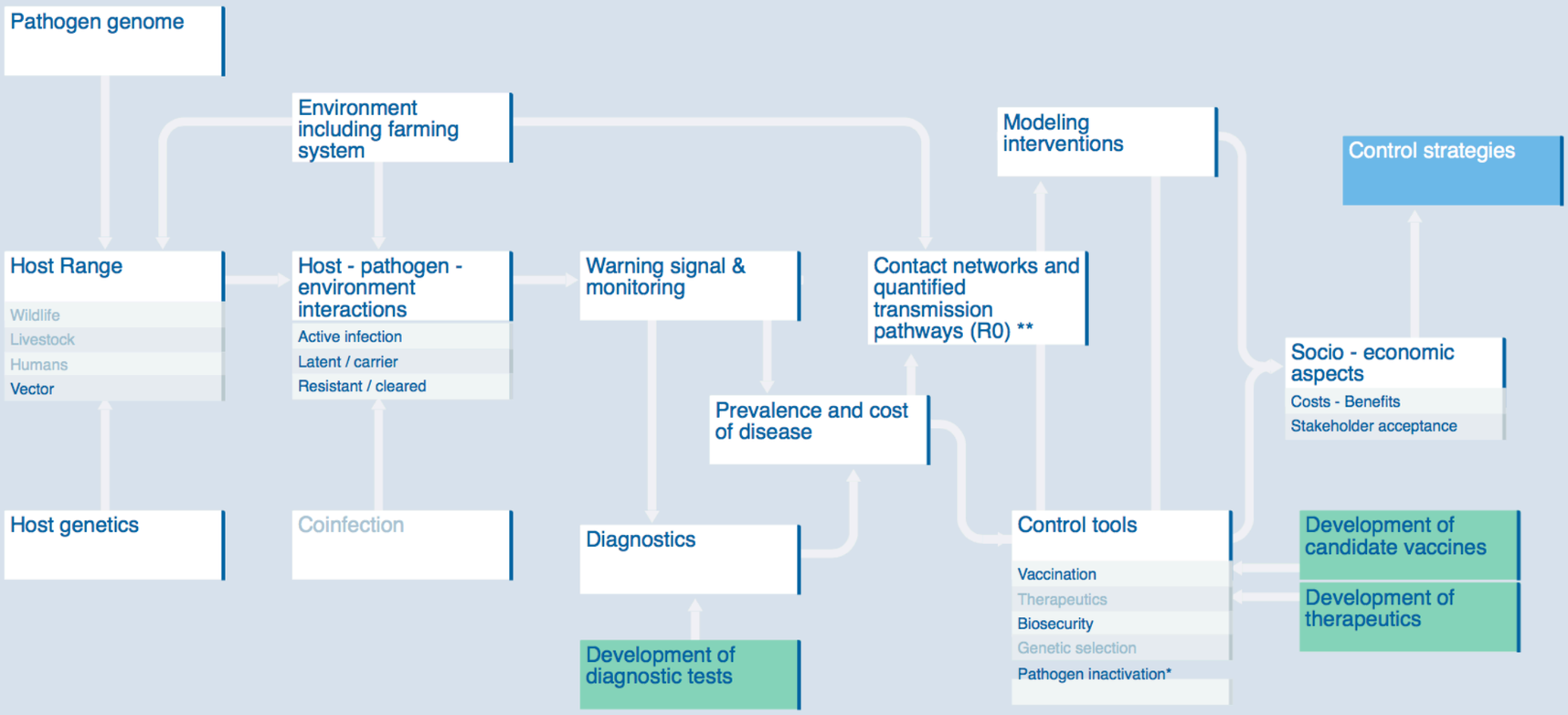

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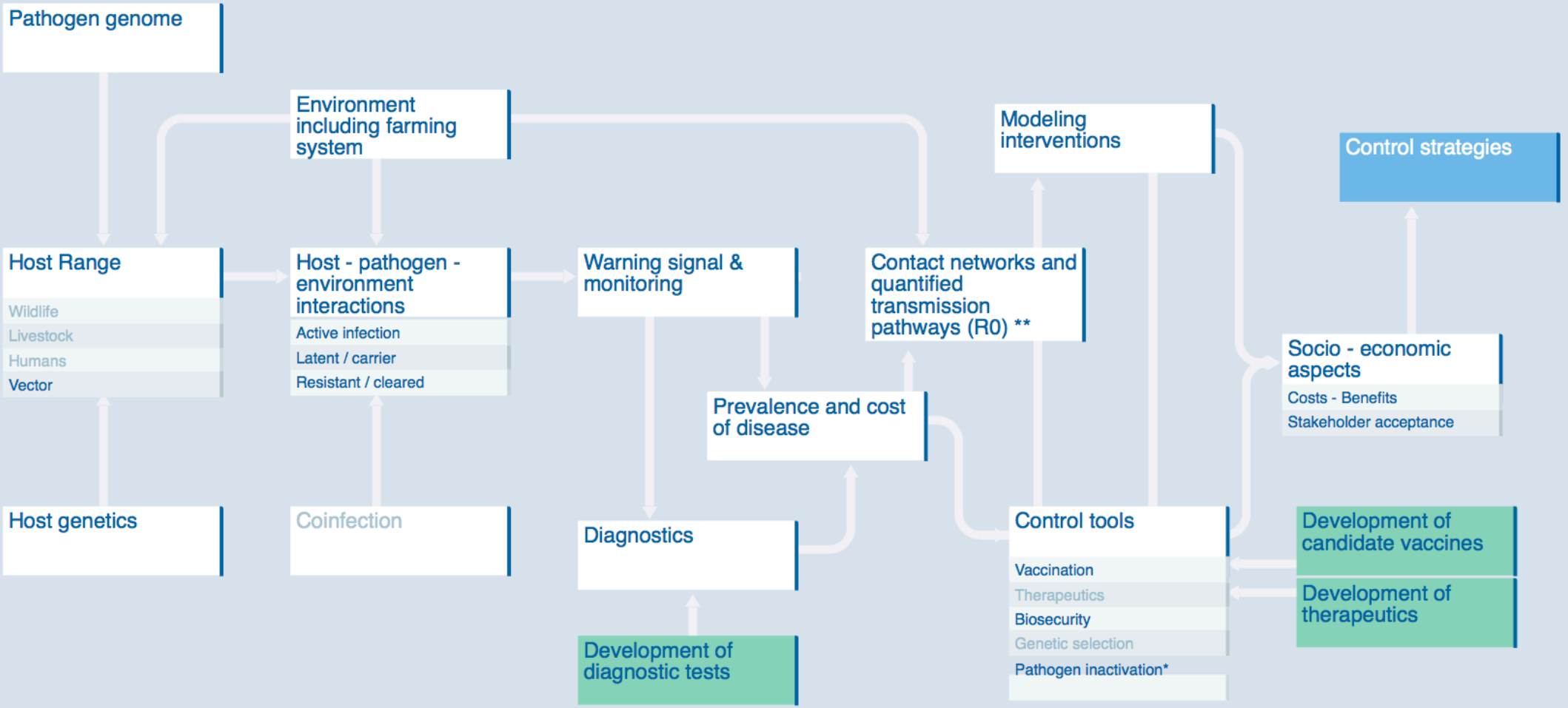

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