Innovation brief

RESEARCH PROGRAM ON Livestock

Photo K. Dhanji/ILRI

GETTING TO GRIPS WITH AFRICAN SWINE FEVER

BUILDING THE EVIDENCE TO CONTROL THE SPREAD OF THE PIG SECTOR'S MOST DAMAGING DISEASE

KEY MESSAGES

African swine fever (ASF) is a viral disease that threatens food security in sub-Saharan Africa and pork production worldwide. There is no prospect of eradication, not least because the virus cannot be maintained in infected areas in wild pigs and soft ticks.

Over the past two decades, molecular and field epidemiology conducted at the International Livestock Research Institute (ILRI) and elsewhere has provided a thorough understanding of ASF's genetic complexity and modes of transmission.

Scientists at ILRI have helped to sequence genomes of the ASF virus, which provides a significant increase in the number and variety of full genomes available for use by the scientific community.

Field studies in East Africa played an important role in designing an Africa-wide strategy to tackle the disease, jointly published by ILRI, the African Union-Interafrican Bureau for Animal Resources (AU-IBAR) and the Food and Agriculture Organization of the United Nations (FAO).

Scientists at ILRI are in the process of developing both live and subunit vaccines to control the disease.

SUMMARY

African swine fever (ASF) poses a serious threat to food security, especially in sub-Saharan Africa. In its most virulent form, it kills all naive pigs, with disastrous consequences for the livelihoods of smallholder farmers. Since 2007, the disease has spread to Europe, Asia and Central America, threatening global pork production. The International Livestock Research Institute (ILRI) has made a significant contribution to understanding the nature of disease, how it spreads and the strategies for control. It has also been involved in researching and developing vaccines which could ensure a better future for Africa's pig sector.

Photo ILRI/Kabir Dhanji

African swine fever is highly contagious. Contaminated farm material, including the urine and manure of infected pigs, can carry and spread African swine fever.

Banner photo: Young Cambra pigs in their pen in Kazinga Village, Mukono, Uganda. Mukono is one of the target districts of the More Pork project under the CGIAR Research Program on Livestock.

ILRI INTERNATIONAL LIVESTOCK RESEARCH INSTITUTE

INTRODUCTION

First identified in imported European pigs in Kenya in 1910, ASF is a large DNA virus belonging to the *Asfaviridae* family. Its more virulent strains — there are 24 currently known genotypes in Africa, two of which have spread to Europe and Asia - kill pigs within 6 to 13 days of infection. Clinical symptoms include high fever and haemorrhaging. Less virulent strains kill between 30% to 70% of infected animals. There are currently no vaccines for ASF and there is no effective treatment.

Recently there has been a dramatic growth in the pig sector in sub-Saharan Africa, and subsequently a significant increase in the number of ASF outbreaks. Between 2016 to 2020, the disease was present in 32 African countries as reported to the World Organization for Animal Health (OIE), and caused particularly heavy losses in countries where pigs are kept in traditional free-range scavenging systems. Besides depriving poor farmers of an income, ASF also reduces the availability of cheap animal protein. Complete eradication of ASF is impossible as the virus is also found in warthogs and other wild suids in Africa in a complex sylvatic cycle involving soft ticks belonging to the genus *Ornithodoros*, and in wild boar in Europe and Asia.

ASF is now a global problem. The virus was introduced to Portugal in 1957 and it soon spread across the Iberian Peninsula. By 1995, the disease had been eradicated in Europe except in Sardinia, but its arrival in 2007 in the Caucasus, most probably in pig swill containing infected pork from Africa, presaged its spread both east and west. The first outbreaks in the Czech Republic occurred in 2017 and it was reported in Belgium the following year. The first outbreaks in China occurred in 2018, since then ASF has caused widespread damage to the agricultural economies of many Asian countries, including Cambodia, North Korea, the Philippines, Vietnam and India. Between 2016 and 2020, eight million pigs were killed by the disease or culled under eradication programmes.

DEVELOPING DIAGNOSTIC TESTS

ILRI's research on ASF began in 2003 when it collaborated with the EU Reference Laboratory for ASF Diagnostics, based at the Centre for Animal Health Research (CISA) in Spain, on the testing of a diagnostic kit in East Africa. Scientists were surprised to find that none of the samples taken from outbreak areas tested positive for ASF antibodies. This may have been related to the characteristics of African pigs, or the fact that the kits had been designed to test for the genotype which had been prevalent in Europe before eradication, rather than Genotype IX, which is found in East Africa.

Photo ILRI/Apollo Habtamu

African swine fever is spread to pigs in many ways, including through contaminated feed.

Unfortunately, diagnostic kits took too long to identify positive cases of ASF — three weeks from the time when symptoms were observed to laboratory confirmation. During this period, the disease was likely to spread, not least because farmers would sell their sick pigs in the market rather than wait for them to be slaughtered as a biosecurity measure. To overcome these problems, ILRI scientists helped to refine diagnostic tests, using a polymerase chain reaction (PCR) assay, and they were part of a Swedish-led team which developed a portable, commercial, real-time PCR kit for use on farms. This has enabled much earlier detection and greatly improved disease control. Diagnostic tests have now been validated by national veterinary services in most East African countries.

Photo ILRI/Kabir Dhanji

A footbath with disinfectant at the entrance to a pig farm ensures that people do not enter with contaminated material on their shoes.

Following ILRI's early research on diagnostics, its scientists focused on the epidemiology — the incidence, distribution and control — of the disease. This involved work at both the molecular and field levels. The use of molecular epidemiology enabled scientists to gain a thorough understanding of the virus's complex genetic profile and the ways in which the disease is transmitted. Work in the field explored, among other things, the role of carrier pigs, modes of transmission, farmer response to the disease, risk factors leading to its spread and methods of control.

UNDERSTANDING TRANSMISSION

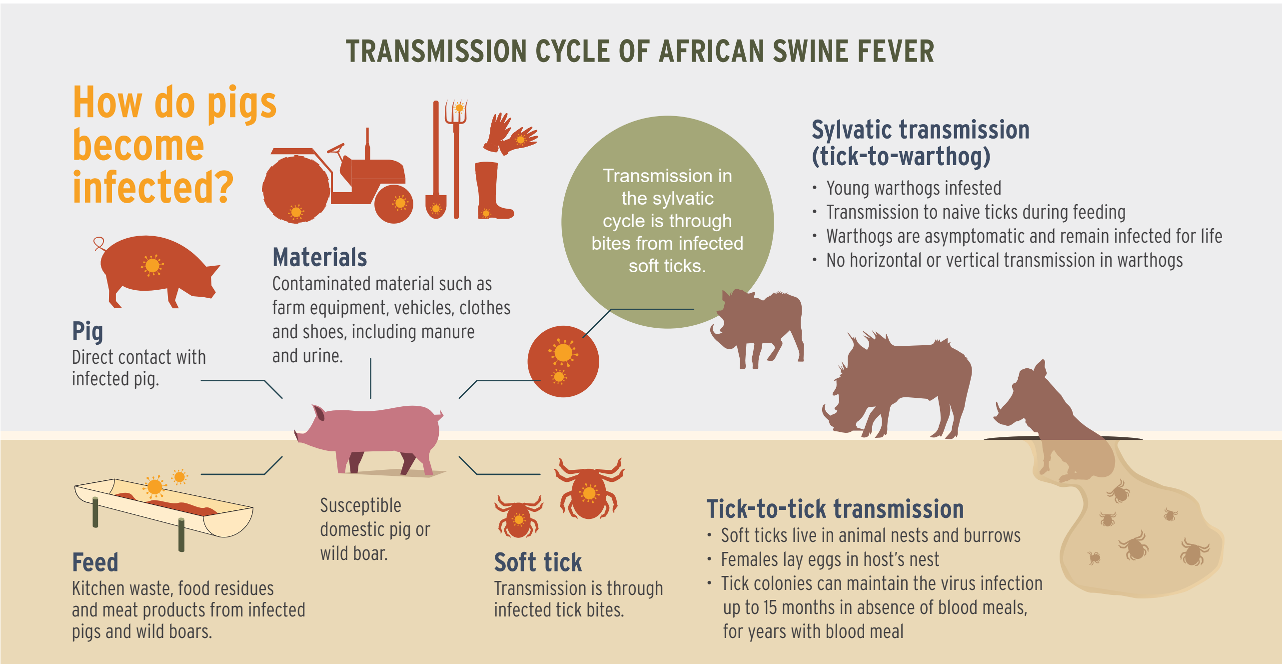
Controlling the spread of ASF is only possible if the dynamics of transmission are clearly understood. Research conducted at ILRI from 2007 onwards used whole-genome phylogenetics – these help to trace the ancestry of a disease – to identify two distinct clusters. One contained South African isolates from ticks and warthogs, and the other contained isolates from West Africa and the Iberian Peninsula. The former suggested a sylvatic cycle, with wildlife transmitting the disease to domestic pigs; the latter suggested a pig-to-pig transmission cycle. Where the disease is spread through a sylvatic cycle, as in East and Southern Africa, it is more difficult to control than pig-to-pig transmission.

Having identified and characterised the different genotypes, scientists could track the spread of the disease across landscapes, frequently over long distances. For example, an outbreak in Kampala swiftly moved eastwards across Uganda to Central Kenya. This had important implications for control and led to closer cooperation between the governments of Uganda and Kenya.

Scientists were puzzled by the fact that outbreaks of the disease sometimes occurred in areas where there were no obvious sources of transmission, such as clinically ill pigs or nearby populations of African warthogs. The discovery of high levels of ASF virus DNA in pigs slaughtered in Kenya, during a period when there were no outbreaks, suggested that the virus could be maintained in carrier pigs which showed no outer manifestation of the disease. Confirmation of this contributed to more effective surveillance and control strategies, indicating that measures such as restrictions on pig movements needed to be always in place, not just when outbreaks occur.

TICKS, WARTHOGS, PIGS AND PEOPLE

The primary host for the ASF virus is a soft tick which lives in the burrows of warthogs, and the warthogs are a source of blood for the ticks when they are laying eggs. Warthogs and other wild relatives such as bush pigs may show mild clinical symptoms of ASF, but one dose of the disease is enough to give them lifelong immunity. Transmission between the two species helps to maintain the virus in the wild, but it doesn't explain how it gets into domestic pigs. However, epidemiological work and social network surveys shed new light on how the disease can spread from wildlife to domestic animals. In Uganda, a focus of research on the sylvatic cycle, wildlife is protected within the national parks, but outside the park boundaries warthogs and bushpigs are frequently killed for food. It is almost certain that when pigs eat scraps of infected game meat they can succumb to the disease.



There are also other routes of transmission. Most obviously, pigs can develop ASF when they are bitten by infected ticks, and the disease can be swiftly passed around the herd in secretions and excretions, including urine and faeces. In East Africa, grandparents visiting their families will often make a present of a piglet and this can be another mode of transmission, as is the sharing of boars when farming families want to have their sows inseminated. During the dry season, agisting is a common practice, involving those without sufficient fodder transferring their stock to those who have. This can lead to the transmission of ASF. The feeding of infected swill to pigs has long been known to be a common source of ASF and the virus can also be spread by fomites, such as vehicles, farm equipment, clothes and footwear.

BUILDING THE GENEBANK

A decade of research by ILRI and its partners in East Africa established a large library of isolates of the virus taken from both domestic and wild pigs. A three-year project, launched in 2013 and funded by US Defence Threat Reduction Agency (DTRA), enabled scientists to add to the publicly available genome bank with sequences from East Africa and elsewhere on the continent. When the research began, 15 genotypes had been sequenced. Since then, a further nine have been added to the gene bank and fully sequenced. This now provides a significant increase in the number and, more importantly, in the variety of full genomes available for use by the scientific community. The 24 genotypes tend to cluster by region. For example, two genotypes (IX and X) found in Kenya constitute a distinct cluster which is genetically distinct from the virus in other regions.

A better understanding of the virus's genetics has been important for several reasons. First, it helps veterinary authorities to track movements of the virus across the landscape during outbreaks. For those countries where the virus isolates are similar, such as Kenya and Uganda, the control strategy requires a regional approach. Detailed knowledge about the genetic make-up of ASF also improves global surveillance by helping the authorities identify breaches in transboundary disease control. Finally, the sequencing of ASF genotypes has been of critical importance to developing new diagnostic tools and vaccines.

Photo ILRI/Kabir Dhanji

Cambra pigs in their pens in Kazinga Village, Mukono, Uganda.

REDUCING RISK, ENHANCING CONTROL

Field studies undertaken in Uganda and Kenya identified some of the key drivers of ASF outbreaks. These included panic sales of pigs when farmers realised that the disease was in their area and the inadequate disposal of dead pigs. The studies also highlighted the important role of commerce in spreading the virus between farms and across regions. Combining data from various studies, scientists were able to estimate disease transmission dynamics using mathematical modelling and geospatial mapping. The same methods were also used to assess the effectiveness of different control strategies and identify the ideal timing of interventions to minimise losses following an outbreak of the disease.

A similar approach was taken by ILRI and its partners in Vietnam, where the disease was first reported in 2019 and has since spread rapidly throughout the country leading to the loss of at least 15% of the national herd. Evaluating the impact of control strategies using the North American Animal Disease Spread Model, the scientists were able to calculate the level that pig movement restrictions had to reach – between 50% and 75% – to control the disease. Their evaluation suggested that if pig farms kept to the same trading partners for at least six months, this would significantly reduce transmission. Timely culling and a reduction in the number of trading partners were also recommended.

The evidence generated by the East African studies had a significant influence on the development of *The Regional Strategy for the Control of African Swine Fever in Africa*, formulated by ILRI in partnership with the UN Food and Agricultural Organization (FAO) and the African Union-Interafrican Bureau for Animal Resources (AU-IBAR) and published in 2017. The strategy prioritised the strengthening of technical services, the improvement of production systems – with a shift away from free-range to more biosecure modern systems of pig husbandry – and a strong focus on the sort of control measures that had already been advocated during outbreaks, such as the introduction of footbaths, quarantine and fencing.

Social surveys in East Africa revealed that translating words into action is no easy task. For example, public information and training programmes on either side of the Kenya-Uganda border were devised to improve farmer knowledge about measures to tackle ASF. A randomised control trial found that farmer knowledge did indeed improve, but their practices often did not. This was confirmed by another study in northern Uganda. Almost 600 people were interviewed in 64 different villages in a series of participatory rural appraisals. Farmers, butchers and traders were aware of the clinical signs of ASF, how the disease spreads and the measures required to control it. However, this did not guarantee their implementation. Indeed, most middlemen and butchers admitted they had sold live pigs and meat infected by ASF. The researchers concluded that new initiatives were required to stimulate changes in management practice. However, the failure to adopt control measures was largely the result of poverty and as that persists it is unlikely that those involved in the breeding and sale of pigs and pork will change their ways.

THE FUTURE

Introducing biosecurity measures – avoiding contact with wild pigs, washing boots when entering enclosures, introducing quarantine pens for new arrivals – is much harder in most African countries, where free-range, scavenging systems prevail, than in countries that have adopted modern indoor pig production methods. Developing a vaccine, or series of vaccines, for ASF is therefore essential. At present, there are somewhere in the region of 40 million pigs in sub-Saharan Africa and it is estimated that a vaccine could benefit between 6 and 17 million smallholder farmers and their families. As the pig population continues to rise, the disease is likely to take an even greater toll if no vaccines are available.

Research on vaccines for ASF at ILRI involves two approaches. These are described in greater detail in another innovation brief https://hdl.handle.net/10568/118052. One approach involves developing a live attenuated vaccine to stimulate antibodies which will kill the virus when it enters the pig's cells. The other focuses on developing a subunit vaccine, consisting of purified fragments of virus antigens, which will stimulate an immune response to prevent the disease entering the system.

By 2021 ILRI had identified 7 to 10 attenuated virus candidates for the live vaccine; viruses strong enough to stimulate an immune response but not so strong that they kill the animals or seriously weaken them. Two of these had been tested on live pigs. They were partially successful in preventing the disease from killing animals, but they still suffered serious clinical symptoms. Further work on attenuation was required. It is hoped that by the end of 2022 ILRI will have a successful vaccine candidate which could then be commercially launched. Work on the subunit vaccine is still in progress. This has involved identifying candidate antigens in three groups of animals: warthogs that are resistant to the disease and only suffer mild infection, pigs that have been killed by the disease and pigs which have caught the disease and recovered. This should help scientists to establish which antigens stimulate a response from the antibodies which provides immunity.

Both approaches are aimed at developing a vaccine to provide immunity to Genotype IX, which is prevalent in East Africa. There is no guarantee that this would work for genotypes in West Africa, Europe and Asia. Likewise, vaccines which are in the process of development in the US and UK are designed to tackle Genotype II, the Georgia strain which is affecting Eurasia. This may not be effective for Genotype IX. This is not a vaccine race where one organisation or research institute will win. Regardless of what happens elsewhere, ILRI's vaccine research will remain vitally important, particularly when it comes to developing a vaccine for use in Africa.

ILRI's two decades of research have involved numerous collaborations with scientific institutes in the US, the UK, Denmark, Germany, Sweden, Spain, Australia and elsewhere. ILRI has benefited from the expertise of these institutions, while the institutions have benefited from ILRI's extensive network of local and regional partners and its long experience of working in the field in Africa. Most of the achievements so far – whether in molecular or field epidemiology or developing new vaccines – have been based on partnership and collaboration.

Photo ILRI/Stevie Mann

A farmer in the Tete province of Mozambique feeds her pigs.

Acknowledgements

ILRI's research on African swine fever has involved many scientists working in collaboration with several groups around the world, with funding coming from multiple sources. The work has been conducted as part of the CGIAR Research Program on Livestock, which is supported by contributors to the CGIAR Trust Fund. https://www.cgiar.org/funders/.

ILRI Scientists

Edward Okoth, Michel Dione, Kristina Roesel, Lee Hu Suk, Cynthia Onzere, Milton Owido, Gideon Ndambuki, Edwina Bochere, Lucilla Steinaa, Anna Lacasta, Jacqueline Lichoti, Mike Barongo, Noelina Nantima, Karl Stahl, Charles Masembe, Patrick Atimnedi, Harry Oyas, Isaac Lekolool, Dominic Mijele, Sam Okuthe, Hiver Bousini, Jocelyne Davies, Richard Bishop.

Collaborators

CISA-INIA: Carmina Gajardo; Univasidad Cuplutense: Jose Manuel Sanchez-Vizcaino Rodriguez; FAO-ECTAD: Sam Okuthe; AU-IBAR; Hiver Bousini; Makerere University: Charles Masembe; CSIRO-Australia: Jocelyne Davies; Department Of Veterinary Cervices Kenya: Harry Oyas; Department of Veterinary Services Uganda: Anna Rose Okurut; Sokoine University of Agriculture: Emma Njau; SLU-Sweden: Karl Stahl, Neil Leblanc; Friedrich Loefler Institute; Walter Fuchs, Sandra Blome; Pirbright Institute: Linda Dixon; US Defense Threat Reduction Agency (DTRA).

Authors

Charlie Pye-Smith[1], Edward Okoth[2], Lucilla Steinaa[3] and Anna Lacasta-Marin[4].

[1]Science writer, CGIAR Research Program on Livestock.
[2]Scientist, International Livestock Research Institute.
[3]Principal scientist, International Livestock Research Institute.
[4]Scientist, International Livestock Research Institute.

Publications

Bishop, R.P. et al. 2015. Comparative analysis of the complete genome sequences of Kenyan African swine fever virus isolates within p72 genotypes IX and X. Virus Genes 50(2):1156-7 10.1007/s11262-014-1156-7.

Dione, M.M. et al. 2015. Risk factors for African swine fever in smallholder pig production systems in Uganda. Transboundary and Emerging Diseases. 64 (3): 872–882. https://hdl.handle.net/10568/69415.

Okoth et al., 2017. Detection of African swine fever virus in the tissues of asymptomatic pigs in smallholder farming systems along the Kenya-Uganda border: Implications for transmission in endemic areas and ASF surveillance in East Africa. Journal of General Virology. DOI: 10.1099/jgv.0.000848.

Gallardo, C. et al. 2009, Enhanced discrimination of African swine fever virus isolates through nucleotide sequencing of the p54, p72, and pB602L (CVR) genes. Virus Genes 38: 85-95. DOI: 10.1007/s11262-008-0293-2.

FAO, AU-IBAR, ILRI. 2017. Regional strategy for the control of African swine fever in Africa. Rome, Italy: FAO. https://hdl.handle.net/10568/80187.

CONTACT

Edward Okoth
E.Okoth@cgiar.org
ILRI