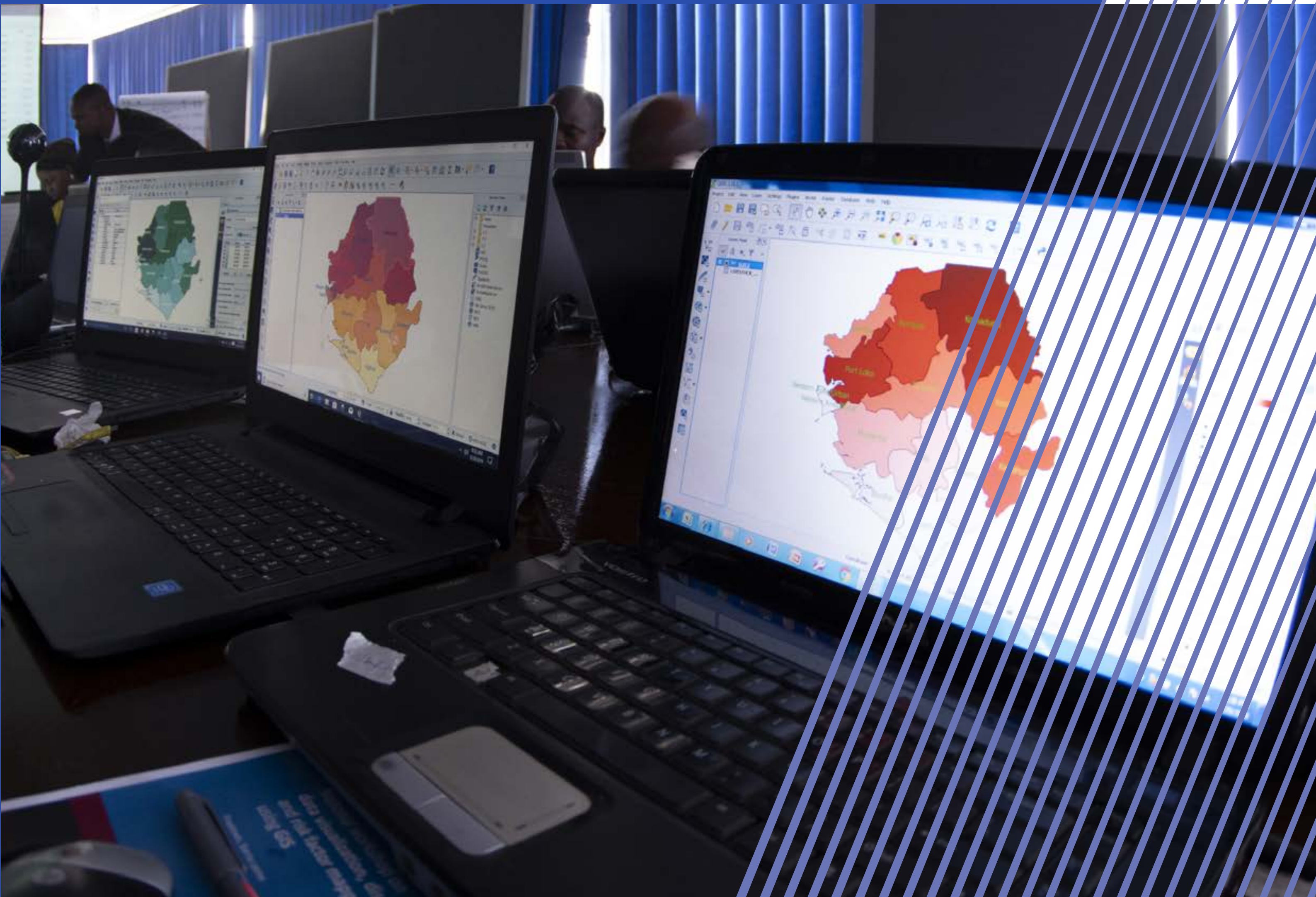
Food and Agriculture
Organization of the
United Nations

African swine fever epidemiology and geographic information systems

Application for disease management

FAO ANIMAL PRODUCTION AND HEALTH / **HANDBOOKS 1**



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African swine fever epidemiology and geographic information systems

Application for disease management

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Abbreviations

ASF	African swine fever
ASFV	African swine fever virus
GIS	Geographic information systems
EFSA	European Food Safety Authority
GLW	Gridded Livestock of the World
MAUP	Modifiable areal unit problem
MS	Member States
EU	European Union
MCDA	Multi-criteria decision analysis
FAO	Food and Agriculture Organization of the United Nations
WOAH	The World Organisation for Animal Health

Introduction

In the last few decades, the world has seen several animal health crises that necessitated the pre-emptive slaughter or culling of many animals as part of control and eradication measures. Among other infectious transboundary diseases, African swine fever (ASF) has significantly impacted the pig production sector in many countries, particularly developing ones. There is a growing concern about the need to address infectious disease outbreaks in domestic livestock populations swiftly, efficiently and proactively. For this to occur, animal health authorities must have access to accurate information to prepare for possible animal health hazards as well as guide complex decision-making processes. These processes often involve actors and stakeholders beyond just the animal health and production sectors.

The utility and wide range of advantages of using geographic information systems (GIS) in the animal health domain, along with the development of spatial animal health information systems, have been emphasized in the literature for several decades (Clarke *et al.*, 1996; Pfeiffer, 2004; Mengistu & Haile, 2017). GIS has proven to be highly suitable and versatile for collecting, processing and presenting information related to disease management. They aid in designing control and preventive approaches and have been widely used, though predominantly by the animal health research community. There are countless examples illustrating the power of GIS in supporting surveillance, risk assessment and disease management applications worldwide. The success of such stories critically depends on the availability and quality of baseline geographic data, as well as the accessibility of affordable information management technologies.

These challenges have hindered the integration of GIS into the routine practices of national animal health services, especially in developing countries where it was most needed. For a long time, geospatial technologies remained a highly technical area. The development of GIS applications required expensive software and special expertise, which were often unaffordable. Additionally, baseline geospatial datasets were scarce or of poor quality, further limiting the routine use of geospatial technologies in the everyday work of the veterinary authorities.

However, in the last decade, a global "geospatial revolution" transpired. The precursor was the transition from conventional paper maps to GIS-based desktop digital maps. A massive increase in remote sensing coverage, quality and resolution, along with the increasing availability of various geographic data, revolutionized the underlying concepts and functionality of early GIS software applications. Shortly after, web mapping technologies became prevalent, which gave way to cloud-based GIS and geospatial applications and mobile maps. Conventional desktop GIS that required large capital investments, special training and skills gave way to web-based geospatial services, which were optimized for mainstream use. Concurrently, the wide proliferation of open-source geospatial data and inexpensive applications made it far easier to collect, manage, manipulate and visualize geospatial data, while sharing interactive maps with users did not require special skills. Advances in hardware and software development, particularly the availability of inexpensive mobile devices such as smartphones, tablets and laptops have spurred the use of data collection. This has transformed how many organizations and businesses conduct field surveys, organize reporting and communicate information to subordinate units and workers.

All these technological advances now make it possible to design and implement flexible, inexpensive and practical spatial information systems to support disease management decisions and interventions in almost any country. FAO has prepared this publication topromote the use of GIS technologies in managing animal diseases, especially ASF. It aims to create a reference document (handbook) demonstrating the advantages of using GIS and explaining the necessary steps for data collection and proper organization of such information. This handbook is not intended to provide a comprehensive overview of all GIS applications in ASF management, nor is it a review of spatial analysis or risk mapping in ASF research. It presents real-world examples of GIS to describe population distribution, map disease occurrence, and assess and visualize the risk of disease spread. The handbook introduces basic concepts of risk mapping and modelling without delving deeply into technical details. It serves as an entry-level resource, bridging ASF epidemiology GIS basics, applicable to other swine and livestock diseases.

The document provides guidance, recommendations and tips on how to prepare the essential datasets and organize them into a GIS that would be epidemiologically consistent, flexible and practical, based on FAO's experience in developing such systems for the management of ASF and other diseases. It is an invitation and gentle foray into the fascinating world of using GIS for the management of animal diseases. The handbook targets officials, animal health professionals, pig farmers, wildlife managers, hunters, GIS experts, students, and other stakeholders involved in the prevention and control of ASF worldwide. It encourages them to create their own decision-supporting GIS to improve the management of ASF and reduce the disease burden and its negative impacts.

Chapter 1

How geographic information systems can help with African swine fever management

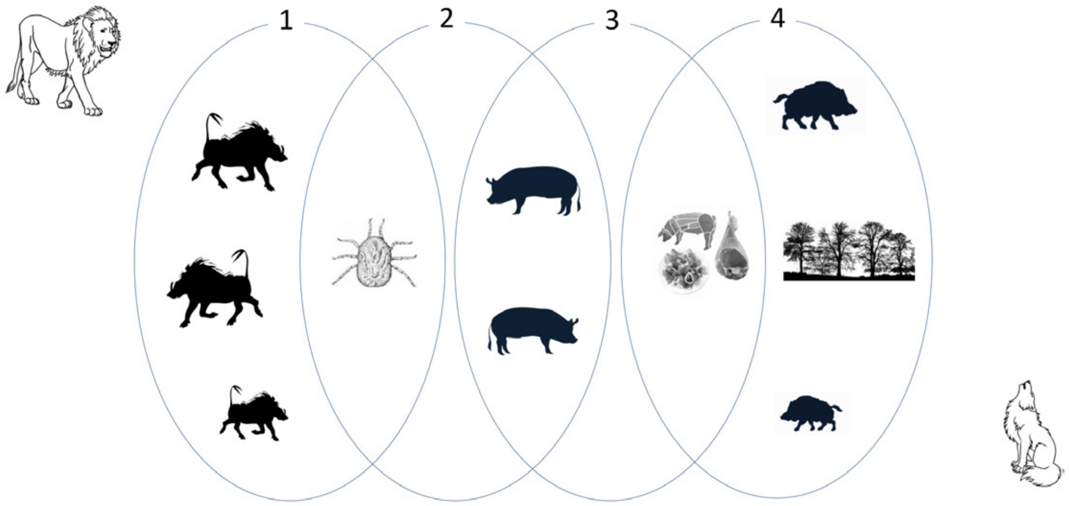
This chapter briefly discusses the epidemiological complexity of African swine fever, one of the major animal health threats in the world, and how GIS can help improve the management of this disease. It encourages them to create their own decision-supporting GIS to improve the management of ASF and reduce the disease burden and its negative impacts. It explains how GIS can be particularly useful and the prerequisites for widening its application in the management of this disease.

AFRICAN SWINE FEVER AS A COMPLEX ANIMAL HEALTH CHALLENGE

African swine fever, an endemic disease that was once largely limited to sub-Saharan Africa, has now become one of the major global animal health problems. Since 2007, the Genotype II virus of ASF has been spreading around the globe in a panzootic manner, resulting in thousands of outbreaks and causing unprecedented economic losses. It is now a transboundary animal disease with complex epidemiology and a profound negative impact on pig production, the livelihoods of people and the viability of trade. In the absence of vaccines, available disease control tools are limited to tightening biosecurity and culling pigs in infected and at-risk farms. Once ASF enters a country, it often becomes a persistent problem, establishing itself endemically if not controlled promptly and effectively. The virus can survive in meat, pig byproducts or carcasses of wild pigs, sustaining low-prevalence endemic transmission.

ASF now has several self-sustaining epidemiological cycles involving three different reservoirs: a) *Ornithodoros* ticks in parts of Africa; b) low biosecurity pig production systems in Africa and elsewhere; and c) wild boar in Eurasia. Each reservoir can sustain infection indefinitely (Figure 1). Some cycles co-occur in certain areas, while others predominate elsewhere. ASF is also adapted to trade in live animals and byproducts, facilitating its geographic spread, especially across borders (Beltran-Alcrudo *et al.*, 2019). The longevity of the virus in non-heat-treated pork products makes its spread invisible to conventional surveillance methods and difficult to control. Value chains involving domestic and wild pigs and their byproducts create new opportunities for

FIGURE 1
From warthogs to wild boars: Adaptive modification of African swine fever virus transmission cycles on the way from Africa to Europe



Cycle 1: The natural African sylvatic cycle; Cycle 2: The anthropogenic cycle involving ticks (Africa and the Iberian Peninsula); Cycle 3: The pure anthropogenic cycle (western Africa, eastern Europe, Sardinia, Asia); Cycle 4: The wild boar-habitat cycle (northeastern Europe, North Korea, 2014 to present).

Source: **Chenais, E., Ståhl, K., Guberti, V. & Depner, K.** 2018. Identification of Wild Boar-Habitat Epidemiologic Cycle in African swine fever Epizootic. *Emerg Infect Dis.*, 24(4): 810-812. doi: 10.3201/eid2404.172127. PMID: 29553337; PMCID: PMC5875284.

disease propagation and transmission, unlike the naturally evolved host–parasite systems, such as ASF's original ecological niche in Africa. Human behaviour is thus a key element in both the geographic spread of ASF and its local dynamics.

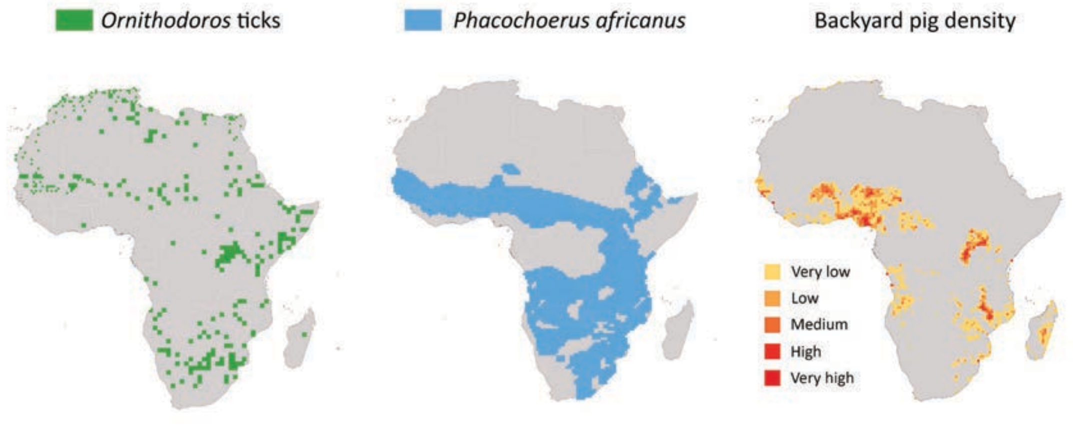
What and how humans do often affect outcomes of ASF spillover into a novel environment more than what any natural, climatic or ecological factors would normally allow (FAO, 2013). Humans have created a system that appears far more suitable for the propagation of ASF compared to its original niche in the African ecosystem, rendering it a panzootic problem. The ongoing global ASF crisis should be considered in all its complexity. This includes human activities and behaviours that impact host–pathogen interactions, production systems, ecology of reservoir or vector species, geographical and climatic factors, trade and socioeconomic contexts. Understanding these multifaceted elements is crucial to effectively manage and control the spread of ASF. In its conquest of the world, ASF takes on many different "faces". We remain oblivious to the changes in its epidemiology, making it difficult to pre-empt a response as it continues to spread to new countries, continents and environments.

The "One Health" approach was developed some time ago to address complex health problems and was initially only focused on zoonotic diseases. It promotes joint expertise and knowledge from disparate disciplines to find practical solutions to the challenges of complex animal and human diseases. Over the years, One Health evolved beyond zoonotic diseases (Calistri *et al.*, 2013). Today, modern biomedical science has broadened the One Health lens to include diseases that do not directly affect humans but still require joint expertise, coordination and management efforts from various disciplines and sectors (Cimino *et al.*, 2021; Tucker *et al.*, 2022). It aims to address such diseases holistically by considering a wide range of factors involved in the emergence, spread and persistence of pathogens. This approach goes beyond conventional wildlife management, veterinary practices and human health strategies, integrating these disciplines to create a more comprehensive and effective strategy for disease prevention and control. ASF is a very clear case of a disease that should be addressed in the spirit of the One Health approach, even though it does not affect humans directly (Cimino *et al.*, 2021).

Approaches to control ASF and the information required to manage it vary across continents and even within a single country. On the one hand, they rely on understanding local transmission cycles, which requires information on the distribution of host or vector species, specific pig husbandry practices, trade patterns and environmental factors. On the other hand, the resources available and the type of surveillance system in place determine the kind of data collected and the level of detail employed. For example, in sub-Saharan Africa, ASF was originally associated with the ecological niche of the ticks of the genus *Ornithodoros* and the common warthog (*Phacochoerus africanus*). Warthogs are naturally resistant to the effects of the ASF virus (ASFV) and do not usually develop clinical disease. Infection in young warthogs occurs exclusively within burrows through tick bites. In this system, the epidemiological reservoir of infection exists due to an ancient, naturally evolved symbiosis between ticks and warthog (Figure 2). Although the presence of both host and vector are

FIGURE 2

The occurrence of *Ornithodoros* ticks, common warthog *Phacochoerus africanus* and backyard pig density in Africa as some of the relevant risk factors contributing to the endemic circulation of African swine fever on the African continent



Note: Refer to the disclaimer on page ii for the names and boundaries used in this map.

Source: Author's own elaboration. Maps are generalizations created based on maps and data from Vial *et al.*, 2017; Walker *et al.*, 2003; Trape *et al.*, 2013; de Jong, 2017; Gilbert *et al.*, 2015.

required to sustain the circulation of the virus, their co-occurrence does not always imply the presence of ASF. As such, eradication of ASF where it is naturally present is impossible.

With the increase of domestic pig husbandry in Africa, the virus has shifted towards a more anthropogenic cycle (Figure 1, Cycle 2) in which domestic pigs started playing a major epidemiological role, with the occasional involvement of *Ornithodoros* ticks. This transmission cycle was also reported from the Iberian Peninsula during the 1960s and 1970s (Sánchez-Vizcaíno *et al.*, 2012), where pig husbandry practices and breaches in biosecurity are the main factors sustaining the endemicity of the ASF virus. Data show that the disease can be eliminated in these settings, albeit with a lot of time and effort invested.

The growing human population and increasing numbers of domestic pigs has led to the expansion of ASF in Africa. Its novel transmission cycle in the continent has become fully dependent on human activity (Figure 1, Cycle 3). Swill feeding, trade in live pigs or infected meat, and free-range pig farming are the main risk factors in this system. This domestic pig cycle has also developed in the Caucasus since 2007 (European Food Safety Authority [EFSA], 2010, 2015) and since then, ASF spread around significantly across the globe on a scale never seen before.

Most recently, in northern and eastern Europe, the disease has evolved further into the so-called “wild boar–habitat cycle” (Figure 1, Cycle 4. See also Figure 3). This novel host–pathogen–environment system has steadily expanded the range of ASF in Europe (EFSA, 2017) and is also emerging in Asia (Cowled *et al.*, 2022). Its successful expansion in wild boar populations was facilitated by the exceptional stability and resilience of the ASF virus in the environment and infected carcasses of animals (Chenais *et al.*, 2018; Guberti *et al.*, 2022). It is still unclear how the ASF virus will behave in warmer Asian or Mediterranean climates, where ecological conditions differ from central and northern Europe (Cowled *et al.*, 2022).

The evolution of ASF over the last decade demonstrates that all countries where pig production is important should prepare for a prolonged and challenging battle against the threat and consequences of the ASF pandemic. ASF will likely become established in the populations of wild boar, at least in Eurasia, for many years to come (Gervasi & Guberti, 2021). Even the development of safe and efficient ASF vaccines, which the global pig industry is in desperate need of, will not alone successfully resolve the problem. The complex epidemiology of ASF, especially where several transmission cycles exist (Figure 3), necessitates tailored interventions that are well-coordinated between the different stakeholders, both spatially and temporally.

Management of ASF, with or without a vaccine, is unlikely to succeed without well-informed and carefully considered decisions regarding what actions should be taken and where to reduce disease risks, bring it under control and/or eradicate it. The extent to which information is both available and promptly deployed to support effective analysis is a key prerequisite to effective decision-making.

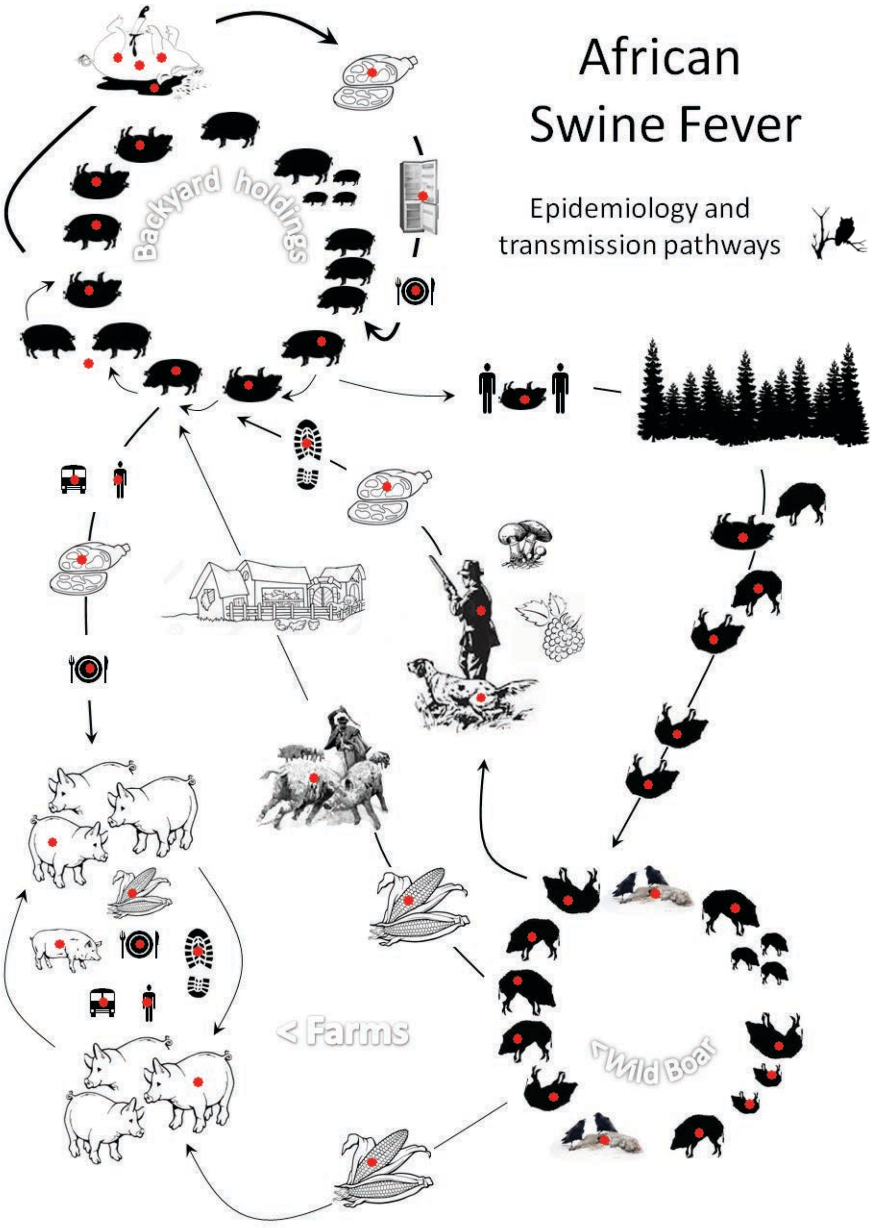
APPLICATIONS OF GEOGRAHIC INFORMATION SYSTEMS IN AFRICAN SWINE FEVER MANAGEMENT

Geographic visualizations, especially around disease control, are probably the most appealing and useful means of communicating complex information. However, maps and geographic visualizations can also be misleading (Monmonier, 2018) and even harmful for decision-making if produced using poor or unreliable data, or if they ignore epidemiological nuances and the specifics of the mapping subject. An extensive body of literature demonstrates various successful applications of geographical information systems to support the control of diseases, including problems related to the management of ASF. However, one of the most widespread obstacles for veterinary authorities in many countries in using GIS in their work is the lack of correctly organized spatially explicit data and/or recommendations on how to prepare them in a way that fully takes advantage of GIS technology. FAO has prepared this guidance document with recommendations, examples, and case illustrations on how to most effectively use the powerful potential of GIS to avoid critical mistakes and optimize data collection and management efforts to achieve the best results possible.

Complex problems such as managing ASF require mutually agreed-upon well-informed and coordinated actions on various fronts relevant to disease control. Even if they are taken by the most qualified experts in the field, decisions that are based purely on subjective judgement without a careful analysis of the data and factoring in the relevant context can be erroneous and costly. This may result in significant economic and social implications that affect thousands of people while damaging the reputation of authorities. High-quality information and the ability to assess the implications of disease spread allow competent veterinary authorities to better understand the underlying risks. This in turn allows them to set up more effective surveillance systems and make far more appropriate decisions both during routine activities and when animal health crises occur. Application of GIS in the prevention, control, risk assessment, and management of ASF provides a strategic vision of the problem and helps resolve multiple practical issues of dealing with ASF outbreaks in different settings and situations.

For example, countries that are not affected by this disease can use GIS to organize and visualize updated information on the distribution of susceptible populations. They can conduct various assessments, such as evaluating the risk of disease introduction and defining areas most at risk. Additionally, GIS can help improve the sensitivity of surveillance systems by

FIGURE 3
Complex epidemiological factors and transmission pathways involved in sustaining endemicity and facilitating the geographical expansion of the African swine fever virus in eastern Europe (Cycles 3 and 4, Figure 1)



Source: **Guberti, V., Khomenko, S., Masiulis, M. & Kerba S.** 2019. *African swine fever in wild boar ecology and biosecurity*. FAO Animal Production and Health Manual No. 22. Rome, FAO, OIE and EC.. https://openknowledge.fao.org/server/api/core/bitstreams/3e77c9c3-0d3b-414c-881eb71253648a8d/content

organizing appropriate surveillance efforts. It can also assist in introducing preventive measures where they are most needed. Available geographic datasets can immediately offer the necessary context and promptly supply decision-makers with the data needed to localize the spread of infection when it occurs. If the disease is already present in the country, targeting surveillance, implementing stand-still operations, culling and eradication of outbreaks require baseline information. This includes data on the distribution of susceptible populations, risk assessments of further spread, and the epidemiological or economic implications of the interventions conducted.

Accurately documented epidemics enable learning from experience by retrospectively analysing disease risk and defining gaps in control or surveillance strategy. This enhances disease intelligence, saves time and resources, and ultimately achieves better results in managing the disease. A better understanding of the specific local risk factors of disease spread and persistence mechanisms are important prerequisites for rendering pig production or wildlife management sectors less susceptible to infection. That said learning from epidemiological experience better prepares the competent authorities to be more effective in organizing their workflow, reviewing surveillance or control protocols, adapting legislation, etc.

The rise of cloud computing in recent years, as well as the birth of new paradigms of software distribution (SaaS [Software as a Service], PaaS [Platform as a Service] and DaaS [Data as a Service]), have given rise to new platforms and models of information dissemination in many spheres, including animal health. The flexibility and simplicity of service platforms, combined with the evolution of web technologies and the widespread use of mobile devices, have prompted the application of GIS as a powerful tool for data collection, integration, analysis and information dissemination. GIS can assist in the management of complex problems and connecting teams of professionals from diverse areas and disciplines, which is crucial during unfolding animal health crises. Modern web-based GIS applications offer endless opportunities, transforming GIS from a tool traditionally restricted to the scientific and expert community into a tool that can be used as part of daily routine. Web-GIS applications and cloud technologies can effectively address two major challenges hindering the effective application of GIS in disease management: the systematic collection of reliable geographic data from the field (e.g. disease events, epidemiological unit mapping, vaccination) and the dissemination of geographic data to support practical collaborative decision-making (e.g. risk maps, notifications, early warnings).

Data collection is the most laborious, time-consuming and difficult phase in the development of any information system. Preparing host population estimates may initially require substantial effort, however, the results are rewarding. Population data contextualize information about the disease and make it possible to interpret observations more accurately, calculate various epidemiological metrics and reach objective conclusions on disease spread patterns observed. Datasets on animal movements, trade and value chains might require even more time to develop, but they too will greatly assist with ASF management by providing a vision of commodity flow directions and critical nodes in the network of movements. Mapping disease occurrence patterns is an essential real-time task that should be organized to combine precision with accuracy. It must supply surveillance with a timely and adequate understanding of an unfolding epidemic threat or the scope of an endemic disease burden. Retrospective analysis of disease dynamics in space and time usually requires classification, normalization, transformation, deriving rates, proportions, estimating sample sizes for surveillance purposes, etc. These operations are impossible without datasets on population and risk factors that put disease observations into a broader epidemiological context. All these tasks can be effectively solved with GIS, provided the underlying information is correctly and carefully assembled into datasets. This process transforms the data into a digital model that accurately reflects reality, enabling well-justified decision-making (Figure 4).

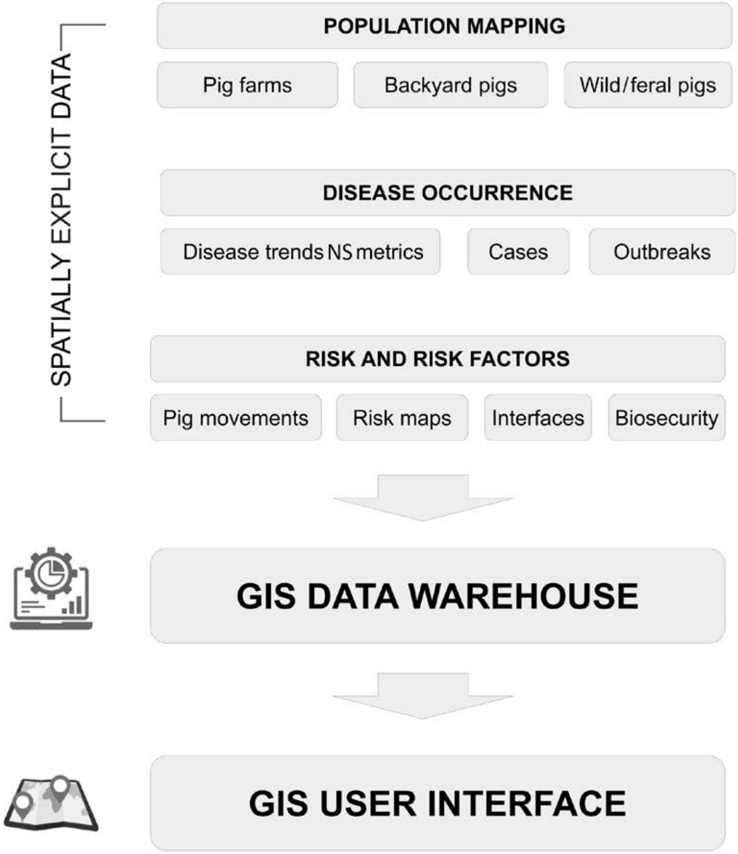
Identifying relevant spatial data layers that represent known risk factors or are likely to affect disease dynamics, and arranging them in formats suitable for mapping, visualization and analysis, is crucial. This must be done in a manner compatible with information on disease occurrence and host population distribution patterns. This task is best assigned to epidemiologists with a background in GIS or spatial analysis. Risk factor maps triangulate disease observations within populations. They place disease dynamics into a broader environmental or geographical context. This approach is known as "disease intelligence"– a data and analysis-driven method for managing infectious diseases and their risks. Anticipating the likely implications of disease introduction and spread is crucial for designing control measures. It is also essential for building up the resources needed to mitigate disease events promptly. The goal is to develop knowledge on where, when and what actions can be taken before the spread evolves into a large-scale crisis.

The data warehouse of a decision-support GIS allows for visualizing and interacting with the different data sets. It enables spatial processing, identifying or filtering out objects or areas that meet certain conditions. Data can be downloaded and exported to other devices and applications. Appropriately organized information can then be used to evaluate the epidemiological and economic implications of outbreaks. It can also be used to conduct in-depth analysis using more robust methods of spatial epidemiology and statistics. Decision support GIS ensures that epidemiologically relevant information can be accessed when needed conveniently and practically.

Below you will find guidance, recommendations and tips on how to prepare the data and organize them into a GIS that would be epidemiologically consistent, flexible and practical. The material is structured around three main mapping topics: distribution of the population (Chapter 2); occurrence of the disease (Chapter 3); and risk and risk factor mapping (Chapter 4). They are built on FAO's practical experience in developing such systems for the management of ASF and other swine diseases. The material is predominantly illustrated with epidemiological situations based on real data.

FIGURE 4

Main data contents and information modules of a decision support geographic information systems focused on African swine fever management



Source: Author's own elaboration.

Key messages:

- The ASF virus can persist for long in meat or carcasses and thus maintain endemic transmission. ASF epidemiology grew in complexity as it was expanding its range. It now has four self-sustaining epidemiological cycles involving three different reservoirs: (a) *Ornithodoros* ticks and wild suids (sub-Saharan Africa); (b) low biosecurity pig production systems (Africa and elsewhere); and (c) wild boar (Eurasia).
- Domestic and wild ASF cycles can co-occur and may re-initiate each other. Effective disease control in several domains is required to get rid of it entirely. Management of ASF should expand to address all its complexity including people's activities and behaviours, the type of production system in place, the ecology of the species involved, geographic and climatic factors, the impact of trade and the socioeconomic context, etc. All this requires management efforts coordinated between the different sectors, stakeholders and players involved.
- The complex epidemiology of ASF requires very well-coordinated situation-tailored interventions between various stakeholders, both spatially and temporally. This necessitates well-informed and carefully considered decisions on what actions should be taken and where to reduce disease risks, bring it under control, and/or eradicate it. GIS is a technology capable of assisting with these tasks.
- One of the most widespread obstacles for the veterinary authorities in many countries to use GIS in their work is the lack of correctly organized spatially explicit data, and/or recommendations on how to

prepare them in a way that allow GIS technology to be exploited.

- Data collection is the most laborious, time-consuming and challenging phase in developing any GIS. It must be undertaken in a way that is consistent with the nature of the disease, the basic requirements of data management, as well as the relevant cartographic and epidemiological rules.
- Three essential data elements are required to set up and start developing an ASF management GIS: distribution of the population, occurrence of the disease, and risk and risk factor mapping.
- GIS-supporting ASF management is developed to visualize and interact with the different layers of information, conduct spatial requests, filter out units that meet specific criteria, and exchange data with other devices and applications. It should help evaluate the implications of outbreaks, including epidemiological and economic ones. By developing such a GIS, we organize and make all epidemiologically relevant information easily accessible and convenient to use practically.
- Managing ASF in many countries already requires close collaboration between veterinary authorities and wildlife, forestry, and hunting agencies or services. This collaboration necessitates literally “sharing maps of operations” making GIS an indispensable tool for support.

Chapter 2

Population mapping

This chapter introduces the concepts of epidemiological units, aggregation and disaggregation of population data, and normalization. It describes the importance of choosing appropriate spatial resolution and data collection units when preparing data for a GIS project. Throughout this chapter, the reader will be walked through a series of real-world case examples of mapping that illustrate various pig populations, including backyard and commercial sectors, as well as wild or feral pigs at different levels of aggregation. It also explores various visualization approaches, offering a comprehensive understanding of how to effectively interpret population data.

Good knowledge of the distribution of susceptible populations is of paramount importance for any disease control programme. Depending on the disease epidemiology, it may be necessary to map some species or production systems that play a key role in sustaining its transmission cycle (epidemiological reservoir) separately from other susceptible populations (spillover or accidental hosts). Extensive and intensive animal production systems often differ in their epidemiological roles. This approach is reasonable and well-justified epidemiologically in the case of ASF.

For example, backyard and free-range pig production typically constitute a reservoir of African swine fever in eastern Europe and many African countries, while pig farms in the commercial sector with generally higher biosecurity are infected less frequently. In some African countries, this disease is maintained through a transmission cycle involving wild suids and ticks of *Ornithodoros moubata* complex, for example when sustained in a natural host–pathogen–environment system with a reservoir represented by arthropods (Costard *et al.*, 2013). Therefore, when mapping the distribution of ASF hosts, a clear discrimination between different species or production systems is needed to account for their respective epidemiological roles (Figure 5).

The epidemiological reservoir is "one or more epidemiologically connected populations or environments in which the pathogen can be permanently maintained and from which infection is transmitted to the defined target population," (Hydon *et al.*, 2002). Some pathogens can sustain their amplification within one or several host species without any additional conditions, while others would require vectors or humans to facilitate that process through their ecological traits, activities or trade. Careful consideration of all available disease data and epidemiological indications, including results of special studies, is sometimes required to identify the reservoir (Hydon *et al.*, 2002).

Currently, three potential reservoirs of ASF can be identified (Figure 5, Costard *et al.*, 2013; Chenais *et al.*, 2018): (1) a symbiotic system between warthogs and *Ornithodoros* ticks; (2) the low biosecurity pig production systems (free-range, outdoor, backyard), where sustained virus transmission depends on human actions; and (3) wild boar populations, where ASF cycle is naturally maintained through environmental transmission (carcass to live animal).

The occurrence of the epidemiologically important species (ticks, warthogs, wild or feral pigs) or production system (low-biosecurity pigs) naturally defines the geographic distribution of the transmission cycle in question and helps define the epidemiological situation. At the same time, other less abundant but still susceptible pigs, such as farmed domestic pigs or free-ranging wild/feral pigs, may act predominantly as accidental hosts of the infection, yet still contribute to disease spread and dynamics.

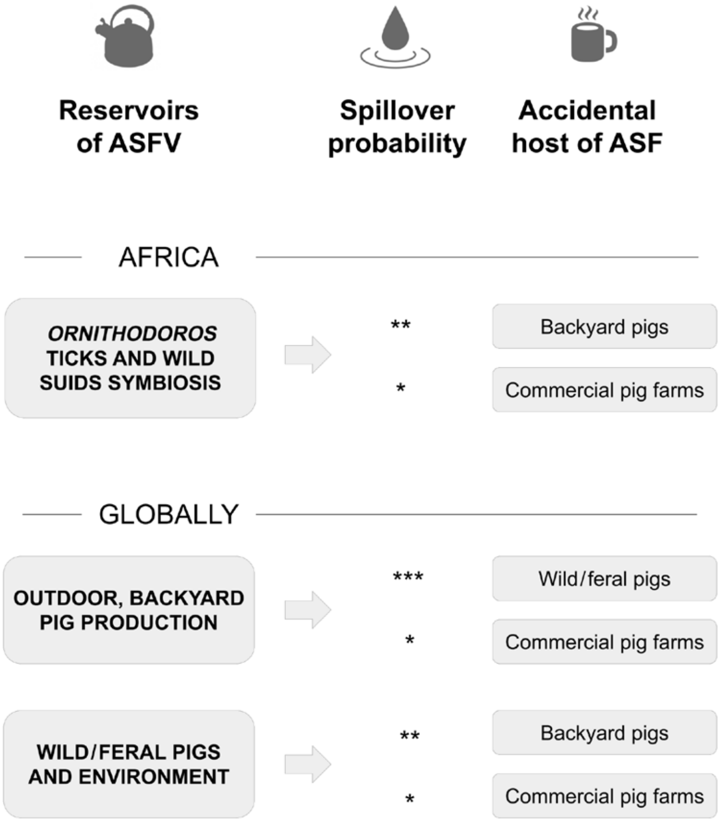
ASF generally tends to spread against the gradient of biosecurity, meaning that populations and epidemiological units with lower biosecurity are more likely to be impacted by the disease. The likelihood of pathogen spillover from an ASF reservoir to other populations varies between sectors due to their differing biosecurity statuses (Figure 5). For example, infection from backyard pigs is more likely to spread to wild boar than to commercial farms, provided the latter sustains a level of biosecurity. When infection is predominantly found in wild boar, less rigorously safeguarded backyard holdings are more vulnerable to ASF outbreaks compared to commercial farms. Therefore, by mapping subpopulations of susceptible hosts separately one can roughly assess the probabilities of certain epidemiological scenarios (Figure 5).

DATA COLLECTION UNITS AND SPATIAL RESOLUTION

The spatial units in a GIS system may range from objects represented as discrete points (farms, markets, slaughterhouses and alike) to subnational administrative units or production zones, represented by polygons where data is aggregated. From an epidemiological perspective, a clear distinction should be made between different types of these units based on characteristics such as husbandry systems, level of biosecurity, population, purpose and other relevant attributes.

FIGURE 5

Three main epidemiological reservoirs of African swine fever virus as sources of infection with different African swine fever spillover probabilities to the populations of other species and categories of susceptible animals, which typically act as spillover or accidental hosts



Spillover probabilities are: * - low, ** - moderate, *** - high. They are provided as an illustration of the importance of distinguishing populations with different levels of biosecurity and based on common sense assumptions that the virus is more likely to spread to populations with lower biosecurity.

Source: Author's own elaboration.

The choice of the spatial unit (resolution) at which population data collection takes place is key as it will define the level of precision at which surveillance and analysis are conducted, as well as the decisions made (Figure 6). Choosing the appropriate data granularity presents a two-fold challenge: using too coarse a resolution results in overly generic outcomes unsuitable for practical disease management, while collecting and maintaining high-resolution data is time-consuming and often impractical. Although higher resolution data would always be preferred to the aggregated statistics, preparation and maintenance of such detailed information might not always be a feasible and cost-effective solution for disease management. Finding a reasonable compromise, or better yet, having a range of options, can help build a more versatile, flexible and intelligent information system. Decisions on these issues should be taken at a planning phase, considering the availability of both geographical data and attribute information on animal populations.

Mapping animal populations to manage disease must account for specific traits of the diseases in question and adhere to general principles of infectious disease epidemiology. One such tool is the concept of "epidemiological unit", or "epi unit" (Box 1).

In the context of managing infectious diseases in swine, any professional pig farm (whether a herd or holding), where animals share the same likelihood of exposure to a pathogen and irrespective of its size, level of biosecurity or any other characteristics, is considered a distinct epidemiological unit. When it comes to non-professional pig holdings, such as backyard or free-range scavenging pigs, the definition of epi unit is mostly not applicable to single holdings because they rarely maintain an appropriate level of biosecurity or are not sufficiently isolated from similar neighbouring holdings. Backyard pig herds are usually aggregated into epidemiological units consisting of multiple holdings. Their boundaries are defined by the distribution patterns of pig owners, such as hamlets, villages, rural settlements and similar areas. Typically, rural populations that keep backyard pigs are clustered, resulting in spatial gaps between different populated places. On other occasions, limits of such rural epi units are difficult or impossible to identify because pigs (together with their owners) are distributed continuously.

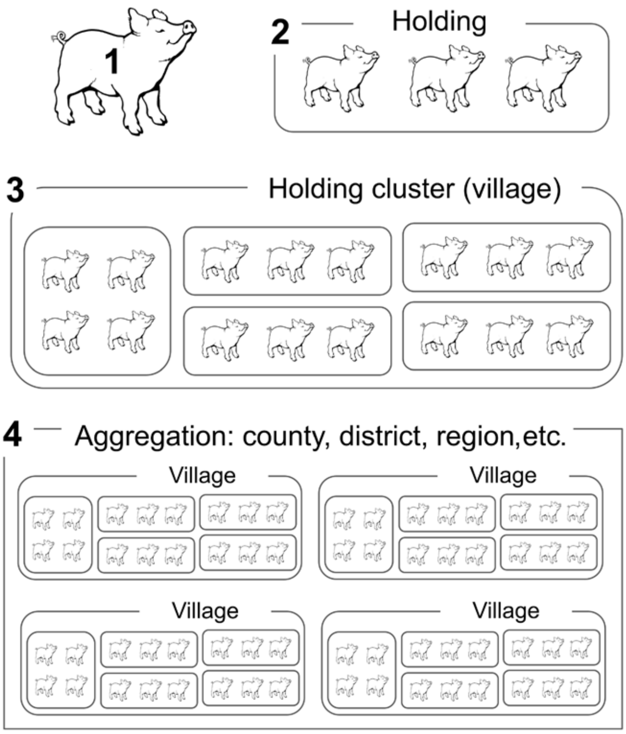
Defining what constitutes an epidemiological unit in the case of wild boar is usually impossible or can be done in a very approximate way and not without compromising the The World Organisation for Animal Health (WOAH) definition. Wild boar may have a continuous distribution, making it impossible to draw borders between subpopulations in areas where habitats are minimally fragmented. Conversely, wild boar can also exhibit a clustered distribution, with groups of animals inhabiting fragments of suitable habitats surrounded by unsuitable terrain, forming quasi-epidemiological units. Decisions on how to delineate epidemiological units or subdivide areas of wild boar occurrence may involve additional considerations, such as terrain features, natural borders, administrative boundaries (e.g. rural community lands) or management boundaries (e.g. hunting grounds or property lines).

BOX 1
Importance of the epidemiological unit

Defining the relevant epidemiological unit is crucial for the surveillance system. The sampling unit chosen for testing should align with this defined epidemiological context. Animals may be grouped as an epidemiological unit based on their shared environment or management practices. Typically, this unit is a herd or a flock. However, it can also be a group of animals in a pen, those belonging to residents of a village, those sharing a communal animal handling facility, or, in some cases, a single animal. The epidemiological relationship may vary depending on the disease or even the strain of the pathogenic agent.

Source: **World Organisation for Animal Health (WOAH).** 2024. *General principles of animal disease surveillance.* [Cited 12 July 2024]. Available from: https://www.woah.org/en/what-we-do/standards/codes-and-manuals/terrestrial-code-online-access/?id=169&L=1&htmfile=chapitre_surveillance_general.htm.

FIGURE 6
Possible resolutions of disease observation and reporting based on levels of aggregation



1 - individual animals; 2 - holdings, herds; 3 - holdings clusters (villages); and 4 - aggregated population units). Please, note that in the epidemiological sense, an individual animal can also be a "herd" or a "holding" and constitute a single epidemiological unit provided it is kept sufficiently separate from other herds or holdings to reduce the probability of infection.

Source: Author's own elaboration.

DESCRIBING PIG POPULATION DISTRIBUTION

GIS has three main ways to describe the distribution of host populations: (a) discrete point units representing farms, villages, markets and slaughterhouses; (b) discrete polygons or area units most often identical to administrative division and representing spatial extent of villages, counties, districts and provinces; and (c) continuous grids or regular standardized rectangular polygons not related to administrative division depicting populations as a continuous spatial variable representing a population or abundance metrics (numbers, density, probability of occurrence). Pig populations involved in African swine fever transmission cycles can be typically classified into three main categories or subpopulations: professionally reared pigs (commercial farms), non-professional holdings (backyard, free-range pigs), and free-living populations of wild or feral pigs. Approaches and tips to mapping these three categories and relevant epidemiological considerations are described below.

PIG FARM SURVEYS AND REGISTERS

Pigs kept in professional holdings (commercially farmed pigs) have an owner and are confined to a certain territory (property, farm, premises). The species, breeds, age categories and purpose of commercial pig farms may vary, and so may their biosecurity characteristics. Typically, commercial farms are treated as a single holding (a single herd) and an epidemiological unit. The farm location can be exactly defined in space using a pair of geographical coordinates and represented on a map as a point object with certain characteristics (attributes). Rare exceptions are commercial herds of free-range pigs, such as East-Balkan pigs in Bulgaria or Iberian pigs in Spain raised in forests. However, even in these cases, animals have defined premises where they breed and spend a part of their life.

It is strongly advisable to map and properly describe all professional swine farms across the country. There are many types of pig husbandry systems worldwide, and it might not always be easy to decide what constitutes a "commercial" or "professional" farm. Pig farm classification adopted in different countries may vary depending on the national legislation. Their official registration might be compulsory in some countries (including recording their principal characteristics), while in others, criteria and definitions are loose or non-existent. Creating and maintaining an up-to-date, georeferenced pig farm register is a crucial component of pig population mapping. This is especially important if a country's pig production systems are at risk or have already been affected by African swine fever or other swine diseases. Preventing disease from entering pig farms is well-justified epidemiologically and economically. Interventions in the commercial sector are generally more cost-effective, practical, and feasible than those in the backyard sector. Knowing the exact location of farms and their main characteristics will facilitate disease prevention and control activities, such as surveillance or vaccination.

An extreme example of a highly biosecure epidemiological unit is a "compartment", which can include several spatial objects with complex geometry. A compartment might consist of multiple premises, or premises combined with meat processing facilities. In cases where such multipart epidemiological units exist, it is important to indicate in the attribute table that they belong to a particular compartment, even if they are represented as separate geographic objects.

A compartment is defined in the Terrestrial Code as:

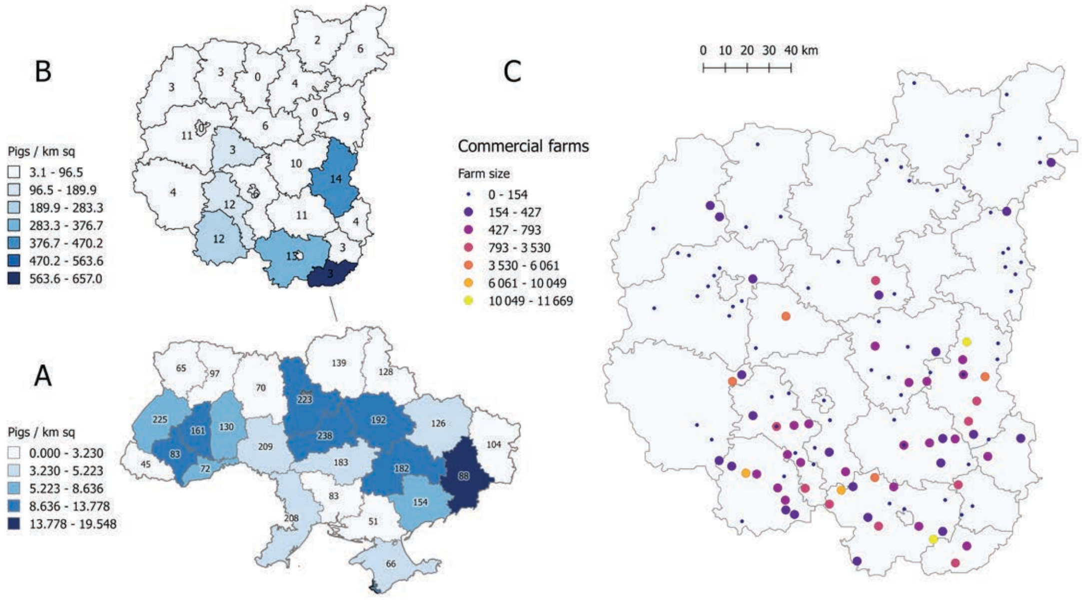
> *"an animal subpopulation contained in one or more establishments under a common biosecurity management system with a distinct health status with respect to a specific disease or specific diseases for which required surveillance, control and biosecurity measures have been applied for the purpose of international trade."*

Data collected in the farm registers or databases should not be mixed up with information on extensive production systems in the same area and typically should contain information on the actual and planned scale of production, breeds, age, specialization, vaccination status, import/export orientation, level of biosecurity, etc. In some countries, wild boar farming is widespread. It is important to include wild boar farms in pig farm registration. Biologically, wild boar is the same species as domestic pigs, and any farm with an owner should qualify as a farm rather than being classified with free-living populations.

In some countries, pig farm registers are maintained and updated every year by the competent veterinary authority or pig farmers' associations, though they are not always precisely and accurately georeferenced and might often require some extra data cleaning effort to make a tabular database suitable for use in a GIS. In the absence of such systematically collected information, special surveys are needed. These are either conducted by the representatives of the veterinary authority or by the farmers themselves. A starting point for such a survey is the development of a comprehensive form that captures key information on the pig farms and any specifics of local pig husbandry practices. Electronic forms/online data collection systems are a very useful tool to gather standardized information on commercial pig farms. With their help, accurate and up-to-date data can be quickly gathered across the country by the employees of authorized veterinary services or by the community of pig farmers.

Raw data on individual pig farms can be aggregated, for example, to provide total population estimates at the regional level or farm counts (Figure 7, A and B). Calculation of farmed pig density (total population per unit of area) at the aggregated level is not strictly speaking "population density" because the distribution of farmed pigs is highly clustered.

FIGURE 7
Commercial pig population in Ukraine at different levels of aggregation



Commercial pig population in Ukraine at different levels of aggregation. A) - Numbers of pigs normalized by unit area and farm counts at oblast level; B) The same at district level in Chernihiv oblast; C) Farms in Chernihiv oblast classified by farm size.

Note: Refer to the disclaimer on page ii for the names and boundaries used in this map.

Source: Author's own elaboration. Country boundaries based on UN Geospatial. 2023. Map of the World. In: United Nations. [Cited: 10 November 2024]. http://www.un.org/geospatial/content/map-world-1

It can be done to compare the relative abundance of this subpopulation between administrative units and account for their area variation. For epidemiological calculations, it is more useful to have farm counts (Figure 7, A and B), if possible, with a breakdown by their types or biosecurity scores.

MAPPING PIGS IN NON-PROFESSIONAL HOLDINGS

Non-professional pig production systems consist of holdings that are normally characterized by small scale of production (most often for subsistence), use of traditional breeds and husbandry practices, low profitability, utilization of kitchen waste or seasonally abound feeds through free-range scavenging, home slaughter, as well as generally low biosecurity. Known under the names of "backyard", "low biosecurity", "free-range", "small-holder" or "traditional" farms, they occur widely around the world, especially in developing and low-income countries. The occurrence of backyard pigs is typically associated with the distribution of rural populations. Non-professional subsistence pig farming is rare in urban settings, except for peri-urban communities in Africa and other developing countries, where pigs may occupy a scavenging niche.

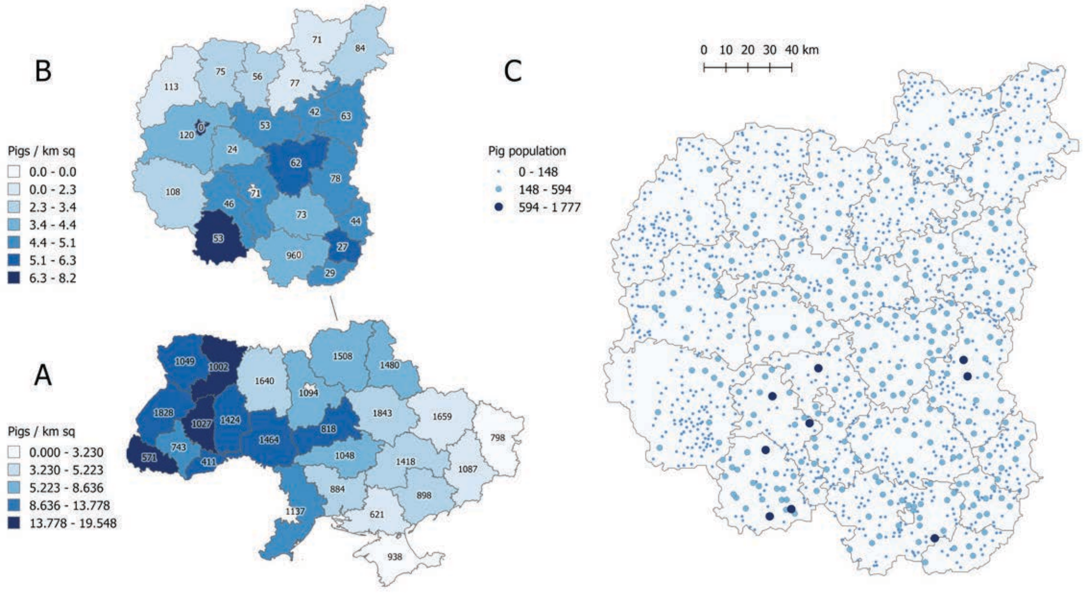
Populated places or villages, which are loose clusters of holdings with similar characteristics, are most often used as a unit for epidemiological purposes and disease control interventions in extensive pig production systems. Animal populations of a village are more likely to interact with each other because of their proximity and animal husbandry routines. In such systems, pigs are raised in the presence of and in direct contact with other livestock species, poultry and other domestic animals, which facilitates virus introduction to farms.

Information on pig numbers in a village can rarely be assessed precisely and regularly. Domestically reared pigs have a short production life span (ranging from months to two years) and there is strong population turnover in any production system. Therefore, rather than being regularly counted, pig populations kept in non-professional holdings are typically estimated. The baseline data (number of pigs per household or farm) is normally collected during agricultural household surveys, which are conducted relatively rarely and are quite expensive. In some countries, they might be outdated by as much as several decades. Such surveys are normally used for further calculations and aggregated data at administrative units of a certain level. Statistical services of the relevant countries subsequently adjust these figures based on various calculations and models.

Animal population statistics for non-professional holdings are often available as aggregated data, such as tables where estimates are provided for an area (an administrative unit such as a province, region, district, county, etc). Visualization of aggregated animal populations (as polygons on

FIGURE 8

Backyard pig population in Ukraine at different levels of aggregation



A) - Average backyard pig density and number of villages at oblast level; B) The same at district level in Chernihiv oblast; C) Villages in Chernihiv oblast classified by pig population estimates.

Note: Refer to the disclaimer on page ii for the names and boundaries used in this map.

Source: Author's own elaboration. Country boundaries based on UN Geospatial. 2023. Map of the World. In: United Nations. [Cited: 10 November 2024]. http://www.un.org/geospatial/content/map-world-1

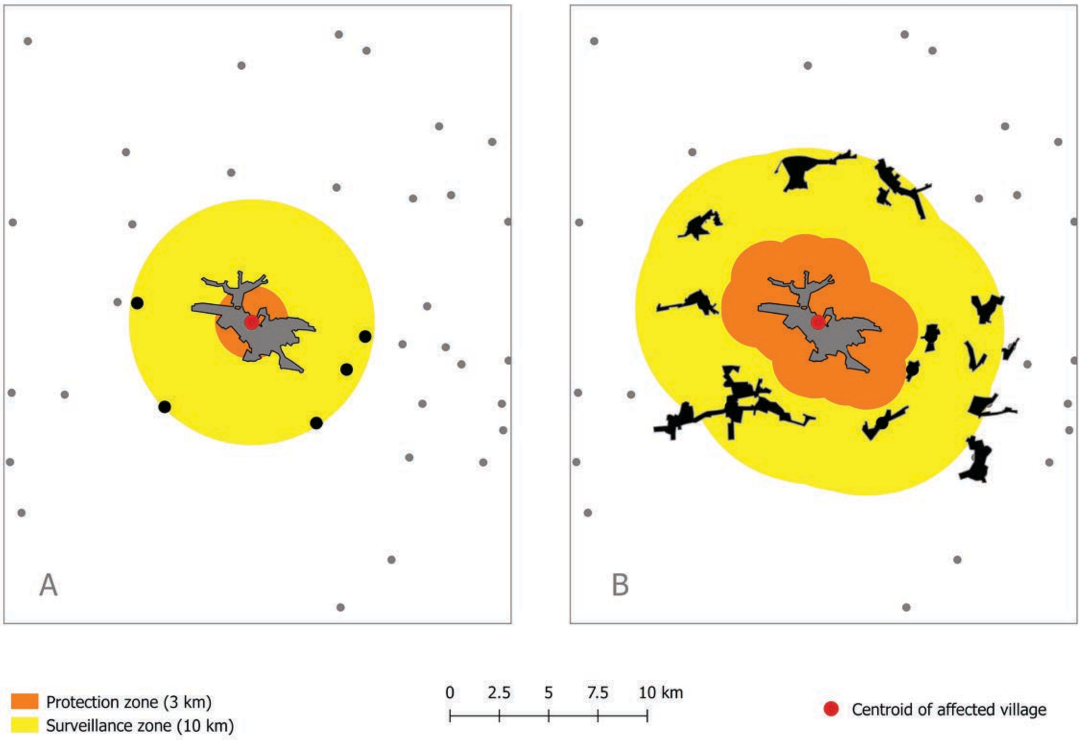
the maps) is commonly used for statistical, economic and administration purposes. Most agricultural statistics or indicators, demographic, economic or public health data are also collected, arranged and updated based on administrative division. In many cases, animal population data is only available at higher levels of aggregation, such as Admin 1 or Admin 2 levels (provinces or districts). This level of data aggregation can be convenient for certain types of national scope analysis and decision-making (Figure 8, A). However, the coarse spatial resolution and lack of essential details make such data less suitable for specific disease control tasks, including surveillance, value chain analysis and intervention planning.

This "low-resolution problem" can be partially resolved through disaggregation. This involves redistributing backyard pig population totals to lower-level administrative or other units based on various statistical methods, ranging from simple to sophisticated. Higher-resolution administrative divisions (smaller size, such as subcounties and counties, Admin 3 and 4) are better suited for practical disease management purposes. However, this varies between countries and depends on human population densities and the way administrative units are subdivided. After all, administrative divisions are designed for purposes other than describing patterns of animal populations or planning disease control activities. Visualization of such aggregated population data or calculating any epidemiological metrics always requires some sort of normalization to account for variation in polygon areas, size of the human population, number of epi units, etc.

Administrative polygons have some drawbacks when it comes to using them as spatial units in a decision support GIS, namely: a) they vary in size and shape across the country and do not always capture the necessary level of detail; b) they are often changed, aggregated or disaggregated, making it difficult to use historical data, as well as conduct prospective predictions; and c) they are often not comparable between neighbouring countries, which complicates regional and transboundary dimensions of analysis. From the technical side, the outlines of administrative units are often produced at various scales and degrees of generalization, which makes it problematic to align them together (both nationally and between neighbouring countries) in a topologically correct manner.

The representation of high-resolution (village-level) backyard pig populations on maps depends on the availability of corresponding geographic datasets. Village or community outlines (polygons) with population estimates would be a more accurate representation of reality (Figure 9). Human settlements often have elongated or otherwise complex geometry, which may have implications for defining the extent of the infected area and creating surveillance or protection zones. Whenever possible, polygons of the lowest level of

FIGURE 9
Effect of geometry type selected for mapping villages



A - when villages are represented as their polygon centroids the protection and surveillance zones cover less area and only five neighbouring villages fall into the 10 km surveillance zone; B - when villages are represented as polygons, both zones are larger and 13 villages fully or partially fall into the surveillance zone.

Source: Author's own elaboration.

administrative division should be used. Alternatively, if such geographic data is not available, village centroids can be used to approximate their locations in geographic space. This solution will reduce accuracy but will provide a better level of spatial resolution for disease management purposes compared to aggregated populations represented as higher-level administrative polygons (Figure 9).

As with farmed pig populations, one may need to compare the relative abundance of backyard pigs between administrative regions of a country by normalizing their total population with the region area. It is also important to have a total count of villages, which makes aggregated estimates of disease occurrence more accurate epidemiologically (e.g. by calculating attack rates, see Chapter 3).

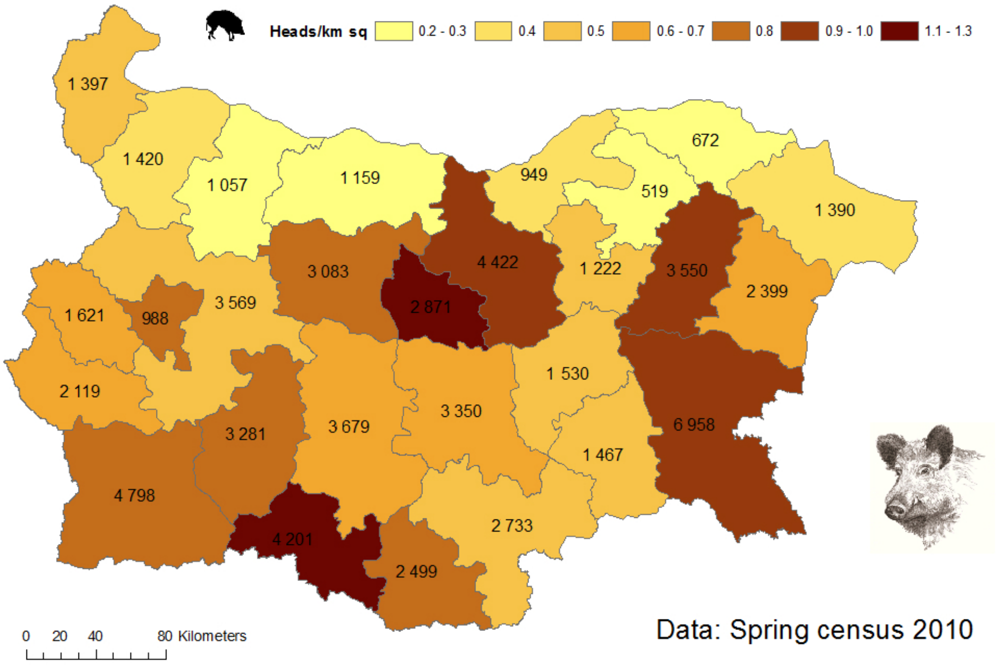
Wild boar/feral pigs aggregated population mapping. For ASF epidemiologists, mapping wild pig distribution patterns is a challenging task, which nonetheless is very important, especially where ASF has established itself as an endemic disease of wild boar. Such information is rarely available to the competent veterinary authorities immediately, apart from where forestry or wildlife management are a part of the same ministry. Obtaining it would normally require cross-sectoral collaboration.

In Europe, where wild boar is a traditional game species, population statistics are usually available from forestry, wildlife or hunting management authorities or hunting organizations. Countries may have different systems in place to estimate the resources of wild animals including special population surveys or record only hunting bags. Some countries include this type of information in their official statistics reports, where they may be associated with polygons of subnational administrative divisions (Figure 10). In this case, they can be easily incorporated into the information system together with domestic pig estimates.

Apart from general availability, common problems associated with using statistics obtained from game or wildlife agencies are that management units adopted by these authorities (forest or hunting districts, hunting grounds, national park boundaries) are poorly aligned with livestock population units. Experience also shows that official data on wild boar numbers are often unreliable, which is related to wild boar biology and the objective difficulties with counting this species.

FIGURE 10

Average wild boar population density and population counts in Bulgaria (2010, spring)



Aggregated at the first level of administrative division.

Note: Refer to the disclaimer on page ii for the names and boundaries used in this map.

Source: Author's own elaboration. Country boundaries based on UN Geospatial. 2023. Map of the World. In: United Nations. [Cited: 10 November 2024]. http://www.un.org/geospatial/content/map-world-1

Another problem with estimating wild boar numbers comes from the different land ownership and stakeholder jurisdiction. While some forests or other types of habitats might be recognized as hunting grounds, others might not. The same applies to agricultural and public or municipal lands that are not used for hunting. The implication is that there is no competent or responsible body to take care of the wildlife in these areas. Another situation arises in nature-protected areas or in the zones along the international border where hunting or visiting is strictly prohibited. Even if reporting wild boar numbers is a compulsory statistic in some countries, such counts are usually incomplete, rarely standardized or reliable. They tend to strongly underestimate wild boar populations.

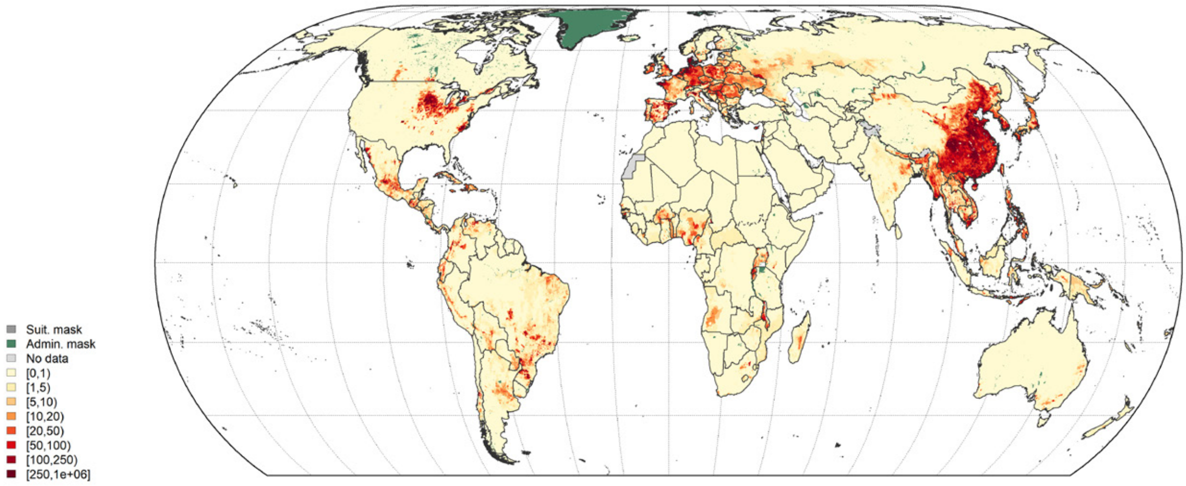
It is more appropriate to regard many of these official numbers as approximate abundance estimates, for example as a relative measure of wild boar numbers, suitable for inter-regional comparisons, but not very useful for informing local disease control operations. As with backyard pig population statistics, it is advisable to have highly detailed maps of wild boar abundance. Achieving this requires close, systematic collaboration among veterinary authorities, wildlife management agencies, biologists, and hunting communities.

Wild boar have continuous distribution patterns with highly variable population densities across space. Those tend to fluctuate naturally, show upward trends or be in decline (e.g. also because of ASF-induced mortality). All this makes estimating their numbers and population parameters a complex and rather challenging research task, requiring staff with disparate qualifications and application of locally appropriate methodology. Wildlife or game biologists have specific methodological solutions for estimating wild animal populations, such as counts at feeding sites and trace or driven counts. They are now working on developing more standardized and reliable methods to count wild boar. Some of those include the use of camera traps or drones, others apply spatial modelling approaches to analyses of occurrence, numbers or habitat preferences of wild boar.

In predominantly Muslim countries or Asia, the traditions of organized hunting are weak to non-existent, though hunting does occur. Statistics such as hunting bag surveys or any other occurrence recording system for wild boar might not be readily available in this context. There is also less attention paid by authorities and the research community to wild pigs and swine diseases. In the United States of America and Australia, where wild pigs are treated as an invasive pest species, special monitoring programmes are in place to provide data and observations for agriculture and wildlife authorities and researchers. The global expansion of ASF creates a strong

FIGURE 11

The global distribution of pigs in 2015



Expressed in total number of pigs per pixel (5 min of arc) according to the Gridded Livestock of the Country boundaries based on UN Geospatial. 2023. Map of the World. In: United Nations. [Cited: 10 November 2024]. www.un.org/geospatial/content/map-world-1. World database (v4). The processing was carried out at 0.0083333 (approx. 1 km at the equator) and aggregated at 0.083333 (approx. 10 km at the equator).

Note: Dotted line represents approximately the Line of Control in Jammu and Kashmir agreed upon by India and Pakistan. The final status of Jammu and Kashmir has not yet been agreed upon by the parties. A dispute exists between the Governments of Argentina and the United Kingdom of Great Britain and Northern Ireland concerning sovereignty over the Falkland Islands (Malvinas). Final boundary between the Republic of Sudan and the Republic of South Sudan has not yet been determined.

Source: **Gilbert, M., Cinardi, G., Da Re, D., Wint, W.G.R., Wisser, D. & Robinson, T.P.** 2022. Global pigs distribution in 2015 (5 minutes of arc). https://doi.org/10.7910/DVN/CIVCPB, Harvard Dataverse, V1.

demand for systematic efforts to collect and analyse wild boar occurrence data in a manner most suitable for each country's local context, traditions and research capacities (see, for instance, the European initiative ENETWILD [ENETWILD, n.d.]). The coming years will likely bring more progress in this area, including in parts of the world where the epidemiological role of wild boar has been neglected. Geographic information systems play a significant role in empirically mapping and modelling patterns of wild boar occurrence at various spatial scales (see ENETWILD, 2019).

Captive and semi-captive populations, such as wildlife farms, ranches and zoos are a category of wildlife that sometimes falls into the cracks between responsibilities of different agencies. Wild boar are often raised in captivity in many countries, either for production or as breeding stock for hunting grounds. In some countries, the wild boar farming sector might be large and managed intensively for hunting, tourism or production reasons. Wild boar raised in captive and semi-captive conditions may have higher risks of certain diseases compared to free-living populations because of unusually high population density, age composition and other factors. For this reason, this type of holding must be included in overall pig population mapping: either as a part of domestic pig farm surveys (when used for production) or as wild boar specialized farms under wildlife or hunting management agencies or communities. In the European Union, fenced wild boar are legally considered domestic pigs. However, the World Organisation for Animal Health treats them as wildlife. Despite this classification, ASF must be managed in these situations similarly to domestic pigs, involving measures such as culling and disinfection.

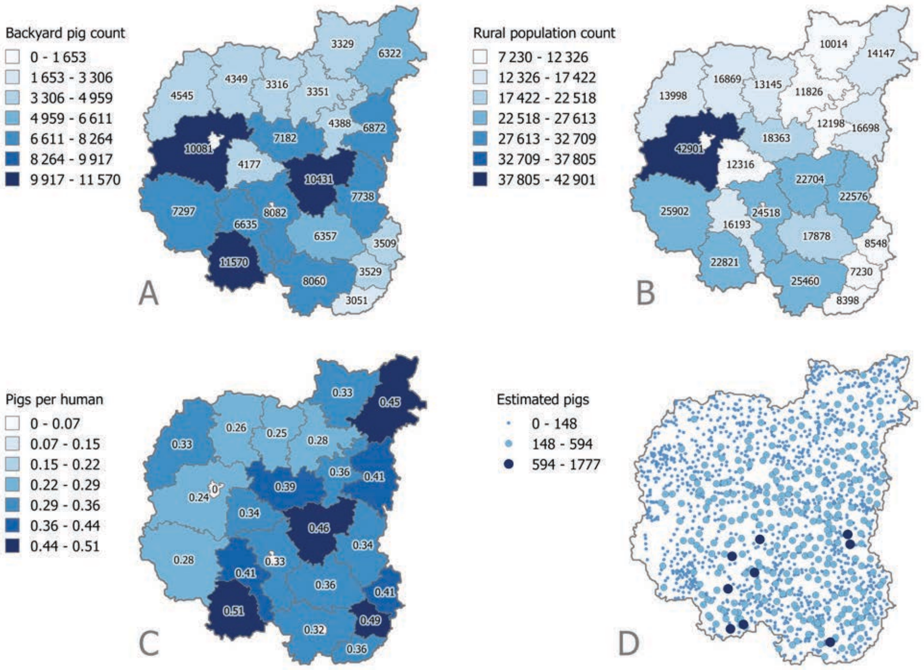
GRIDDED POPULATION MAPS, DISAGGREGATION AND MODELLING

Backyard pigs. Agricultural surveys are not conducted in every country regularly. In some countries, livestock statistics can be outdated and unreliable. A good solution to overcome these data gaps and increase the spatial resolution of livestock distribution maps is the use of rasters. Rasters consist of a matrix of pixels (also called cells), each containing a value that represents the conditions for the area covered by that cell. In livestock mapping, these grid cells have population estimate data expressed as the number of animals in a grid cell or as a density (head/km^2). FAO pioneered the production of livestock gridded maps in 2007 (GLW1, FAO, 2007). Since then, these maps have been frequently used in data-deficient regions and for regional to global analyses, serving epidemiological and other purposes.

Global gridded livestock population (GLW) datasets are produced by FAO and collaborators using constantly evolving modelling approaches. These datasets disaggregate population totals available at the polygon level and distribute them within these spatial units based on identified predictors (FAO, 2007; Robinson *et al.*, 2014). The precision

FIGURE 12

Example of vector-to-vector disaggregation of backyard pig population totals based on district-level pig-to-human ratios in Chernihiv oblast, Ukraine



A - Total pig count at district level; B - Rural population count; C - Number of pigs per rural inhabitant; D - Result of estimating numbers of backyard pigs at village level as village population size multiplied by C.

Note: Refer to the disclaimer on page ii for the names and boundaries used in this map.

Source: Author's own elaboration. Country boundaries based on UN Geospatial. 2023. Map of the World. In: United Nations. [Cited: 10 November 2024]. http://www.un.org/geospatial/content/map-world-1

and applicability of these maps have their limitations, generally related to the fact that the accuracy of predictions naturally declines with increasing scale. Gridded livestock maps are overall a more flexible way to deal with population data, especially on the larger spatial scales. Gridded pig distributions enable the development of statistically robust models and predictions, avoiding problems related to frequent changes in administrative borders.

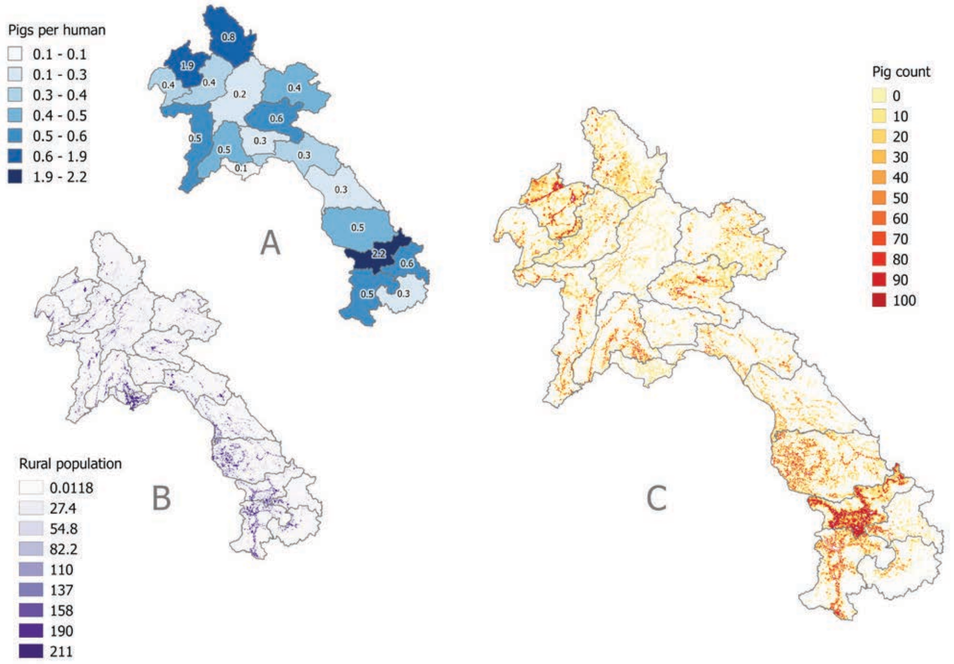
Several versions of the GLW database have been released, reflecting the most recently compiled and harmonized subnational livestock distribution data at each time. This work is developed and maintained by FAO's Livestock Information, Sector Analysis and Policy Branch (NSAL) within the NSA division's regular programme and various projects. It has been developed in collaboration with the Spatial Epidemiology Lab (SpELL) at Université Libre de Bruxelles.

Depending on their purpose, the spatial resolution of gridded livestock data may vary. Livestock population models are continuously developed to make them more accurate and cover a wider range of domestic species and production systems. For some, including swine, extensive, semi-intensive and intensive production systems have been already mapped separately (GLW 2, Gilbert *et al*., 2015). Most recently efforts have been made by the research community to produce country-specific livestock distribution models (Zhao *et al*., 2019; Zhao *et al*., 2022; Meisner *et al*., 2022). By reducing the geographic scope of the modelling exercise and using more detailed, up-to-date and accurate input data (household surveys, segregated populations by sectors), researchers were able to substantially improve the quality of livestock models. There is also a growing understanding that the modelling methods are more suitable for ruminants and extensive farming systems, while industrial animal husbandry follows different distribution patterns and requires different mapping approaches.

For monogastric species, such as pigs, whose backyard populations are very closely spatially associated with the distribution of rural populations, one can use a relatively simple approach to disaggregation. The idea behind this is that numbers of rural inhabitants are used as a predictor variable when totals are redistributed over subordinate administrative units or grid cells. It assumes that the ratio of pigs to humans (including rural population only) at higher levels (e.g. admin 1) roughly remains constant across subnational administrative units of lower order (e.g. admin 2). Given the known numbers of rural inhabitants in each subordinate administrative unit, one can then calculate the approximate number of backyard pigs in each unit (Figure 12).

FIGURE 13

Example of vector-to-raster disaggregation in Lao People's Democratic Republic



A - Number of pigs per rural inhabitant at the provincial level; B - Rural population count represented as 30 arc-seconds grid (WorldPop, 2020). Available at: https://hub.worldpop.org/ [Cited 13 July 2024]) includes only grid cells with below 300 persons per km² which are considered rural areas as per recommendations: Anonymous, 2020); C - Pig population count obtained because of raster calculations.

Note: Refer to the disclaimer on page ii for the names and boundaries used in this map.

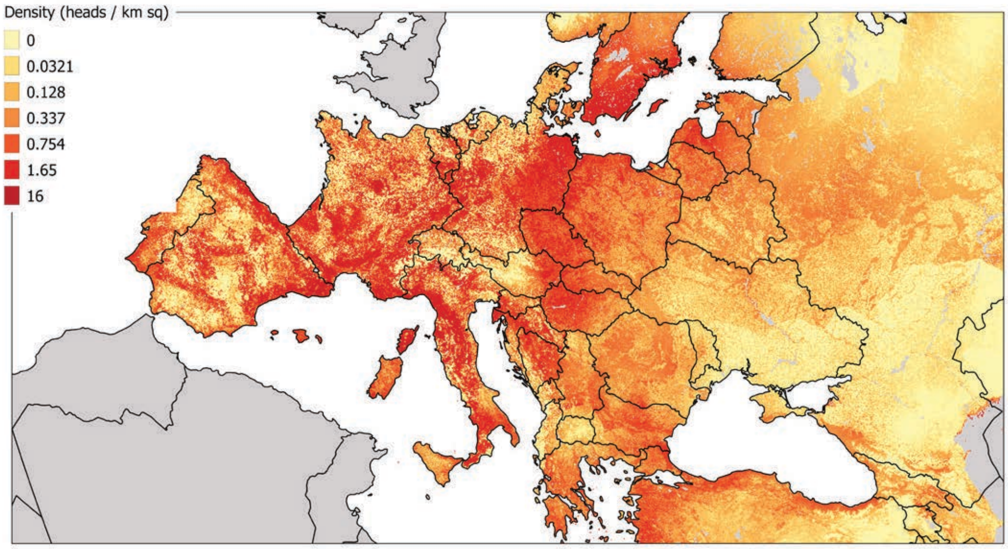
Source: Author's own elaboration. Country boundaries based on UN Geospatial. 2023. Map of the World. In: United Nations. [Cited: 10 November 2024]. http://www.un.org/geospatial/content/map-world-1

The same logic applies to other levels of administrative division, such as disaggregation from admin 2 to admin 3, provided that empirical data for level 2 is available. Similarly, one can downscale backyard pig population totals from a given level of administrative division (the finer the better) to a rural human population raster, thereby obtaining pig population estimates at the resolution of the human population raster (Figure 13).

Wild boar/feral pigs. Biologists are widely using GIS to analyse wildlife species occurrence patterns and make predictions of their range extents or abundance estimates, especially where empirical data is not available because of insufficient count coverage, accessibility or other reasons. Often their research outcomes are produced as raster maps (grids) that can be integrated into GIS and to support practical decisions. Wild boar numbers and distribution are becoming an increasingly more popular subject of such research, ranging from local projects in national parks or parts of a country (Lee *et al*., 2022) to regional or global scope modelling exercises (Pittiglio *et al*., 2018; Lewis *et al*., 2018; ENETWILD consortium, 2021). It is a good idea to establish close collaboration with wildlife biologists experienced in modelling species distribution within any respective country. This collaboration can help advance the decision support system for ASF management by using wild boar population maps with the most appropriate approach based on the available data. Such collaborations would be mutually beneficial and results can be used by stakeholders well beyond the animal disease epidemiology domain.

Several types of data can be used by biologists for predictive mapping of wild boar. The simplest option is presence data, such as georeferenced locations with confirmed occurrences of the species. Potential sources of such data sets include records on road kills, hunting locations, tracks or dang records, sightings by the public, crop damage locations, etc. Given that the probability of finding different types of evidence for wild boar presence varies, presence data should ideally be collected using the same method. Collection of presence/absence data is somewhat more complicated as people in general are less reliable in reporting the absence of wild boar. More effort is typically required to confirm the absence rather than the presence of a particular species. Questionnaire-based surveys or camera trap observations can generate presence/absence data that are suitable for modelling wild boar occurrence at different spatial scales. In some areas, such as national parks, nature

FIGURE 14
Disaggregated (modelled) population density of wild boar in Europe at a resolution of 5 km per pixel



Based on statistical data originally collected at the sub-national level of administrative division (Data: Pittiglio *et al*., 2018).
Note: Refer to the disclaimer on page ii for the names and boundaries used in this map.
Source: Author's own elaboration. Country boundaries based on UN Geospatial. 2023. Map of the World. In: United Nations. [Cited: 10 November 2024]. http://www.un.org/geospatial/content/map-world-1

reserves or hunting grounds, population counts are well-designed, systematic and reliable to produce local population density estimates (head per unit of area) of acceptable quality. In the presence of a sufficient number of those, one can build a model that would generate predicted density estimates as opposed to "presence only" or "presence/absence" models whose outputs come as the probability of occurrence maps (0–1). Where population data on wild boar is available as polygon-level aggregate statistics, a disaggregation approach resembling that of the one used in livestock population mapping becomes possible (Figure 14; Pittiglio *et al*., 2018; ENETWILD consortium, 2021).

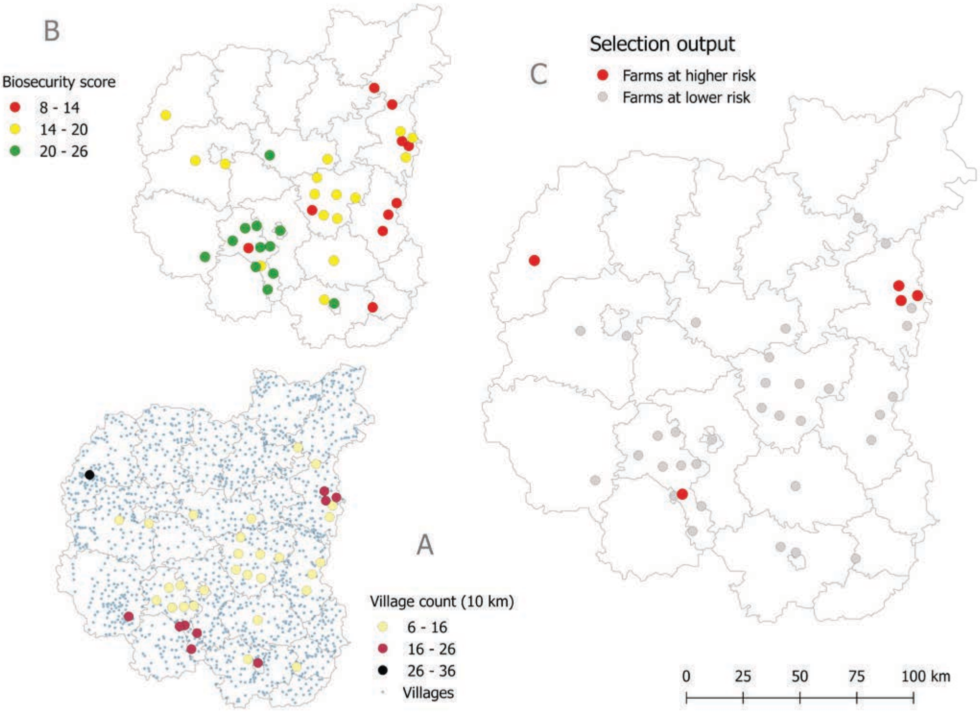
HUMAN POPULATION

Human population data are a very important characteristic of the unit of analysis. Humans are involved in the epidemiology of ASF in multiple ways: as pig owners or consumers of products, hunters or farmers, traders or customers. Maintaining up-to-date statistics on human populations at various levels of aggregation is a good idea. This data helps with tasks such as correcting the visualization of spatial patterns, normalizing animal population data (e.g. pig-to-human ratios), disaggregation, risk analysis and estimating the probability of finding dead wild boar carcasses. A distinction should be made between rural and urban populations, as their interactions with animals, other humans and environmental or risk factors of concern usually differ significantly. Urban populations are typically not involved with pig production or hunting, while in rural areas pig breeding is often a significant part of subsistence strategy or wild pig hunting is a common occurrence. In some countries, ethnic composition or religion can be good predictors of population involvement in or avoidance of pig breeding, as well as certain consumer preferences and cultural needs related to the treatment or utilization of wild or domestic pigs. Some of these factors might be of epidemiological significance.

Human population data are normally regularly collected by governments as population or household surveys and agricultural censuses. In between censuses, statistical models and projections are often used to correct estimates based on known relationships with demographics, economics or other variables. Data sets are arranged following administrative division from the highest units (villages, subcounties) to the lowest ones (districts, provinces) and would be most often accessible from the countries' statistical offices, although not always in a format that is ready for use in the geographical information systems. Human demographics, health and socioeconomic indicators are also routinely collected by many international institutions and research organizations and can be accessed from multiple online databases.

Raster maps of the human population of various spatial resolutions are now also available, including projected population change. These models become increasingly more robust, accurate and reliable and can be recommended for use where national statistics are poor or outdated (see WorldPop, 2020).

FIGURE 15
Finding pig farms with lower biosecurity located in the areas with high density of villages



Vulnerable farms were identified based on their characteristics combined with village counts in the zone of 10 km around the farms obtained from the village layer using GIS tools in Chernihiv Oblast, Ukraine.

Note: Refer to the disclaimer on page ii for the names and boundaries used in this map.

Source: Author's own elaboration. Country boundaries based on UN Geospatial. 2023. Map of the World. In: United Nations. [Cited: 10 November 2024]. http://www.un.org/geospatial/content/map-world-1

ADDITIONAL ATTRIBUTES OF EPIDEMIOLOGICAL UNITS

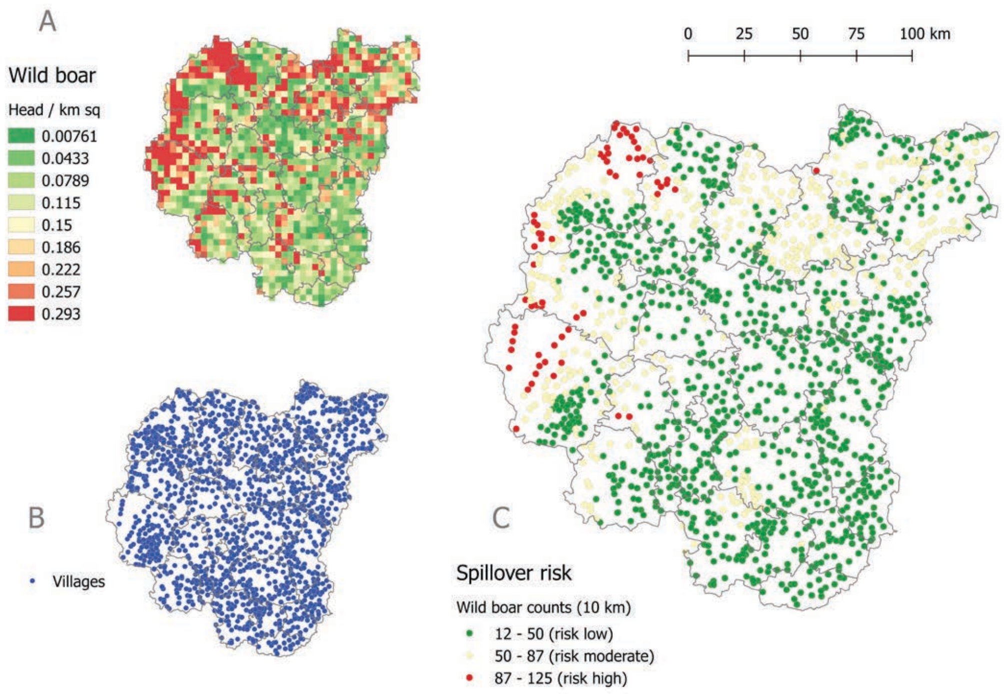
Attributes of the epidemiological units involved in pig production can be additionally enriched by contextual information from other layers using simple geoprocessing tools. For example, in addition to available characteristics of pig farms (specialization, size, biosecurity) one may calculate simple population metrics for the backyard production sector in the zone of selected radius around the farms. Indicators such as the number of villages and their total estimated pig populations can be added to farm attributes to provide additional classification criteria for risk evaluation. The task that can be solved with this information can be, for instance, formulated as follows: "Select pig farms with lower biosecurity score situated in the areas with high density of villages" (Figure 15).

Making such a selection can be a reasonable solution in a situation when ASF is spreading in the backyard sector of the country or region in question and authorities want to inspect the most vulnerable farms, conduct additional surveillance or spread educational materials to the farmers whose properties are most at risk.

The same kind of calculations can be performed to pre-define backyard pig population metrics within a 1, 5 or 10 km radius from each village in the dataset. Then, upon detection of disease in any village, authorities can immediately find out how many epi units of each type are in the infected zone, the population size to be destroyed or which resources are required to conduct surveillance in the affected village's vicinity according to official protocols. Using GIS functionality to assist with disease management planning can have many applications relevant to different epidemiological situations. For enhancing surveillance, it might be useful to identify villages located in areas with high wild boar population estimates. Zonal statistics of the wild boar population layer can be added to the attributes of these villages, enabling their classification by additional indicators (Figure 16).

FIGURE 16

Classification of villages to identify the risk of African swine fever spillover (either from domestic pigs to wild boar or vice versa) in Chernihiv oblast, Ukraine



Using zonal statistics calculated in the radius of 10 km around each village from the raster layer with wild boar population estimates (Pittiglio *et al.*, 2018).

Note: Refer to the disclaimer on page ii for the names and boundaries used in this map.

Source: Author's own elaboration. Country boundaries based on UN Geospatial. 2023. Map of the World. In: United Nations. [Cited: 10 November 2024]. http://www.un.org/geospatial/content/map-world-1

AGGREGATION OF POPULATION METRICS

The availability of granular population data (e.g. fine-scale mapping of epidemiological units) significantly increases the functionality of decision-support GIS and is therefore highly recommended. However, some management and analytical tasks require aggregation of pig population metrics. For example, it is important to know regional or district summary statistics such as the total number of villages, counts of farms of different categories, total population sizes of pigs in professional holdings and the backyard sector, etc. (Table 1, Figure 17). Such a task can be easily implemented with the help of standard GIS functionality. The attribute table of the regional summary layer should be regularly updated to reflect changes.

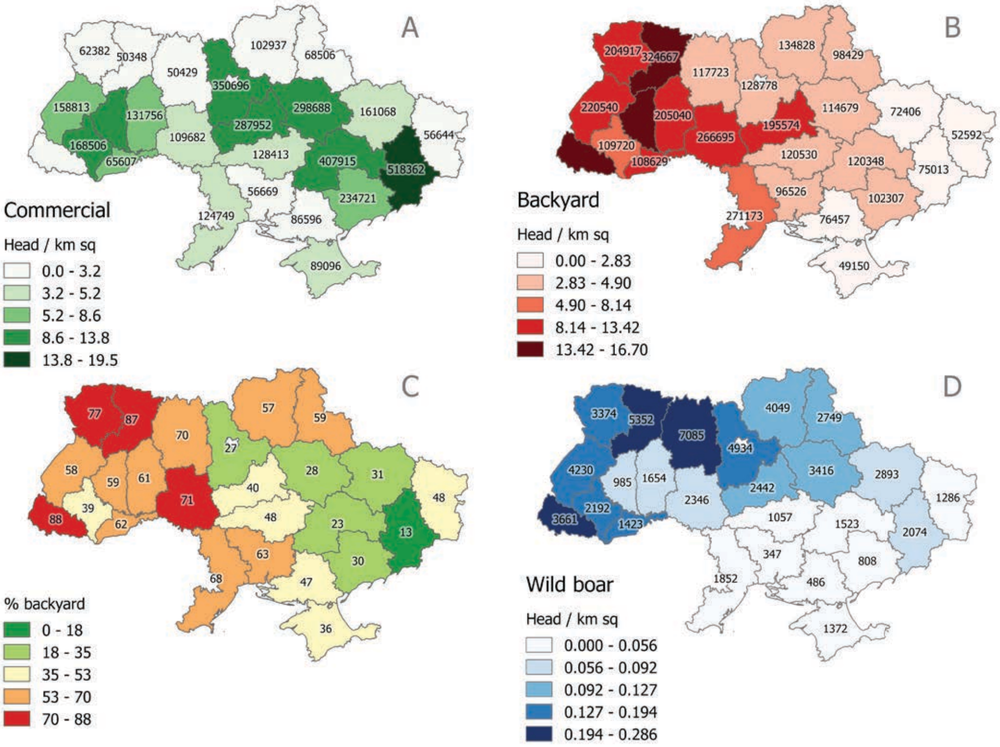
Correct cartographic visualization of aggregated data always requires some variables that can be used to minimize the effect of the modifiable areal unit problem (MAUP, Pfeiffer *et al.*, 2008). The variation in the areas and other characteristics of summary polygons can be compensated by the calculation of normalized population metrics to make comparisons correctly and generate maps or visualizations that reflect the spatial variation of the parameters of interest without bias (Figure 17). For example, instead of making a map of total pig farm counts, one may normalize farm count totals by the unit area (e.g. calculate the density of farms). Normalization by area is always required to correctly present patterns in the distribution of population. Sometimes human population totals (e.g. rural population) can be a better or more appropriate denominator for normalization. Provided with raw summary statistics, one may also calculate various proportions. For example, it is possible to show how the share of professional holdings with a low biosecurity score or the proportion of backyard pigs (Figure 17, C) varies between different regions of the country.

Key messages:

- It is essential to treat and map the three pig populations (backyard, commercial and wild/feral pigs) involved in the ASF transmission cycle separately, to effectively evaluate the probabilities of certain epidemiological scenarios and facilitate tailored appropriate interventions in each sector.

FIGURE 17

Aggregated pig population statistics in Ukraine at oblast level (2014)



A - Commercial pig population counts and density; B - Average backyard pig population counts and density; C - Proportion of backyard pig population in the total pig population counts; D - Population counts and average density of wild boar.

Note: Refer to the disclaimer on page ii for the names and boundaries used in this map.

Source: Author's own elaboration. Country boundaries based on UN Geospatial. 2023. Map of the World. In: United Nations. [Cited: 10 November 2024]. http://www.un.org/geospatial/content/map-world-1

- An epidemiological (epi) unit is a group of animals with approximately the same probability of exposure to a pathogen because they share a common environment or management. It can be a herd, farm, all animals in a village, individual barns or pens. Defining an epi unit in the case of free wild pigs is usually impossible. The decision on what constitutes an epi unit in a particular case may involve additional considerations.
- Aggregation of population data can be useful for purposes such as planning, calculating statistics, etc. However, it is crucial to ensure that this aggregation is performed accurately, especially when considering the diverse pig populations involved.
- Creating and regularly updating a georeferenced pig farm register is crucial for pig population mapping, especially in countries at risk of ASF or other swine diseases. This register aids in disease prevention and control activities.
- The integration of the village layer with pig estimates into GIS systems is crucial for effective disease control interventions, focusing on specific at-risk epidemiological villages.
- Mapping wild pig distribution patterns is crucial for managing ASF. However, it presents a considerable challenge. Effective data gathering requires collaboration across sectors, involving forestry, wildlife management, hunting organizations and other relevant entities.
- Maintaining up-to-date human population data, particularly on rural populations, is crucial for disease management GIS and epidemiology of ASF. It helps visualize spatial patterns, normalize animal population data and analyse risk.
- The attributes of epidemiological units in pig production can be significantly enriched by integrating information from other layers, such as the number of villages and the total estimated pig populations. These additional details aid veterinary authorities in assessing the level of risk and resources needed in the event of outbreaks.

TABLE 1

An indicative list of summary indicators and aggregated pig population statistics to be maintained in a geographic information systems at a regional level of aggregation

Group	Aggregated unit indicator	Metrics	Description
Unit characteristics	Unit area	Km^2	Estimated terrestrial area of the unit of aggregation (excluding any water areas)
	Rural population counts	Number	Most recent count of rural population as per national statistical data
	Rural population density	Persons per km^2	Rural population totals divided by total unit area (excluding cities)
Epi Unit counts	Total epiunit count	Number of epi units	Total number of epi units including both farms and villages
	Low biosecurity epi units (villages) counts	Number of villages	Total number low biosecurity epi units (villages)
	Commercial farms total count	Number of farms	Total number of commercial farms
	Commercial farms (by biosecurity class) counts	Number of farms	Numbers of commercial farms of each biosecurity type
	Commercial farms (by production type) counts	Number of farms	Numbers of commercial farms of each production type
Pig population counts	Total domestic pig count	Number of heads	Total number of domestic pigs of all categories
	Backyard pig count	Number of heads	Total number of backyard pigs
	Commercial pig count	Number of heads	Total number of commercial pigs
	Wild / feral pig count	Number of heads	Total number of wild/feral pigs
Normalized counts	Village density	Villages per km^2	Number of villages divided by unit area
	Farm density	Farms per km^2	Number of farms divided by unit area
	Backyard pig density	Head per km^2	Backyard pig population counts divided by unit area
	Commercial pig density	Head per km^2	Commercial pig population counts divided by unit area
	Wild / feral pig density	Head per km^2	Wild or feral pig population counts divided by unit area
	Backyard pigs per rural inhabitant	Head per person	Backyard pig population counts divided by total rural population counts

Source: Author's own elaboration.

Chapter 3

Disease occurrence mapping

This chapter introduces the key concepts of disease surveillance based on epidemiological units. It explains the importance of accurately identifying different types of disease events, choosing appropriate spatial resolution, and disease reporting or visualization units under different epidemiological circumstances. Throughout, you will be guided through several hypothetical and real-world scenarios, illustrating the mapping of disease occurrence in backyard and commercial sectors, as well as in wild or feral pigs. It also guides effectively summarizing or aggregating disease event observations, facilitating meaningful comparisons across epidemiological units in both space and time.

How disease surveillance is organized strongly influences the way the epidemiological situation will be visualized on maps. The standardized approach to recording and then mapping disease events is critically important. In theory, several resolution levels of presenting information of disease occurrence in space from most granular to most generic are possible: (1) individual animals ->; (2) individual herds or holdings ->; (3) holding or herd clusters (farms, villages) ->; and (4) artificial population units (counties, districts, provinces, countries). From the cartographic perspective, those may be looked at as "zoom" levels with gradually decreasing scale and increasing levels of data aggregation (see Chapter 2. Population mapping). These levels should never be mixed up when geographical visualizations are produced (see Escobar & Craft, 2016). In practical veterinary epidemiology, reporting and mapping of disease events in domestic animals typically need to be performed at the level of epidemiological units (farms and villages), unless disease notifications refer to finding infectious agents in animal remnants (pathogen detections, see below). In any case, empirical mapping of disease occurrence should be closely correlated with the distribution of host populations.

Reporting disease in individual domestic animals (level 1) is rare, however, when ASF or other diseases spread in wild animals, epidemiological investigations require a very fine-scale resolution of all observations, including mapping locations of finding affected individual animals or their groups. This is the main approach to describe the spatial extent of an outbreak and formulate epidemiological hypotheses. Fine-scale mapping of carcasses with outcomes of laboratory investigations, as well as the results of testing hunter-harvested wild boar, are instrumental to determining the extent and duration of the disease spread in an area. High-resolution disease event mapping is particularly important at the beginning of the ASF epidemic. Disease control interventions in wild boar critically depend on knowing the location of each single case of ASF. This information shows the spatial progress of infection and directly influences the control measures and their locations. During forward and backward tracing, it helps to identify index, primary and secondary cases.

DISEASE EVENT TYPES AND THEIR NOTIFICATION

Location-based animal disease event reporting is the basis for epidemiological surveillance at the national and international levels. Well-organized and consistent disease observation enables correct interpretation and analysis of collected data, facilitates risk assessments and modelling, and thus provides evidence-based background for the development of disease control strategies. The more precise and accurate the collected information is, the more intelligent and efficient practical measures to deal with the problem can be developed.

Inconsistencies in disease observation are often due to poor quality information, inaccurate location data, or improper data aggregation, rather than just under-reporting of events. Issues related to location data quality, the accuracy of basic attribute information on disease events (type of epi unit affected, species, dates, etc.) and other important epidemiological details are unfortunately very common in reporting ASF. The situations encountered with this disease can be very complex epidemiologically, requiring proper investigation and careful consideration of all details.

Consider the following hypothetical, yet realistic, scenario involving the discovery of several disease events caused by the ASF virus and their proper interpretation and recording (Box 2 and Figure 18).

An epidemiologist must identify events based on timing, location and other relevant factors. They need to determine which events are pathogen detections, which are cases of disease and which are outbreaks (see Box 3). This distinction is crucial for accurately describing, recording,and mapping disease events to ultimately develop a sound epidemiological explanation.

Analysing the hypothetical situation above requires first defining the primary case or outbreak – the earliest event that can be traced back and defined in space and time, at least approximately. Here, the most likely primary case is Event B: five three-week-old carcasses of domestic pigs

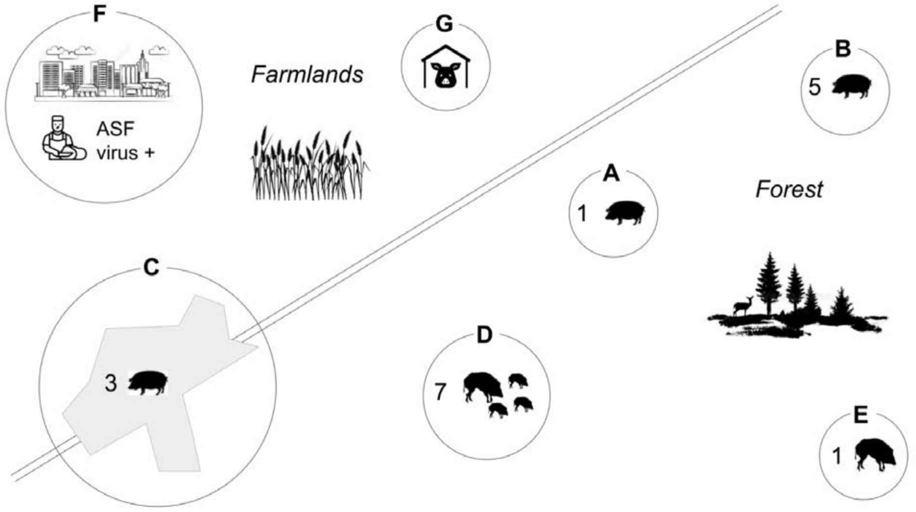
BOX 2

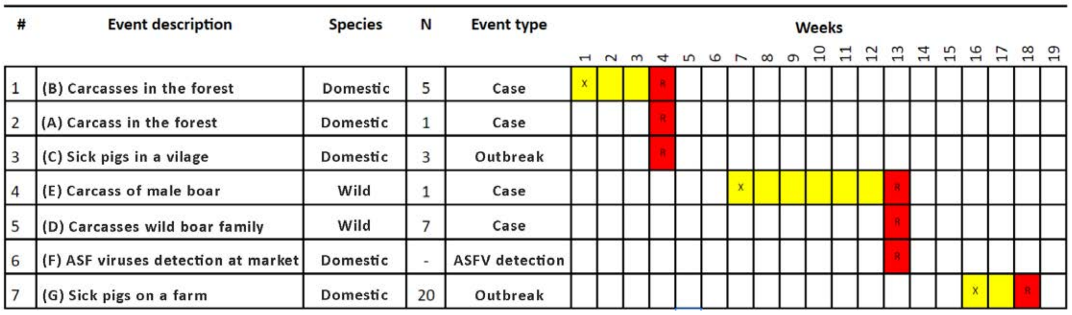
Hypothetical African swine fever disease episode

Hikers found a freshly dead domestic pig in a roadside forest and reported it to authorities. Tests confirmed the pig was positive for ASF. Follow-up surveillance on the next day showed that this was not an isolated case: (B) Approximately three weeks post-mortem, five more decomposed carcasses of domestic pigs were discovered along the road in the same forest, but 2 km away from the first carcass. At the same time, (C) in a village 7 km away from the second carcass finding, a local veterinarian was alerted of sick pigs. Clinical examination and laboratory results confirmed the diagnosis of ASF. The three pigs in the affected holding and the entire backyard pig population of the village were culled and destroyed. However, nine weeks later after the detection of an ASF outbreak in the village, a game manager (D) found a whole family group of seven dead wild boar in one location in the same forest where the first dead pigs were reported. The carcasses were fresh, 1–3 days post-mortem. Further searching in the forest around the site revealed (E) a decomposed carcass of a male boar submerged in a pool of water 7 km away from the dead boar family. It was estimated that death occurred 4–6 weeks prior. Around the same time, testing of (F) environmental samples collected from a butcher's point of sale at a local market in a district capital revealed DNA of the ASF virus. The point of sale was closed for disinfection. Four weeks after the event at the market (G) an outbreak of ASF was reported at a commercial farm not far away from the town. Investigation revealed that mortality started two weeks before the farmer's report.

FIGURE 18

Schematic representation of the hypothetical African swine fever disease episode and the timeline of the events mentioned in the text





#	Event description	Species	N	Event type	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	(B) Carcasses in the forest	Domestic	5	Case	X	🟨	🟨	R															
2	(A) Carcass in the forest	Domestic	1	Case				R															
3	(C) Sick pigs in a vilage	Domestic	3	Outbreak				R															
4	(E) Carcass of male boar	Wild	1	Case							X	🟨	🟨	🟨	🟨	🟨	R						
5	(D) Carcasses wild boar family	Wild	7	Case													R						
6	(F) ASF viruses detection at market	Domestic	-	ASFV detection													R						
7	(G) Sick pigs on a farm	Domestic	20	Outbreak																X	🟨	R	

Weeks

Descriptions are ordered according to the assumed sequence of events (below).

Source: Author's own elaboration.

BOX 3

Disease event types

Pathogen detection – finding specific infectious agents in the tissue or secretions of sick or dead animals, in subproducts, discharges, on fomites or in the environment. It may or may not be successfully traced back to a case or a disease outbreak. Pathogen detection may not always correspond to the geographical locations of cases or outbreaks.

Case of a disease – clinically verified or laboratory-confirmed occurrence of disease in an individual animal. A case may or may not be a part of a detected outbreak (e.g. it can be an imported case). The geographical location of a case is not always the location of the outbreak, although it is often strongly suggestive of a possibility of one nearby. Diseases in wildlife are usually reported as cases, rather than outbreaks.

Disease outbreak – confirmed spread of a pathogen among multiple individuals within one or more epidemiological units. This is the most definitive location of a disease event. Every single village or farm affected by a disease is an outbreak.

Source: Author's own elaboration.

found in the forest. These should be treated as five cases of ASF, not an outbreak. It is usually impossible to associate such findings with a definitive epidemiological unit. The five dead pigs may come from a backyard holding or holdings, or a commercial farm. Illegally disposed animals are typically deprived of any tags or signs that could help trace them back to the owner. While the geographical location of the outbreak cannot be identified, the precise location of the carcasses is still important, as the disease can potentially spill over to wild boar and initiate a new disease incursion. This location, along with the location of the single domestic pig carcass (Event A, also a case), should be carefully recorded to inform further surveillance efforts.

Event C is classified as an outbreak because we know exactly which holding was affected and its location. The village is therefore an infected epidemiological unit in which culling operations are performed. Location data for this outbreak could be either the coordinates of the holding or the village centroid. Seven carcasses of a wild boar family (Event D) were subsequently found. However, the single male boar carcass was much older, suggesting that Event E, the death of the male boar, preceded the boar family's death from infection. Both events are cases of ASF, as wildlife mortalities are usually reported as cases, not outbreaks. Carcass locations should be reported as precisely as possible, given the clear evidence of an ongoing epidemic in the forest. Wild boar carcass locations will define the size and extent of the infected area and thus are key for organizing disease control and guiding further carcass searches.

Detection of the ASF virus in an environmental sample at a butcher shop (Event F) neither indicates the origin of contaminated meat nor does it define the likely timing of contamination. It is important therefore to explicitly indicate in the records where and under which circumstances the positive sample was collected so that it does not get mixed up in the records with cases or outbreaks.

The last in the series is Event G, an outbreak of ASF on a commercial farm, whose diagnosis was delayed by two weeks. The farm is a discrete epidemiological unit and its precise location (not the nearby town or village centroid) should be recorded, as it will be used for defining a follow-up surveillance zone.

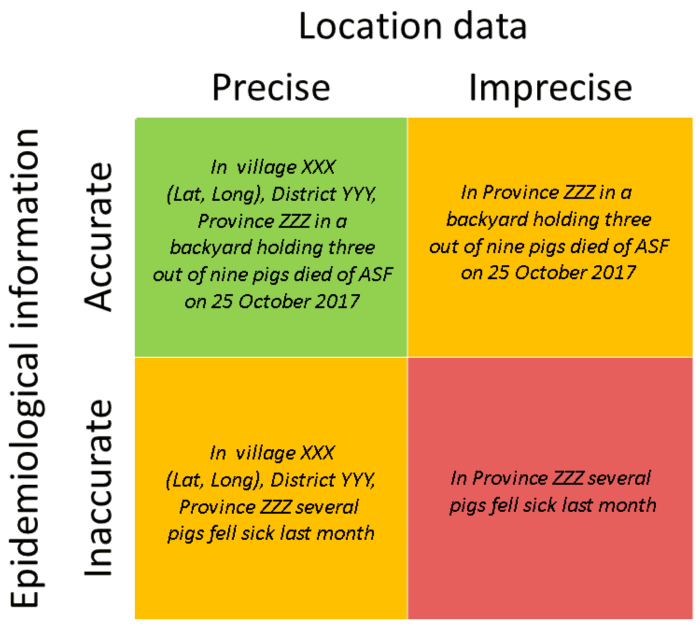
In real life, information about disease events may be incomplete, inconclusive and imprecise (Figure 19). In this case, records should contain remarks that explicitly indicate what and to which extent is an approximation. Decisions on how to record a particular disease event in a geographical space should not be a matter of convenience but based on the careful analysis of all available epidemiological information. Best results for disease event investigation and reporting are achieved by using cloud-based electronic data collection systems and standardized online forms or applications. Data can first be also collected into printed forms and later verified and entered into an online data management system. Electronic disease reporting systems can ensure the availability of the results of epidemiological investigation in a near-real-time fashion, which is a key to success in organizing appropriate and timely disease control operations.

MAPPING AFRICAN SWINE FEVER DISEASE EVENTS IN DOMESTIC PIGS

Recording of disease location data for discrete epidemiological units, such as farms or villages, is usually done using latitude and longitude (e.g. affected units are then visualized on the map as point features). It should not be a problem, provided that the veterinary authority does have a comprehensive up-to-date database of such units (see Chapter 2). The coordinates of affected units can then be quickly assessed from it, based on the name of the populated place and its administrative attribution. However, if the geolocation of commercial farms was originally made based on the centroids of nearby populated places, the farm location coordinates should be verified on the ground or using web maps or other means. Ideally, upon receiving notification of ASF in a particular epidemiological unit, the competent authority should already have information on it in a database. If this is not the case, it is important to collect as much information as possible and indicate in the records

FIGURE 19

Precision versus accuracy: A hypothetical example of four different ways of reporting a disease event



Location data

Epidemiological information		Precise	Imprecise
	Accurate	*In village XXX (Lat, Long), District YYY, Province ZZZ in a backyard holding three out of nine pigs died of ASF on 25 October 2017*	*In Province ZZZ in a backyard holding three out of nine pigs died of ASF on 25 October 2017*
	Inaccurate	*In village XXX (Lat, Long), District YYY, Province ZZZ several pigs fell sick last month*	*In Province ZZZ several pigs fell sick last month*

The box with a green background represents the preferred option, as it is both precise and accurate. This is followed by less favoured descriptions in boxes with a yellow background, which are either imprecise or inaccurate. The text in the red box is the least suitable way to report the disease event, as it is both imprecise and inaccurate.

Source: Author's own elaboration.

whether the affected unit is a commercial or backyard holding. Such information, when accumulated over time, allows for the exploration of epidemiological metrics such as attack rates and the evaluation of different risk factors for each subpopulation separately. Usually, epidemiology and the extent to which commercial and backyard populations are involved in disease dynamics differ between sectors. This has important implications for the management of ASF.

In the areas seriously affected by ASF, it is not unusual to encounter carcasses or other contaminated materials (bones, viscera, skins or similar) of domestic pigs illegally disposed of that test positive for the virus. Such findings provide indirect evidence of disease occurrence in the area; however, the origin of carcasses and locations of affected epi units often remain undiscovered. It is important to account for the fact that in the attempt to get rid of dead pigs or to sell the meat of sick animals, owners can travel considerable distances, especially if restrictions on trade or a standstill are declared in the area. All such disease events involving animals of unknown origin still need to be properly documented, including estimating how long ago the remnants were disposed of and their exact GPS coordinates. They should be recorded in the database as cases of ASF (provided laboratory confirmation of virus detection) but should never be mixed up with statistics on outbreaks (Figure 20). Carcasses of dead pigs should be treated in the same fashion as cases in wild boar (see below), as they can potentially initiate a focal introduction of ASF in the wild in the areas where such risk is expected.

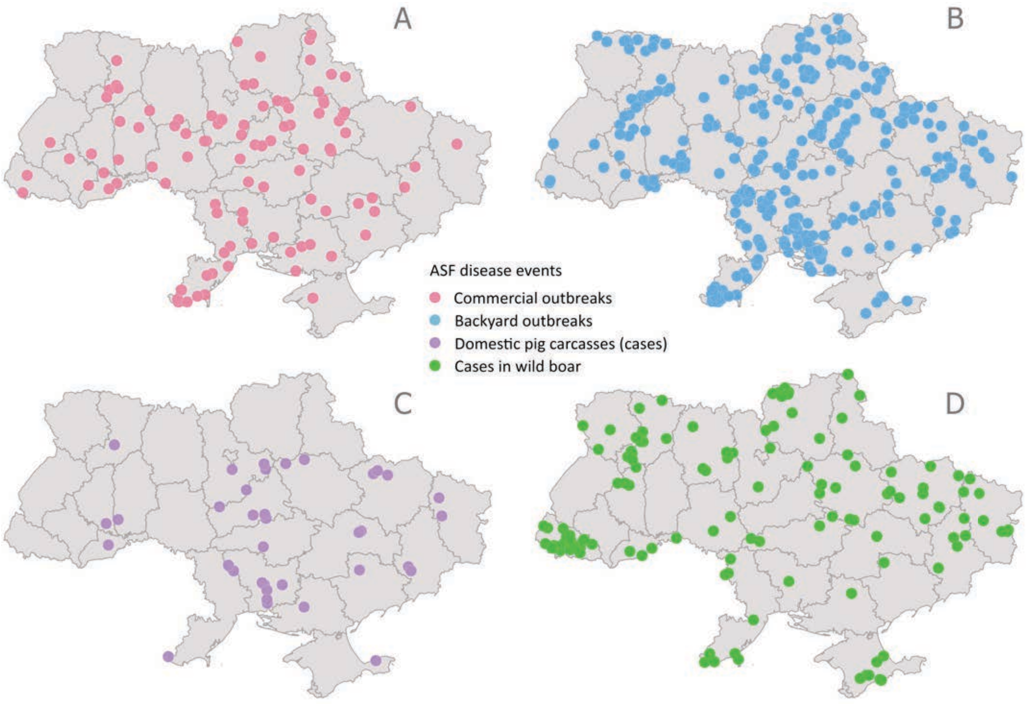
MAPPING AFRICAN SWINE FEVER CASES IN WILD BOAR

Information on most disease events in wildlife usually is due to opportunistic passive surveillance. The effectiveness of such surveillance depends largely on people's incentives to notify them of the morbidities or mortalities they observe to the respective authorities. ASF reporting rates often differ significantly between countries, production systems or subpopulations. They also vary significantly by season and year. This explains why even in neighbouring countries one can observe a sharp contrast between the density of reported cases of ASF in wild boar. Countries that actively search for carcasses report far more cases.

Opportunistically reported ASF disease events are qualitative rather than quantitative metrics of disease occurrence. They tell where and when the disease was present. However, a lack of disease event reports does not necessarily mean the absence of the disease. Geographical and temporal biases in

FIGURE 20

African swine fever notifications in Ukraine (2012–2022) categorized by sector and epidemiological considerations



A - outbreaks on commercial farms; B - outbreaks in the backyard sector; C - ASF virus detections in carcasses of domestic pigs (cases); and D - cases in wild boar including virus detections in carcasses and hunted animals.

Note: Refer to the disclaimer on page ii for the names and boundaries used in this map.

Source: Author's own elaboration. Country boundaries based on UN Geospatial. 2023. Map of the World. In: United Nations. [Cited: 10 November 2024]. http://www.un.org/geospatial/content/map-world-1”www.un.org/geospatial/content/map-world-1

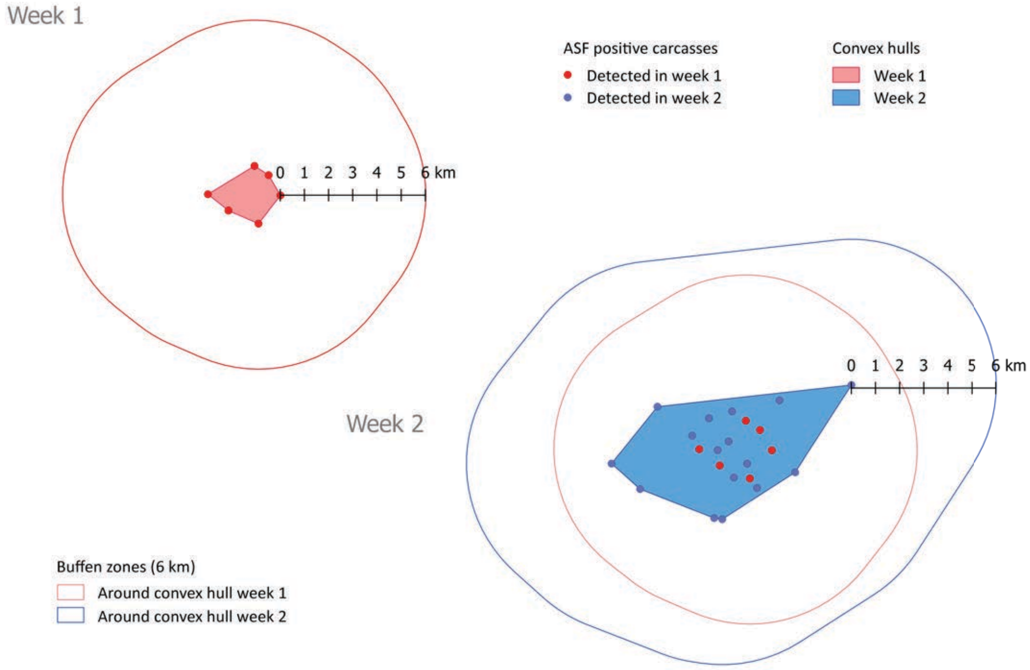
disease reporting are a common problem in many countries and with many wildlife diseases. Surveillance for ASF in wild boar is a very clear example of this problem.

The specifics of the Genotype II ASF virus epidemiology in wild boar, particularly its extremely high lethality, mean that information on the spatial extent of an outbreak mainly comes from testing carcasses for the virus. Such detections are always considered cases. ASF epidemics in wild boar are essentially large outbreaks occurring in a continuously distributed population. If uncontrolled, they can evolve into an endemic state, with sporadic cases continuing for months or years, provided the wild boar population is large enough to supply new victims. New outbreaks are evident only when the primary disease incursion occurs far from previously infected areas.

Searching for carcasses and their safe disposal is the major disease control intervention, which at the same time, is the only effective way to conduct passive surveillance for ASF in wild boar (Guberti *et al.*, 2022). It is important to understand that wildlife mortality events caused by ASF, which are occasionally detected by the public, usually represent just the tip of the iceberg of the unfolding epidemic process. Sick animals often choose to die in poorly accessible forest habitats or wetlands. Carcasses may quickly disappear or become inaccessible due to predators or scavengers, decomposition, bad weather or rough terrain. Prompt and active carcass search in an infected area typically reveals many more cases whose location needs to be recorded as precisely as possible to immediately guide management decisions and further surveillance.

The application of GIS is thus instrumental for understanding the spatial extent of an ASF epidemic in wild boar, identifying possible new incursions or tracing the effectiveness of interventions. The most important management objective that is achieved through mapping positive carcasses is defining the spatial extent of the area of virus circulation. Usually, after finding the first positive carcass (which may or may not be the index case), additional searches reveal more dead animals. Epidemiological investigation should help to estimate the timing of the likely onset of the outbreak, but this task can be tricky and might require considerable time and effort before the picture becomes clearer. Precisely mapped positive cases should be processed to generate a convex hull (smallest convex polygon containing

FIGURE 21
Identification of the area of virus circulation in wild boar or feral pigs



This is achieved through mapping positive carcasses of wild boar, creating a convex hull and a 6 km buffer zone (week 1) and an iteration of the process after finding new positive carcasses in a week (week 2).

Source: Author's own elaboration.

all of them). Next, a buffer zone around the convex polygon should be created that accounts for the likely progress of infection during the time that elapsed since the estimated onset of the epidemic. The constant suggested by Guberti *et al*. (2022) is 6 km, which corresponds to the maximum annual home range of an adult male wild boar or several months of an epidemic wave progression. This empirically identified area of virus circulation should be revised whenever new cases are detected outside of it by re-generating the convex polygon and buffer zone (e.g. every week) to account for new epidemiological findings. GIS makes this task straightforward: provided with a subset of positive carcass locations, one can easily generate both convex polygons and buffer zones to guide surveillance and further risk assessments (Figure 21).

Along with sample collection, searching for carcasses and documenting ASF cases in wild boar requires gathering information on the dating of carcasses (stage of decomposition) and, whenever possible, identifying the sex and age of the animals. It is important that this data set can be correctly aligned with laboratory results and that it contains precise and accurate coordinates. This is best achieved using mobile forms or applications but still requires substantial coordination and close collaboration between those working in the field, the lab and the office. Ideally, carcass search teams should be trained on the agreed data collection and reporting approach before the start of field operations and specifically informed on the correct way to record location coordinates. It is important to record and map all carcasses, even if not all of them test positive for the virus. Laboratory methods cannot guarantee 100 percent sensitivity, especially with poor-quality samples, which is common with diagnostic material collected from decomposed carcasses of wild boar. Retesting such samples is rarely possible as carcasses are usually destroyed quickly. However, an epidemiologist reviewing both positive and negative findings may have reasons to treat negatives as suspected or unconfirmed cases and may have a better idea of the likely spatial progress of the disease.

Some affected countries suspend hunting wild boar in the areas defined as infected, while others continue or intensify it. In any case, active surveillance through hunting or trapping wild boar and testing animals virologically and/or serologically is another source of information on the disease occurrence, though much less sensitive compared to passive surveillance. Of course, such surveillance results are most useful and informative when they are presented as a map, rather than a table.

As it is with carcass locations, it is important to record the exact coordinates of the places where animals were hunted, but not approximations, such as a game dressing/storage centre, a centroid of a hunting ground or coordinates of a nearby village. The best result would be achieved if hunters recorded information on the hunted boars right at the hunting spot using an electronic form or application. If hunting is taking place from the towers, their coordinates can be predefined and associated with a particular hunted animal afterwards. Hunters familiar with the terrain can also identify the coordinates of the hunting spot using web mapping tools like Google Maps. Mapping results of active surveillance in wild boar should always include both positive and negative testing outcomes. It is important to distinguish in the database between samples collected from carcasses and those taken from hunted animals. These requirements are often neglected, especially when the number of tested animals is high. Hunters and laboratory staff should be aware of the need to provide consistent information on all tested animals, regardless of the testing results, and understand that without accurate data, the interpretation of epidemiological information will be significantly compromised, and much of their effort will be largely wasted.

Research shows that the ASF virus can be detected in various biological matrices, including faeces, tissues and saliva using methods of non-invasive surveillance for ASF in wild boar. Where such methods are adopted and used in routine sampling activities, reporting of precise geographical coordinates is essential, even if such disease events are virus detections, not cases or outbreaks.

VISUALIZATION OF DISEASE EVENTS IN DOMESTIC PIGS

Visualization of disease occurrence data is a very powerful method of basic epidemiological analysis. By simply placing disease event notification in the geographic context, we obtain a much more informative picture of the epidemiological developments. This immediately prompts us to build hypotheses, look for explanations or ask questions and make assumptions. However, the accuracy of disease event descriptions can strongly compromise visualizations and may lead to erroneous conclusions. The most common mistake is the misclassification of disease events. For example, carcasses of domestic pigs of unknown origin might be incorrectly recorded as outbreaks and associated geographically with a nearby village. Similarly, cases in wild boar could be aggregated with an outbreak in domestic pigs and reported as a single disease event. It is not uncommon to aggregate disease events that not only occur in distinctly different locations and subpopulations but also those that are separated by considerable time gaps. Accumulation of such errors in the database compromises the quality of data and any attempts to analyse information consistently.

Complications often arise when it comes to visualization and aggregation of disease information at some level of administrative division. It is common to see ASF occurrence maps where locations of outbreaks in domestic pigs (affected farms or villages) are mixed up with case detections in wild boar. Not all GIS experts and animal health professionals consider such outbreaks and cases as phenomena that distinctly differ from the epidemiological point of view and cannot be directly compared, particularly when aggregated. Reports and maps generated without this important distinction are misleading, especially when disease occurrence metrics are compared between different subpopulations or regions.

Information on disease events can be aggregated based on some spatial classification criteria, such as administrative division or any other polygon outlines of interest. Since most statistical indicators are collected and arranged according to administrative divisions, polygons of administrative units (such as subcounties, counties, districts and provinces) are most often used for the aggregation and analysis of disease events. Aggregation is particularly relevant when disease detections are numerous, as simple counts of disease events can be uninformative or even misleading. In such cases, adjustment calculations become important (see examples below).

Typical problems that arise with polygon aggregation are related to the fact that administrative units are not well suited for epidemiological analysis and visualization (e.g. MAUP; see Pfeiffer *et al*., 2008), particularly without prior normalization of data. Polygon areas, host population numbers and their distribution patterns usually vary between polygons. Appropriate denominators such as area, total population, number of farms or holdings and duration of observation period should be used to compensate for various possible biases in the calculation of aggregated disease occurrence metrics.

Two simple examples are provided below to illustrate the importance of normalizing disease event counts with respectively arranged host population data (total counts of epi units). They do not exhaust all the complexity of issues that may arise during aggregation and interpretation of disease observations (Pfeifer *et al*., 2008), but rather, they highlight the need for taking those into account seriously when it comes to visualization of aggregated disease statistics.

Consider the following hypothetical example (Table 2). After aggregating disease events, Province 1, with the highest outbreak count, appears to be the most severely affected. However, a simple calculation of the attack rate (the proportion of epidemiological units affected relative to their total number in each province) reveals a different pattern, suggesting that the situation is worst in Province 3, which

TABLE 2

A hypothetical example of normalization of aggregated outbreak count statistics using population data

UNIT	Total population	Total epi units	Outbreaks	Attack rate (%)
Province 1	56 000	500	50	1.0
Province 2	30 450	680	30	0.4
Province 3	10 000	70	10	1.4

Source: Author’s own elaboration.

TABLE 3

A hypothetical example of the normalization of aggregated outbreak count statistics using population data and accounting for the likely duration of exposure

UNIT	Total epi units	Outbreaks	Attack rate (%)	First occurrence	Last occurrence	Months present	Monthly attack rate (%)
Province 1	500	50	1.0	1 February 2001	30 March 2001	2	0.50
Province 2	680	30	0.4	1 March 2001	30 March 2001	1	0.44
Province 3	70	10	1.4	1 january 2001	30 March 2001	3	0.48

Source: Author’s own elaboration.

has the lowest number of outbreaks. Normalizing disease observations helps avoid biased conclusions based solely on outbreak counts and provides a more accurate and reliable description of the spatial patterns of disease frequency.

Whenever possible, correct aggregation of disease events in domestic pigs should avoid presenting disease occurrence statistics without an appropriate denominator, which is preferably the total number of epidemiological units of the respective type. By using such a denominator, it is possible to calculate the attack rate or “incidence proportion” at the resolution at which surveillance is conducted. With domestic pigs and a disease such as ASF, it is always the level of epiunits. For example, to estimate the attack rate in the backyard sector one would need to divide the total number of outbreaks (affected villages) during a period by the total number of villages with domestic pigs. If this kind of disease metric is consistently calculated across all regions, one can arrive at a much more objective comparison of disease occurrence between parts of the country, draw adequate conclusions and infer more insightful explanations from the observations (Figure 22)

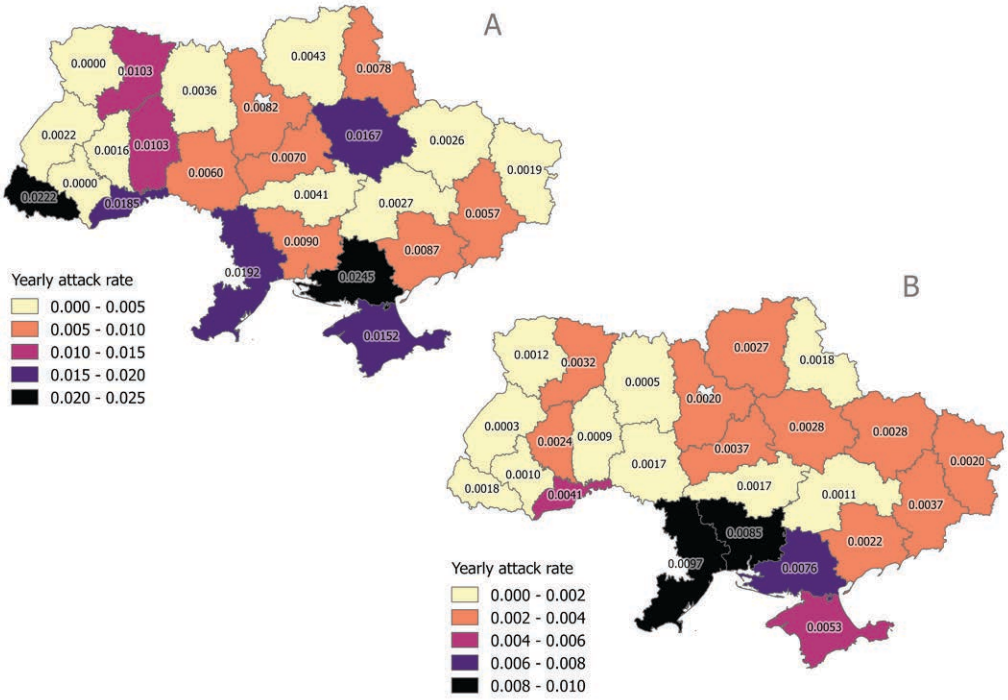
The accuracy of measuring disease occurrence statistics using aggregated data may also be affected by the duration of likely exposure of the population to the pathogen in each spatial unit. If, for example, in the situation described in Table 1, the disease first arrived in Province 3, and then spread through Province 1 to Province 2, it would be reasonable to consider how long animals in each province were exposed to the pathogen. Suppose the disease was likely present for 1, 2 and 3 months in Provinces 2, 1 and 3, respectively. In that case, the average monthly attack rates would not differ significantly between provinces, suggesting that the disease was found almost equally frequently in each of them (Table 3).

VISUALIZATION OF DISEASE EVENTS IN WILD BOAR

Analysis of ASF occurrence in wild boar populations is a challenging task, as is surveillance and disease management. First, it is usually very difficult to obtain reliable information on the numbers of affected animals and the spatial extent of the epidemic. Passive surveillance based on carcass detections is extremely labour-intensive, and it is hard to ensure an equal amount of effort everywhere. In practice, the disease surveillance efficacy highly varies across space: from occasional opportunistic findings to well-organized and funded surveillance programmes, sometimes even involving specially trained dogs. As a result, in some affected populations, findings of positive carcasses might be very abundant, while in others they may be scarce or non-existent. But the latter does not necessarily imply a better epidemiological situation unless it is confirmed by intensive surveillance. Second, with rare exceptions, it is impossible to estimate what proportion of the population (or family groups) was affected by the disease because estimates of the wild boar population size are very unreliable. In addition, ASF is a highly fatal disease that dramatically reduces populations of wild boar, thus quickly rendering any pre-epidemic numbers outdated. Virological surveillance based on apparent virus prevalence in hunted animals faces the same population size uncertainty issue. This is further complicated by the possibility that hunting is not a random sample collection method and can be biased,

FIGURE 22

Calculated average yearly decimal African swine fever attack rates (0.01 = 1%) by regions of Ukraine and adjusted for exposure time



A - in the commercial sector (farms as epi units); B - in the backyard sector (villages as epi units).

Note: Refer to the disclaimer on page ii for the names and boundaries used in this map.

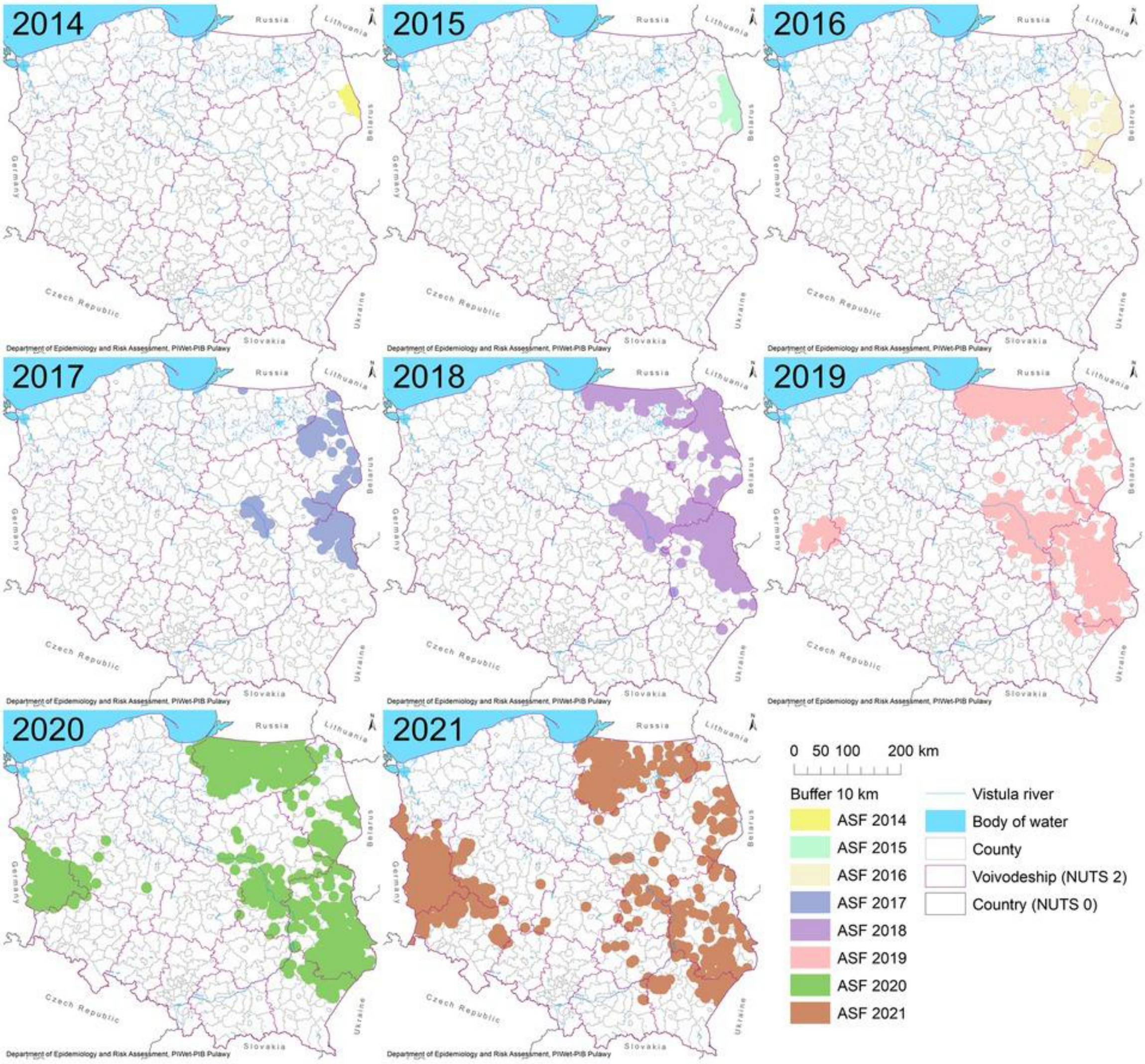
Source: Author's own elaboration. Country boundaries based on UN Geospatial. 2023. Map of the World. In: United Nations. [Cited: 10 November 2024]. http://www.un.org/geospatial/content/map-world-1"www.un.org/geospatial/content/map-world-1

either toward selecting healthy animals or, conversely, selectively targeting sick animals. Even if a few surviving wild boars remain and have life-long immunity to the disease, it is still impractical and nearly impossible to use serological surveillance to obtain standardized epidemiological metrics for comparing disease incidence between different areas or populations. These uncertainties and complications mean that any objective and epidemiologically meaningful estimates of ASF occurrence in the wild boar population are simply impossible.

When it comes to wild boar, a more realistic approach to assessing ASF dynamics in space (and time) is to consider the absolute size of areas affected by the disease at any given period as a measure of disease progression. Such a solution was, for example, adopted by Bocian *et al*. (2022) when describing the dynamics of ASF spread in Poland. By creating 10 km buffer zones around case locations for a given period and dissolving buffers into a single polygon, one can estimate the extent of the disease occurrence in units of area, rather than in cases. This would be a more objective measure of disease dynamics compared to case counts or any other epidemiological metrics (Figure 23). However, this is only possible under the condition that a country's passive surveillance is effective in the identification and constant monitoring of the infected areas (Guberti *et al*., 2022). By consistently applying this approach, one can compare the absolute areas or proportions of areas affected by ASF epidemics in wild boar across different regions of the country. Additionally, one can build temporal graphs to visualize the epidemic's progression both regionally and nationally. GIS is critically important for effectively evaluating these area-based disease spread metrics.

FIGURE 23

Areas of African swine fever occurrence in the years 2014–2021 in Poland



Shown as zones within 10 km of the outbreaks in domestic pigs and wild boars. NUTS – nomenclature of territorial units for statistics

Note: Refer to the disclaimer on page ii for the names and boundaries used in this map.

Source: **Bocian, Ł., Frant, M., Ziêtek-Barszcz, A., Niemczuk, K. & Szczotka-Bochniarz, A.** 2022. Dynamics of the African swine fever spread in Poland. *Journal of Veterinary Research*, 66(4): 459–471. https://doi.org/10.2478/jvetres-2022-0067

Key messages:

- In domestic pigs, ASF reporting is based on epidemiological units, which are: a) pig farms in the commercial sector; and b) villages (or their local equivalents) in the case of backyard pigs. ASF virus can also be found in pig remnants or pork products, in which case no epidemiological unit can usually be identified. In wild or feral pigs, disease occurrence cannot be linked to a discrete epidemiological unit either.
- Disease events are divided into three categories: pathogen detections, cases of disease and disease outbreaks. Pathogen detection involves finding a specific infectious agent in the tissues or secretions of sick or dead animals or the environment. A case of disease is a clinically verified or laboratory-confirmed occurrence of disease in an individual animal. A disease outbreak is the confirmed spread of a pathogen within one or more epidemiological units. These types should always be distinguished.
- Electronic disease reporting systems can ensure availability of the precise and accurate results of epidemiological investigations in a near-real-time fashion, which is a key to success in organizing appropriate and timely disease control operations.
- In domestic pigs, it is important to record whether the affected unit is a commercial or backyard holding.

All disease events involving animals of unknown origin must be recorded, but properly categorized and flagged up not to be mixed up with statistics on outbreaks. ASF cases in wild or feral pigs should not be mixed up with disease events in domestic pigs. A clear distinction based on all important attributes should be always maintained between all disease observations.

- Precisely mapped positive cases in wild boar should be processed to generate a convex hull with a 6 km buffer zone to account for the likely progress of infection. This area of likely virus circulation should be revised whenever new cases are detected outside of it by re-generating the convex polygon and buffer zone (e.g. every week) to account for new epidemiological findings.
- Surveillance for ASF in wild or feral pig carcasses requires gathering information on the stage of decomposition, identification of the sex and age of the animals and other relevant details. It is crucial that this data is correctly aligned with laboratory results and contains precise and accurate coordinates. If wild pigs are hunted for surveillance, it is important to record the exact coordinates of the hunting locations. The best results are achieved when hunters record information on the hunted boars directly at the hunting spot using an electronic form or application.
- Mapping results of active surveillance in wild boar should always include both positive and negative outcomes of testing. It is also important to keep a distinction in the database of ASF cases in wild boar between samples collected from carcasses and those taken from hunted animals to avoid compromising the results.
- Aggregation of disease events in domestic pigs should avoid presenting disease occurrence statistics without an appropriate denominator, which is preferably the total number of epidemiological units of the respective type. By using such a denominator, it is possible to calculate the attack rate or "incidence proportion" at the resolution at which surveillance is conducted. With domestic pigs and ASF, it is always the level of epidemiological units.
- Epidemiologically meaningful estimates of ASF occurrence in the population of wild pigs are challenging. One approach to assess ASF dynamics in space and time is to consider the absolute size of areas affected by the disease at any given period as a measure of disease progression. By creating 10 km buffer zones around case locations over a given period and dissolving buffers into a single polygon, one can estimate the extent of the disease occurrence in units of area, rather than in the number of cases.

Chapter 4

Mapping the risk of African swine fever spread

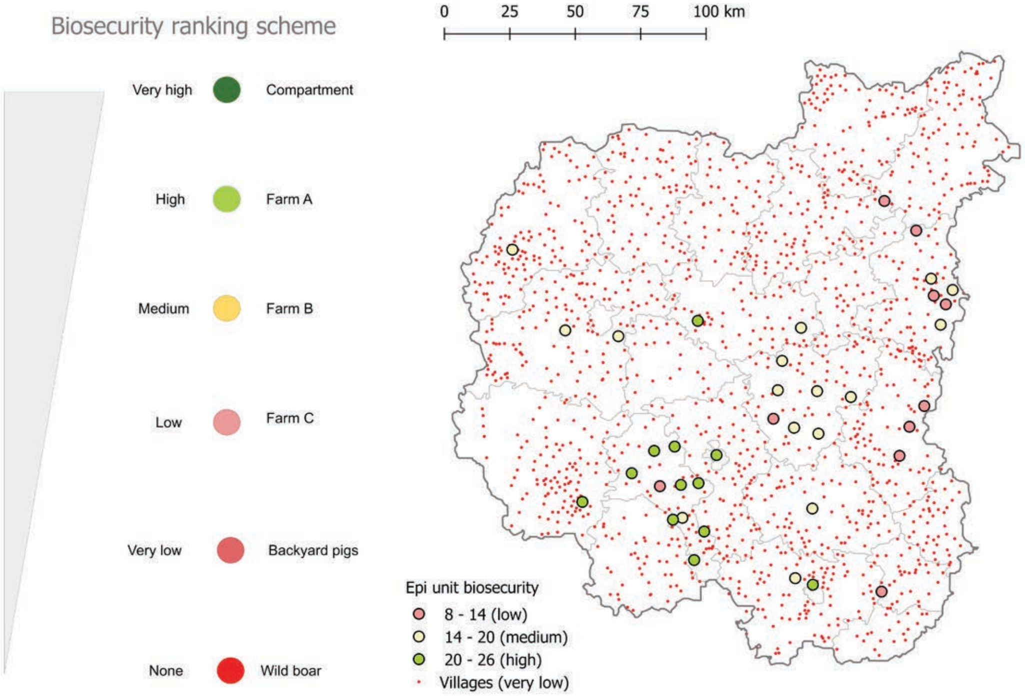
This chapter introduces several concepts important for mapping the risk of ASF spread and creating relevant layers in the ASF management GIS. It points out the importance of evaluating the biosecurity level of epidemiological units as the first and simplest step in risk assessment. The chapter explains how ASF risk changes dynamically with the evolving epidemiological situation and covers spatial risk factors, including proximity, accessibility and adjacency. Real-world examples of zoning and regionalization for mapping ASF risk are provided, along with a basic understanding of risk factor mapping and risk modelling in ASF management.

ASF is an infectious disease capable of developing into large-scale epidemics and establishing itself endemically for a long time in the pig production systems or populations of wild boar. It has a strong capacity to spread in geographic space from one epi unit to another or progress through affecting increasingly more susceptible animals during an epidemic. The risk of this can to a certain degree be predicted, anticipated and managed through disease prevention and control interventions. These management efforts can be effective only if they are targeted appropriately geographically.

An important starting point in the spatial risk assessment for ASF is identifying the vulnerability of the different epidemiological units and animal populations to the disease. In other words, one should try to estimate which of them is more likely to become infected if all other conditions or risk factors are held equal (something that seldom happens in real life). In practice, this means the classification or ranking of epidemiological units by their biosecurity levels (Figure 24).

FIGURE 24

Epidemiological units classified by their biosecurity level in the Chernihiv region in Ukraine



All villages were assigned to the "very low" class while commercial farms (larger dots) were evaluated against a set of 24 questions regarding various aspects of their biosecurity.

Note: Refer to the disclaimer on page ii for the names and boundaries used in this map.

Source: Author's own elaboration. Country boundaries based on UN Geospatial. 2023. Map of the World. In: United Nations. [Cited: 10 November 2024]. http://www.un.org/geospatial/content/map-world-1"www.un.org/geospatial/content/map-world-1

For example, an average pig farm is usually better protected against disease spillovers compared to a village with multiple backyard holdings. Epidemiological units, especially specialized farms, usually differ in some of their characteristics, which intrinsically increase or decrease the chances of disease introduction. Their vulnerability is therefore not particularly related to where they are in geographic space (subject to the effect of spatial risk factors) but is mainly determined by how good their protection against the disease is.

Commercial swine holdings vary immensely in their biosecurity characteristics between countries as well as within the same country. Evaluation of the degree to which they follow biosecurity standards is a very important part of risk assessment, not the least because the knowledge gained can be quickly used to manage risk through improvements to farm biosecurity. National competent authorities normally have a set of requirements on different aspects of farm biosecurity; however, their enforcement and control are not always in place or possible. Typically, a set of questions (criteria) is developed in the form of a questionnaire to measure the overall biosecurity level of each commercial holding. Every effort should be made to collect and maintain an up-to-date georeferenced pig farm register containing information on their biosecurity characteristics. Ideally, each commercial pig holding should be evaluated against formally accepted biosecurity criteria. This allows cumulative vulnerability scores and individual attributes of all holdings to be visualized on a map as distinct classes.

There is much less variation in the vulnerability (biosecurity level) in the extensive pig production systems. Usually, epidemiological units such as villages have equally low protection against diseases, though individual holdings might vary in their adherence to principles of biosecurity. In this situation, it is hardly possible to evaluate an individual village's biosecurity level in a meaningful way. However, certain aspects of pig husbandry may consistently differ between villages as epidemiological units. For example, in some of them, certain free-range breeds can be produced, or the pig production cycle involves seasonal free-ranging periods or regular scavenging. If villages in the country can be consistently classified based on some characteristics that increase their vulnerability to infection, such information should be reflected in their attributes as epidemiological units.

The concept of biosecurity does not apply to populations of wild boar. This pig subpopulation is the most vulnerable to the risk of disease and is equally susceptible across their entire distribution range. That is why wild boar often acts as a sentinel species for the introduction of ASF to a new area, even before any domestic pigs become infected.

EVOLUTION OF RISK IN THE COURSE OF DISEASE SPREAD

There are three distinct stages in the evolution of the epidemiological situation with ASF, as well as with other infectious animal diseases: 1) pathogen introduction (incursion, spillover) to a susceptible (population or subpopulation; 2) epidemic spread (invasion) of a disease; and 3) endemic persistence of a pathogen. Introductions of AFS are the kind of epidemiological events that are rather rare and inconclusive to be predicted with reasonable certainty. "Rare events" are low-frequency, high-severity problems that can have far-reaching consequences. Experience shows that the pathways of introduction, source of infection and risk factors contributing to primary disease incursions on most occasions remain rather obscure. Standard statistical methods do not apply to rare events. Predicting them, despite their extreme importance, remains a very difficult task for epidemiologists. Usually, nothing more than proximity to the disease detections can suggest an elevated risk of its new incursion.

At the same time, some spatial characteristics, such as the distribution of predominant pig husbandry systems or pig population density, have a more predictable effect on the outcomes of an ASF incursion in an area at potential risk. The disease is more likely to develop into an epidemic in those parts of the country where, for example, backyard pig production is prevalent or wild boar population density is high (see Guberti *et al*., 2022). Armed with that knowledge, the competent authorities may initiate an awareness campaign among pig farmers or increase surveillance efforts to test dead wild boar to anticipate ASF outbreaks in time for countermeasures to be effective. The availability of good quality information on the swine population in the format of GIS layers (see Chapter 2) helps to anticipate which subpopulations the disease is more likely to be detected first in case of an introduction and spread. At the epidemic stage, it is important to determine whether the epidemiological process involves a low biosecurity pig production sector or if the epidemic is sylvatic. This distinction has implications for risk evaluation, including its spatial dimension, and the use of appropriate GIS functionality to support decisions.

Failure to control an ASF epidemic at an early stage may lead to the progressive expansion of the disease range and eventually its permanent establishment in the country. The endemic situation significantly changes the risk landscape and requires considering the impact of an increasing number of risk factors affecting disease occurrence. The long-term presence of disease in a country and careful observations of its dynamics can provide a basis for a context-tailored analysis of its spatial patterns and may eventually help to identify significant specific risk factors or drivers of disease spread empirically. In countries where ASF is endemic, it becomes increasingly important to understand and appropriately regulate risks related to trade and value chains.

In spatial epidemiology, a risk factor for disease spread is a spatially explicit variable that is considered relevant to, or found to be statistically associated with, an increased probability of disease events or infection persistence in the host species population. Mapping risk factors is a way to qualify or quantify occurrences of certain spatial phenomena capable of affecting disease dynamics across space. In an epidemic of a disease as complex as ASF, there is always an interplay of multiple risk factors, which acting together eventually result in an outbreak. As one way of using them, the spatial risk factors can be predefined based on expert opinion and processed in a GIS using, for instance, the Multi-Criteria Decision Analysis technique that transforms and combines geographical data and value judgments to solve spatial problems such as risk of disease spread or endemicity.

Mapping spatial risk factors of ASF must be done about specific swine subpopulations (commercial, backyard and wild boar), as disease drivers and epidemiology differ between them. For example, ASF often becomes endemically established in backyard pig production systems, which act as the main epidemiological reservoir of the infection, even if other subpopulations (commercial pigs and wild boar) may occasionally get involved in the transmission cycle too. In this case, the concept of what constitutes a risk for professional pig farms and wild animals is different from the situation where the wild boar is the main reservoir. In the latter case, the risk factors of concern for commercial farms and backyard holdings are directly related to the specifics of the disease transmission cycle and its epidemiology in wild boar.

However, there is also an interplay of risks related to transmission between these subpopulations. Spillovers from backyard pigs to wild boar (and vice versa), or introductions of ASF to a commercial farm from backyard pigs or wild boar, do occur, especially where subpopulations co-occur in high densities. In these situations, risks can be defined by producing maps of interfaces between them, which helps approximate the probability of such events across space. When different ASF transmission cycles co-occur, it can be challenging to unravel the true picture of what is happening. In such complex situations, GIS can provide contextual information and a data environment that helps triangulate observations and build consistent hypotheses.

It is reasonable to consider and evaluate the risk of disease at different epidemiological stages (incursion, epidemic and endemic situation) separately for the subpopulations, carefully examining their actual epidemiological role in the process based on the information coming from the field investigations. Analysis of the relative role of risk factors and the development of consistent epidemiological explanations of the observed disease patterns is not a simple task. It requires good quality properly arranged training data from past epidemics. GIS and methods of spatial epidemiology are indispensable here, helping to find and statistically evaluate correlations between disease patterns and various spatial variables. Spatial epidemiology has much to offer in identifying risk factors for a disease system, provided it has access to accurately recorded spatially explicit disease occurrence data, correct population estimates, relevant spatial risk variables, and an adequate epidemiological hypothesis to test (see more on this below).

Further in this section, some approaches to mapping anticipated risk and some spatial risk analyses are discussed in detail. They are broadly grouped around several main topics, corresponding to situations most often encountered during the implementation of practical disease management interventions. The examples provided are not at all exhaustive, since it will be impossible to describe all possible risk factors, even for diseases with well-known epidemiology. Additionally, risk factors may change over time and space and in relation to the host species involved. Their relative contribution to the probability and outcomes of infection may also vary and are not easy to estimate and quantify in real life, especially in times of a rapidly evolving animal health crisis.

PROXIMITY, ACCESSIBILITY AND ADJACENCY

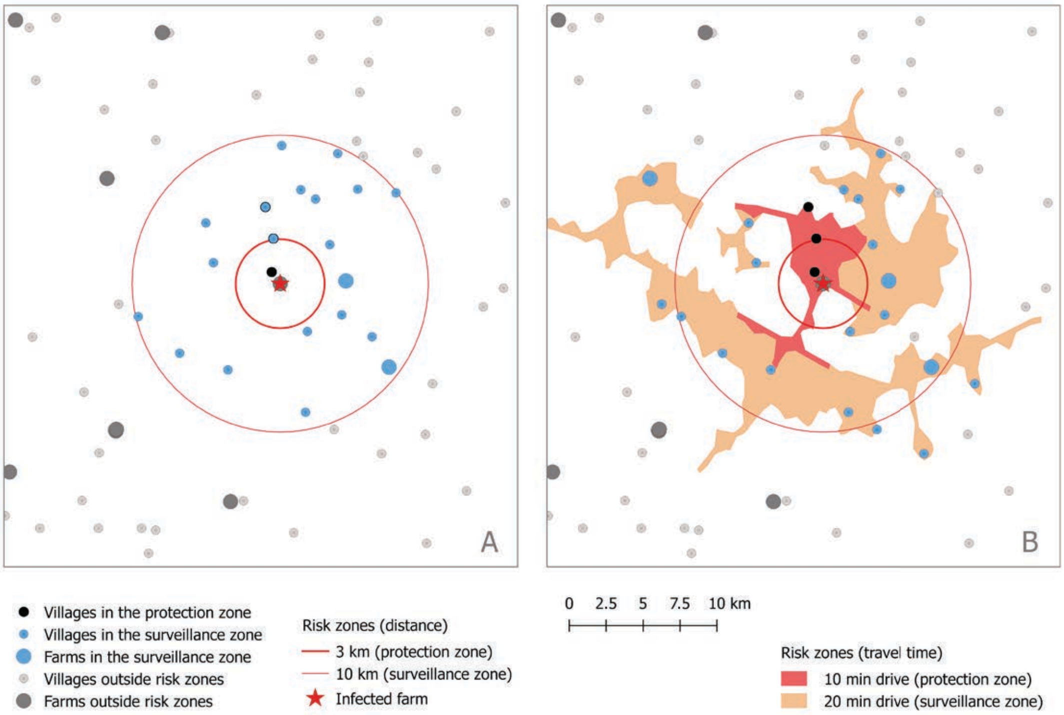
The occurrence of a disease itself always represents an obvious risk factor to the animal population and is often used to classify areas by anticipated risks based on criteria as simple as proximity or accessibility. On many occasions, this is the most practical way of defining areas at risk in case of the introduction of a highly contagious exotic disease. This approach is widely adopted by veterinary and public health authorities worldwide, although the types of zones distinguished, their definitions and the kind of interventions officially required may vary depending on the disease, national legislation and other considerations.

Establishing circular zones around active outbreaks or cases in domestic swine is the simplest formal way to spatially define areas at risk of further disease spread. This approach is based on the commonsense assumption that the closer unaffected epidemiological units are to the affected ones, the higher the risk of disease (so-called "neighbouring infection"). Typically, an area within a radius of 1 to 5 km from the affected epidemiological unit is at very high risk of infection (an infected or potentially infected zone). Beyond this, surveillance zones with a radius ranging from 4–5 km to several tens of kilometres are set up (Figure 25, A). The risk is expected to be lower in the surveillance zone compared to the infected area but still higher than outside the zone. The rest of the country may or may not be free of the disease, depending on its initial status (endemic, epidemic or first occurrence).

When it comes to outbreaks in backyard pigs, instead of proximity criterion, one may also use accessibility as a measure of disease spread risk. The background for this is that infected pigs or contaminated meat can be transported by people (usually for sale or illegal disposal) by roads and usually travels for a

FIGURE 25

Application of different criteria for identification of protection and surveillance zones for a simulated outbreak of African swine fever on a commercial farm



A - the zones were identified as two radiuses 3 and 10 km from the affected location respectively; B - the zones were identified based on accessibility, measured in travel time from the affected location, with 10- and 20-minute drive isochrones respectively. In the first case, farms and villages at risk were selected by the respective circular polygons, while in the second case, selection was made by using the polygons of accessibility. These polygons can be generated in GIS using either publicly available raster datasets or some online isochrone (equal travel time) polygon generation services.

Note: Refer to the disclaimer on page ii for the names and boundaries used in this map.

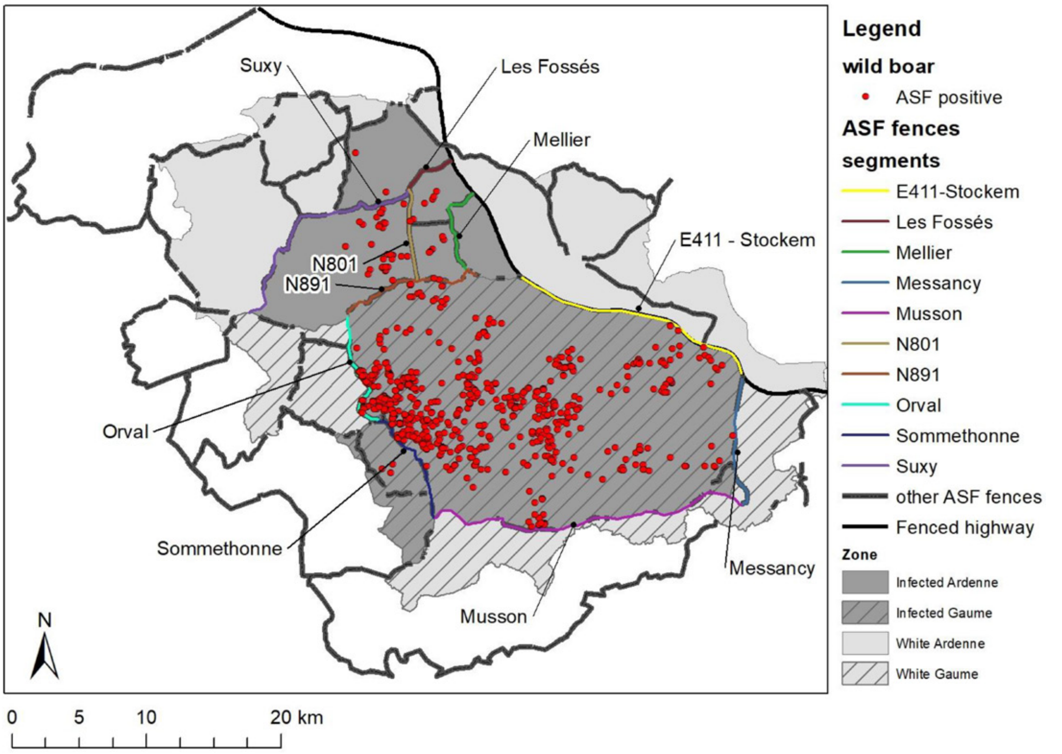
Source: Author's own elaboration. Country boundaries based on UN Geospatial. 2023. Map of the World. In: United Nations. [Cited: 10 November 2024]. http://www.un.org/geospatial/content/map-world-1"www.un.org/geospatial/content/map-world-1

reasonably short distance (e.g. 30–60-minute drive). Following this logic, one may generate accessibility zones around an infected location such as a village, to understand what is in the defined accessibility zone (e.g. a market or other villages). This approach better accounts for the likely behaviour of humans, rather than drawing circular radial zones mechanically, without consideration of existing obstacles and natural limitations of terrain to the spread of ASF (Figure 25, B). Using accessibility zoning instead of circular buffers may save the time and resources needed to define and inspect epidemiological units that are most at risk from a known disease outbreak.

There is a specific aspect of zoning when it comes to ASF cases in wild boar. The epidemiological considerations behind this are discussed elsewhere (Guberti *et al.*, 2022), while here we briefly present how this zoning approach can be implemented with the assistance of GIS. First, all positive carcasses of wild boar should be carefully mapped and the subset of these locations used as an input to generate a convex polygon (see Chapter 3). Second, a buffer area of some 6 km around the convex polygon must be created. These two zones together comprise an infected area where the risk of infection is the highest. Inside this area, management interventions such as carcass search and disposal should be implemented, while hunting and any other activities entirely stopped. If the outbreak is a focal introduction and authorities aim at containing it, next to the infected area a "white area" should be established, at least double the size of the infected one. Its identification involves analysis of local topography, terrain and obstacles for animals, to reduce the number of wild boar as much as possible to minimize the risk of the virus escaping from the infected area. The white area is also the equivalent of the surveillance zone used to control outbreaks of ASF in domestic pigs. The risk of ASF spread is lower than in the infected area but is still considerably high. Therefore, all animals hunted in the white area should be tested and safely disposed of. Ideally, infected and white areas should be isolated from each other at least partially: either by natural physical obstacles that can potentially slow down the spread of infection by an artificial fence or by a combination of both. The zoning setup and its adjustments, apart from implementing simple geoprocessing tasks described above (creation of a convex polygon and a buffer

FIGURE 26

Infected areas and white zones established in Belgium as a part of the management of a focal introduction of African swine fever to wild boar populations



Note: Refer to the disclaimer on page ii for the names and boundaries used in this map.

Source: **Licoppe, A., De Waele, V., Malengreaux, C., Paternostre, J., Van Goethem, A., Desmecht, D., Herman, M. & Linden, A.** 2023. Management of a Focal Introduction of ASF Virus in Wild Boar: The Belgian Experience. *Pathogens*, 12: 152. https://doi.org/10.3390/pathogens12020152.

around it), requires considering various other epidemiological factors (season, population density, duration of the epidemic, availability of resources, anticipated duration of the management efforts, distribution of domestic pig holdings, etc). This is where the task complexity evolves from using a single risk criterion of spatial proximity into a more sophisticated decision-making process. GIS provides the means and tools to place epidemiological data into a broader topographic and general cartographic context, allowing for the analysis of factors such as the presence of forests, occurrence of obstacles or roads, placement of fences, and other relevant considerations (Figure 26).

Regionalization is another disease risk identification approach that looks similar to zoning but uses administrative divisions (e.g. levels of aggregation) and certain epidemiological considerations to differentiate the degree of risk between the infected region and the adjacent regions around it (adjacency criterion).

Both approaches assume that zone boundaries or the selection of regions are systematically updated to reflect the overall evolution of the epidemiological situation. Zoning based on proximity or accessibility is mostly applied at the beginning of an epidemic or in situations of sporadic re-occurrence of disease. In contrast, regionalization is more suitable when the disease shows progressive spread (multiple outbreaks or cases are reported) and evidence suggests its prolonged presence in an area with mixed epidemiology (e.g. involving both domestic and wild pigs). The zoning approach uses simple proximity or accessibility to delineate infected and surveillance zones, while the regionalization approach uses adjacency and additional criteria, such as the presence of natural boundaries, transport infrastructure, trade patterns or some ecological considerations. This particular ASF regionalization approach is described in the respective documents of the European Commission (Document 32023R0594, see Box 4) and adopted by all the Member States of the European Union. It is essentially a risk ranking exercise that classifies administrative sub regions based on disease occurrence patterns, adjacency and some extra epidemiological considerations. It allows for clearly distinguishing affected and non-affected parts of the EU MS and focuses interventions appropriately according to the combined assessment of the level of risk in both domestic pigs and wild boar (Box 4).

BOX 4

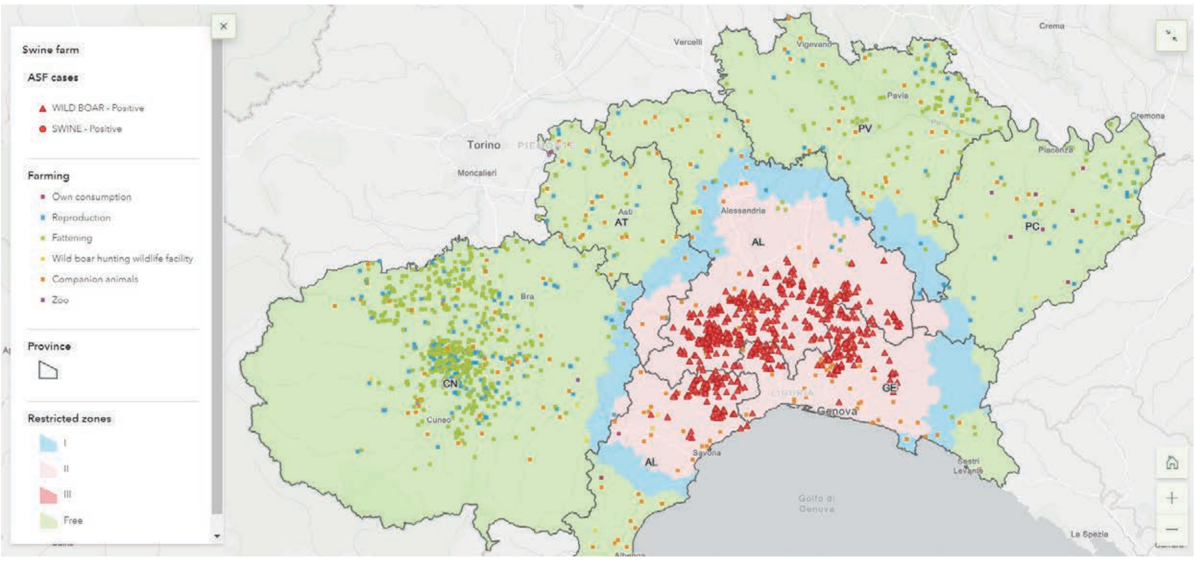
The main criteria for demarcating Parts I, II and III according to Commission Implementing Regulation (EU) 2023/594 of 16 March 2023 laying down special disease control measures for African swine fever

1) Part III: occurrence of ASF in domestic pigs despite the presence or not of the virus in wild boar;
2) Part II: occurrence of ASF only in wild boar;
3) Part I: higher risk area with no cases, nor outbreaks, of ASF and where higher surveillance (in particular passive) is applied adjacent to Part II, III; and
4) The definition of the size and shape of any area, and in particular when wild boars are involved, should consider at least the following factors: a) geographical aspects linked to the location of the outbreaks and wild boar cases; b) ecological factors (e.g. waterways, forests) and the existence of natural and artificial barriers; c) presence and distribution of wild boar; d) epidemiology of the disease; e) results of specific epidemiological studies; f) historical experience gained on ASF spread; g) administrative divisions, territorial continuity and enforceability of the control measures; h) distribution of pig farms (non-commercial farms, commercial farms and outdoor farms) and the existence of protection and surveillance zones (if any); i) hunting practices and other wildlife management considerations.

Source: **European Union.** 2023. *Commission Implementing Regulation (EU) 2023/594 of 16 March 2023 laying down special disease control measures for African swine fever and repealing Implementing Regulation (EU) 2021/605 (Text with EEA relevance).* Available at: https://eur-lex.europa.eu/eli/reg_impl/2023/594/oj

FIGURE 27

An example of the European Union regionalization applied by the national veterinary authorities of Italy in response to the African swine fever epidemic



Note: Refer to the disclaimer on page ii for the names and boundaries used in this map.

Source: **African Swine Fever Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise "G. Caporale", COVEPI.** N.d. *African swine fever. National epidemiological bulletin. An ArcGIS Story Map.* Available at: https://storymaps.arcgis.com/stories/9fe6aa3980ca438cb9c7e8d656358f35. [Cited 13 July 2024]

MOVEMENTS OF LIVE PIGS AND SUBPRODUCTS

Trade in live animals and their subproducts has always been implicated in the spread of disease and its significance in this respect progressively increases globally (Fèvre *et al.*, 2006; FAO, 2013), as well as on the national scale in many countries. Ongoing urbanization, growing consumer markets and commercialization of animal production result in the massive movement of animals outside of their main production areas, which thereby promotes the spread of diseases such as ASF. Trade and movements may also involve wild animals (e.g. relocation, reintroduction) and can produce epidemiological situations impossible or very unlikely to occur in the natural ecosystems.

Value chains in some pig production systems can be extremely complex and involve multiple stakeholders and actors. There is a big variation in how they are organized and how they function in different countries. Value chains by their definition are responsive to the supply–demand dynamic and price differential and change to maximize profit. They are not always restricted to national boundaries and operate across international borders. A significant part of international and national pig and pork trade in some countries can be illegal and out of formal control. Understanding live pig and pork value chains is extremely important in the context of ASF management, as the virus is effectively spread in space with contaminated meat and its epidemiological cycle in domestic pigs is fundamentally sustained by reinfection of animals through the means of infected products and fomites.

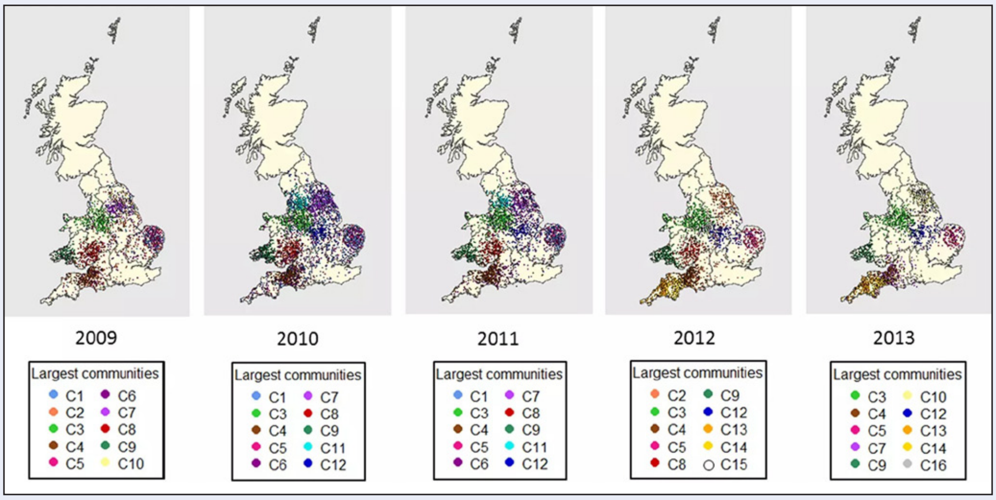
Movements of pigs and their products occur as part of the normal production cycle, driven by regional price differentials, transportation between production and consumption areas for slaughter, and distribution from abattoirs to wholesalers, retailers, various markets, meat selling points and supermarkets before reaching the end consumer. In many countries, some of these movements, especially in the commercial sector, are regulated and documented by veterinary authorities. Where available, data on pig movements can be analysed, appropriately summarized, arranged and included in a GIS to inform about the risk of disease spread. Movements of pigs and products across space occur as a part of the normal production cycle, due to regional price differentials, between production and consumption areas for slaughter, as well as from abattoirs to wholesalers and retailers to a variety of markets, meat selling points, supermarkets etc before the products reach the end consumer. In many countries, some of these movements, especially in the commercial sector, are regulated and documented by the veterinary authorities. Where available, the data on pig movements can be analysed, appropriately summarized, arranged and included as a part of GIS to inform about the risk of disease spread.

Such analysis usually uses raw data containing origin and destination locations, numbers of animals moved, dates and other attributes that can be processed using network analysis techniques. Understanding patterns of pig movements can provide useful insights into how trade flows are directed, which nodes play the most important role, which clusters of premises are most interconnected or identify those premises that mainly gather animals or those that predominantly send out or receive pigs (Box 5).

BOX 5

Analysis of pig movement patterns in the United Kingdom of Great Britain and Northern Ireland

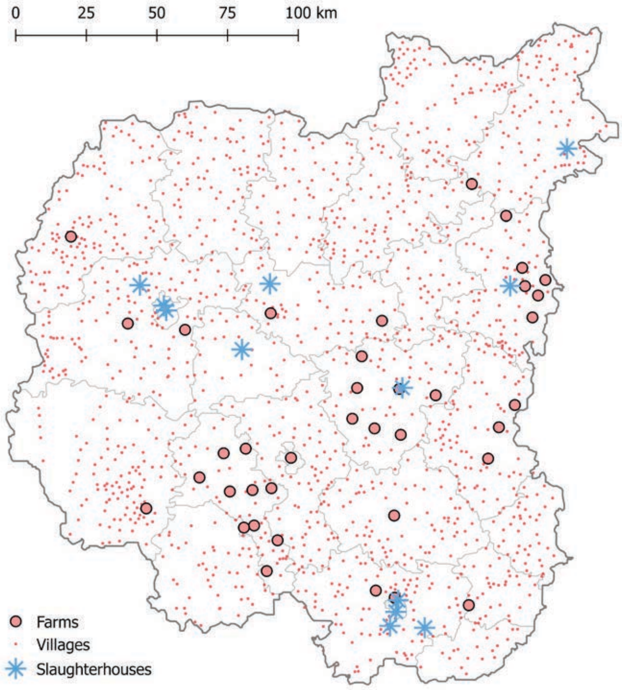
Analysis of the pig movement network in the United Kingdom of Great Britain and Northern Ireland showed that several types of nodes involved in pig movement can be identified. Around 22 000 pig holdings accounted for the absolute majority (98.6 percent) of pig movements. There were also 217 gathering areas, 174 slaughterhouses and 16 markets involved in the movement network. Pigs were usually moved over relatively short distances (tens of kilometres). From pig holdings, most movements were directed to slaughterhouses (68.3 percent) and other pig holdings (23.7 percent). In terms of pig numbers, 56.2 percent of pigs were moved for slaughter and 43.5 percent to other pig holdings. Analysis of the network structure also showed that premises formed “communities.” For example, there were groups of holdings, gathering areas, slaughterhouses and markets that were more intensively connected than would be expected by chance.



Note: Refer to the disclaimer on page ii for the names and boundaries used in this map.

Source: **Guinat, C., Relun, A., Wall, B., *et al.*** 2016. *Exploring pig trade patterns to inform the design of risk-based disease surveillance and control strategies.* Sci Rep, 6: 28429. https://doi.org/10.1038/srep28429. Figure 5. Available at: https://www.nature.com/articles/srep28429/figures/5

FIGURE 28
Localization of officially registered slaughterhouses in Chernihiv region in Ukraine



With the map of epidemiological units in the background

Note: Refer to the disclaimer on page ii for the names and boundaries used in this map.

Source: Author's own elaboration. Country boundaries based on UN Geospatial. 2023. Map of the World. In: United Nations. [Cited: 10 November 2024]. http://www.un.org/geospatial/content/map-world-1"www.un.org/geospatial/content/map-world-1

There are different ways in which the results of pig movement analysis can be incorporated into GIS. Information on the role of each premise in the network, such as their connectedness, attribution to a community of nodes, number of incoming or outgoing movements, totals of moved pigs etc. can be added to the characteristics of farms or other network nodes such as slaughterhouses. Alternatively (or additionally), movement data can be aggregated and summarized at a level of administrative division to provide a generalized picture of production or trade-related flows in the pig industry (Gorsich *et al.*, 2019).

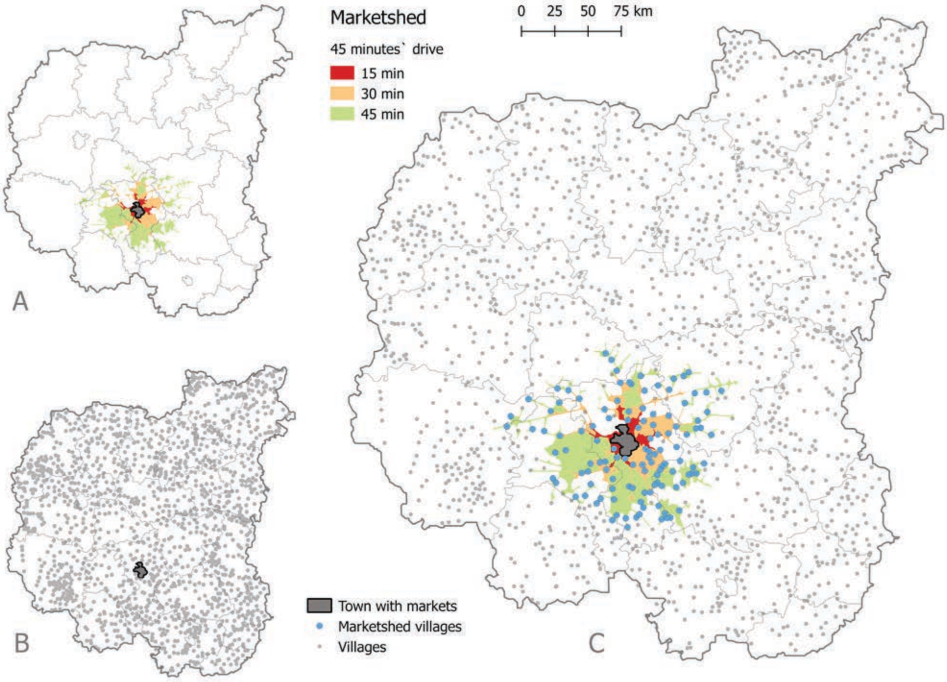
Slaughterhouses and meat processing plants are critical nodes in the pig value chain where live pigs are turned into products that are sold either wholesale or go to the retail market. They may receive pigs from both commercial farms and backyard holdings and can play a significant role in the spread of diseases, with potentially far-reaching implications. Due to their critical role in the epidemiology of ASF and the potential spread of other diseases, all slaughterhouses should be registered, described by their essential characteristics and mapped. While this is usually the case in most developed countries (where abattoirs must be officially registered and licensed for operation), in developing countries many small slaughterhouses may operate unregistered or illegally. Every effort should be made to compile a georeferenced database of slaughter facilities and ensure they are under the supervision and inspection of the competent authorities (Figure 28).

It is usually more difficult to collect data on the movements of pigs in the backyard or small-holder production sector. Trade of smallholder farmers is often irregular, opportunistic and informal. Although backyard pig production is usually subsistence-oriented, some of such holdings do sell pigs at least occasionally, especially during disease outbreaks to compensate for losses. This makes it difficult to obtain reliable data on the value chain organization, as well as puts in question the overall usefulness of such efforts. In some countries, authorities require movement certificates for pigs transported for sale or slaughter issued after examination of animals by a veterinarian. Analysis of this type of information can provide useful insights into general backyard pig movement flows provided that data is made digitally available. However, this system requires animal identification and electronic movement record-keeping databases, which is rare in most countries where backyard pig farming predominates.

A reasonable approach to describing potential risks coming from the transportation of infected pigs or contaminated products in extensive systems is to use market accessibility

FIGURE 29

A fragment of a map of market sheds identified based on travel time to the nearest city with a population of fifty thousand in Chernihiv region, Ukraine



Note: Refer to the disclaimer on page ii for the names and boundaries used in this map.

Source: Author's own elaboration. Country boundaries based on UN Geospatial. 2023. Map of the World. In: United Nations. [Cited: 10 November 2024]. http://www.un.org/geospatial/content/map-world-1"www.un.org/geospatial/content/map-world-1

maps. The assumption behind this is that farmers (or intermediary traders) are most likely to move products from rural areas to the closest (most accessible) urban centre where market opportunities are higher. Based on this assumption, one can classify any epidemiological unit (village or a farm) by the time needed to reach urban centres with markets, identify the one to which the products are most likely to travel from a given location, as well as outline market catchment areas or market sheds (Figure 29).

Conceptually, market sheds are areas in which small small-scale trade flows in various commodities (including livestock and subproducts) tend to concentrate at the markets found in the closest largest city. Such trade normally involves small-holder livestock owners, who travel to the market themselves or sell animals to the local intermediaries. From an epidemiological perspective, the spread of disease through such small-scale trade is more likely to occur within market sheds, rather than between them, because animals and subproducts are usually transported to the most accessible market. Market sheds are identified based on the travel cost or accessibility raster layers and can be produced for markets located in populated places of different varying sizes (e.g. 10 000, 20 000, etc.). They can be used as yet another way to identify the risk of ASF spread in space in situations where trade is expected to play a significant epidemiological role.

Market sheds can be a very useful means of delineating areas for surveillance programmes focused on ASF virus detection in pigs or subproducts that are moved for sale over relatively short distances. Sick animals and contaminated products are often sold quickly and as a priority. In the case of ongoing outbreaks, targeting surveillance on urban markets can be a good strategy to detect pathogens such as ASF.

SPATIAL RISK FACTORS AND RISK MODELS

The development and maintenance of a decision support GIS open perspectives to utilize the full potential and advantages of modern spatial epidemiology and risk mapping. Analysis of disease occurrence patterns and the effect of various spatial factors can be performed at different spatial scales, including local epidemics, country-wide assessments, and regional or even global levels. While most studies that investigated the spatial epidemiology of ASF did manage to find certain combinations of variables that explained disease occurrence either in domestic pigs or in wild boar, it is hardly possible to extrapolate their findings to other areas and epidemiological contexts. Spatial variables that can serve as useful predictors in a decision support

GIS developed for a particular country can only be identified in the process of developing a model that is tailored to suit the country's context and data availability. It is recommended that such spatial risk assessments are outsourced to competent research groups that can prepare relevant datasets and build models that are most appropriate for the situation.

In a review by EFSA (2022), it was identified that the most frequent ASF risk factors in domestic pig populations were various pig population density metrics and biosecurity indicators. Of the socioeconomic factors, demographic characteristics were very frequently found to be significant, followed by human population density indicators and access to laboratory services. In addition to pig farming and anthropogenic factors, other types of variables were found to be significant for ASF in domestic pigs. Among them were those related to the habitat, the area itself (including previous ASF virus infection or presence of abattoirs), wild boar management characteristics and the presence of vectors. Factors related to habitat (i.e. vegetation, waterbodies, fauna and climatic conditions) were significant in a considerable number of studies for the occurrence of ASF in domestic pigs. However, as EFSA concludes, whether that relates directly to the presence of ASF in domestic pigs or indirectly through the wild boar potentially affected population is unclear. The results of spatial risk factor analysis in epidemiology very often reveal correlations or associations which cannot be interpreted as simple straightforward causal relationships.

KNOWLEDGE-DRIVEN RISK MAPPING

There are two distinct situations when it comes to spatial risk assessments of ASF: a) the country is free of disease or the existing surveillance system is not providing sufficient data on the epidemiological situation; and b) the country is already affected or is endemic to ASF. In the first case, the risk assessment can only be based on assumed constellations of risk factors identified from elsewhere or through expert elicitation or review of literature. The typical methodological solution in this case is the application of the "knowledge-driven" risk assessment technique, of which spatial multi-criteria decision analysis is most widespread (Box 6).

Spatial MCDA or conceptually similar approaches have been used to create risk maps of epidemics or likely persistent circulation of many animal diseases, including ASF in Africa, China, Kazakhstan and elsewhere. Whenever disease observations for the area of concern are accumulated, the early predictive risk maps created by MCDA can be statistically validated with empirical observations. The method is most useful and cost-effective as a first approximation of the country's suitability to sustain the ASF transmission cycle. It can be improved as more information on disease occurrence becomes available and better knowledge on its local epidemiology is gained.

BOX 6

Definition of knowledge-driven risk mapping

"Knowledge-driven" risk mapping is an approach that uses literature-based evidence or expert opinion, rather than empirical data exploration, to describe the relative importance of risk factors for a disease. In data-sparse environments, this evidence can be integrated into a formal decision-making process to predict the suitability of a geographic area for disease occurrence based on the presence of identified risk factors. The likelihood of infectious disease occurrence is typically influenced by multiple interacting factors. Therefore, knowledge-driven disease risk mapping should be performed as part of a formal and systematic evaluation framework that considers the relative contribution of each factor to the overall estimation of suitability.

Multi-criteria decision analysis (MCDA) is a methodology that allows the analysis of complex decision problems involving conflicting criteria and has been used within a GIS for this purpose. Broadly, MCDA prioritizes the criteria that influence a decision and provides a framework by which users can reach a decision that reflects these priorities. In the context of risk mapping, "criteria" are risk factors for an undesirable event, such as disease occurrence, while the "decision" relates to the estimation of an area's suitability for the event, and therefore the relative likelihood that it can occur.

"Knowledge-driven'' risk mapping is one such approach that uses literature-based evidence or expert opinion, rather than an empirical exploration of available data, to describe the relative importance of risk factors for a disease. In data-sparse environments, this evidence can be integrated into a formal decision-making process to predict the suitability of a geographic area for disease occurrence based on the presence of the identified risk factors. The likelihood of infectious disease occurrence is typically influenced by multiple interacting factors. Knowledge-driven disease risk mapping should therefore be performed as part of a formal and systematic evaluation framework that considers the relative contribution each factor makes to the overall estimation of suitability.

Source: **De Glanville, W.A., Vial, L., Costard, S., *et al.*** 2014. Spatial multi-criteria decision analysis to predict suitability for African swine fever endemicity in Africa. *BMC Vet Res,* 10: 9. https://doi.org/10.1186/1746-6148-10-9.

In Europe, ASF has become a de facto novel endemic disease of wild boar. Mechanisms of its spread and persistence are much more affected by spatial factors compared to the domestic pig cycle, where socioeconomic factors and human behaviour inevitably introduce a lot of noise. Research has already found many interesting associations with climatic, land cover or human activity-related spatial variables that affect ASF occurrence in wild boar, both in Europe and elsewhere (Bergmann *et al*., 2021; Ito *et al*., 2022). However, it is likely that at different stages of an epidemic and throughout the endemic phase, the role of environmental factors changes in space and time, making extrapolations difficult. To investigate and understand the constellation of risk factors for the endemic persistence of ASF in wild boar in a country, one must account for disease epidemiology and choose potential spatial risk factors based on reasonable assumptions. This involves selecting variables that are relevant and have an underlying hypothesis or explanation. Research already finds many interesting associations with climatic, land cover or human activity-related spatial variables that affect ASF occurrence in wild boar both in Europe and elsewhere (Bergmann *et al*., 2021, Ito *et al*., 2022). However, it is likely that at different stages of the epidemic and throughout the phase of endemicity the role of environmental factors changes in space and time, which again makes it difficult to make any extrapolations. One aiming at investigating and understanding the risk factor constellation for endemic persistence of ASF in wild boar in a country must account for disease epidemiology and choose potential spatial risk factors based on reasonable assumptions, selecting variables that are relevant and have an underlying hypothesis or explanation behind them.

As an example, three spatial risk variables (Figure 30) were chosen in Ukraine to evaluate the suitability of its area for endemic circulation of ASF. The assumptions behind this risk assessment exercise were the following: (A) areas with a higher population density of wild boar are likely to sustain longer epidemic and are more likely to reach conditions of endemic equilibrium (Guberti *et al*., 2022); (B) in colder climate, approximated here by annual mean temperature, contaminated wild boar carcasses are preserved for a longer time and thus contribute to ASF endemicity (Bergmann *et al*., 2021); and (C) the human footprint index is a quantitative measure of human influence across the globe, including natural habitat fragmentation (higher index means higher human impact and fragmentation and slows down spread of disease in space). The logic behind this risk factor mapping exercise came from expert knowledge, not from statistical investigation of disease occurrence patterns. Provided that the accepted assumptions hold true, one can go a step further in the risk assessment and generate a GIS layer that combines all three spatial risk factors in one risk map (Figure 31).

In this simple example, the three spatial risk variables originally available as raster layers with different spatial resolutions were aggregated at the second level of administrative division by calculating their averages for each unit. Then these average values were transformed and rescaled to fit a unitless score ranging from 0 to 1 in such a way that the score would reflect their assumed contribution to ASF suitability in a standardized and comparable way. Areas with lower average values of annual temperature, higher density of wild boar and lower human footprint index correspond to better conditions for ASF persistence and have respectively higher suitability scores. The final step in this risk assessment exercise was to average the suitability scores of the three variables for each district and again rescale values to match the scoring system from 0 to 1 (Figure 31). For the sake of simplicity in this example, all three spatial variables were considered to equally contribute to ASF suitability. In other situations, or with other variables, analysts may consider assigning different weights to the variables if that is foreseen by the assumptions underlying the model design.

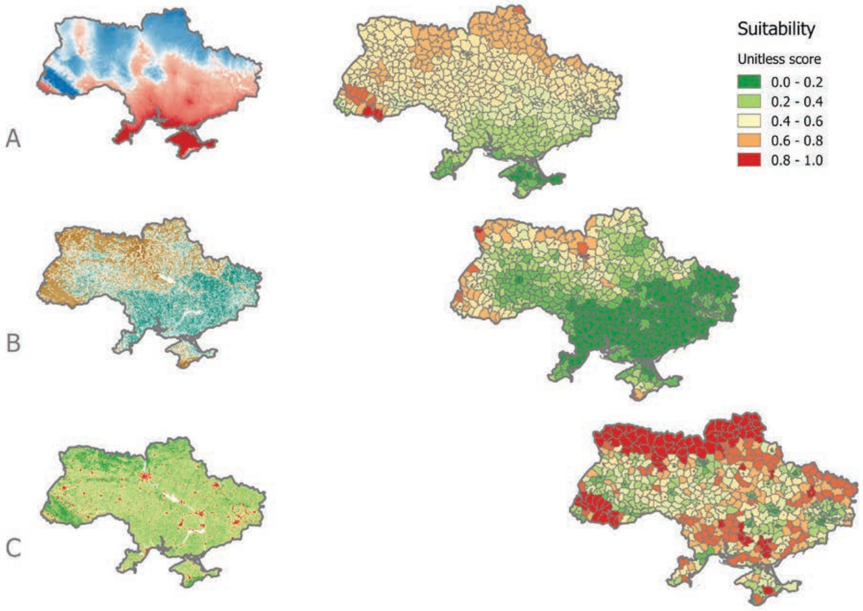
EPIDEMIOLOGICAL INTERFACES

From the perspective of ASF epidemiology interfaces are spatiotemporal domains where pathogen transmission between different subpopulations of pigs can be expected to occur more often than elsewhere (Caron *et al*., 2012). For example, the probability of interactions between domestic and wild pigs in eastern Europe can be estimated based on their respective population densities (Figure 32), which however does not fully account for the complexity of possible ways of interaction, likely to also involve human activities and different pig husbandry systems: such as wild boar hunting, free-ranging of pigs, illegal disposal of contaminated carcasses in the environment etc.

This approach to identifying potential interfaces between two populations is essentially another form of simple knowledge-driven risk mapping, using the population densities of the two ASF host species. In the example from Figure 32, population densities of the two respective populations were rescaled to match the same unitless score system, summed and reclassified into five qualitative categories (from “very unlikely” to “very likely”). Similarly, this kind of interface mapping can be performed using population densities at some level of aggregation. The outcome of such an exercise will be less granular compared to the raster map of the interface in Figure 32 and more similar to the map in Figure 31.

FIGURE 30

Three arbitrarily selected potential spatial risk factors for endemic persistence of African swine fever in the wild boar populations in Ukraine



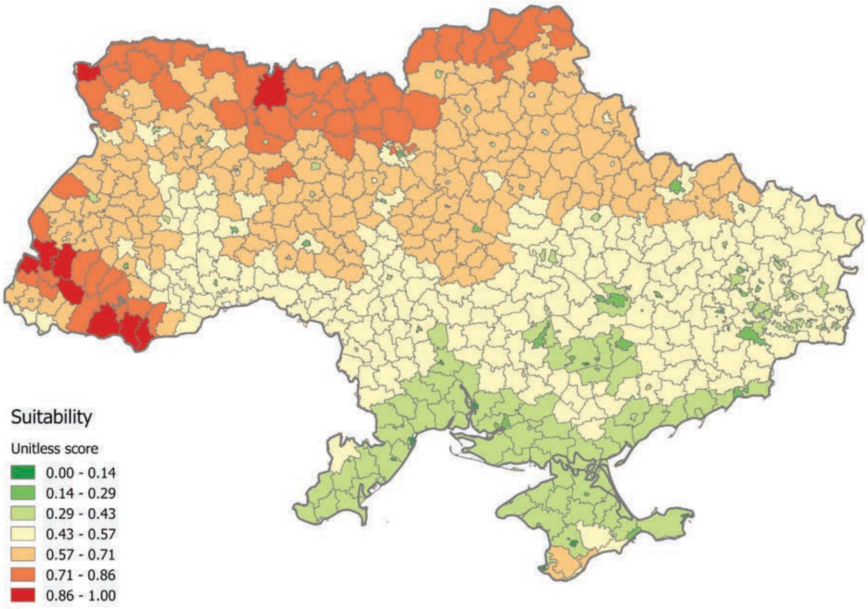
Presented as raster layers (left) and their respective averages at district level rescaled to fit the same unitless scoring system from 0 to 1 (right). A – annual mean temperature (WorldClim Database, Fick, S.E. and R.J. Hijmans, 2017); B – estimated wild boar population density (Pittglio *et al.*, 2018); C – human footprint index (WCS-CIESIN, 2005). Reddish colours on the maps to the right indicate higher suitability for ASF. Greenish colours denote units with lower suitability. Yellowish colours are intermediate scores.

Note: Refer to the disclaimer on page ii for the names and boundaries used in this map.

Source: Author's own elaboration. Country boundaries based on UN Geospatial. 2023. Map of the World. In: United Nations. [Cited: 10 November 2024]. http://www.un.org/geospatial/content/map-world-1"www.un.org/geospatial/content/map-world-1

FIGURE 31

Final risk map of the suitability of Ukraine for endemic persistence of African swine fever in the populations of wild boar



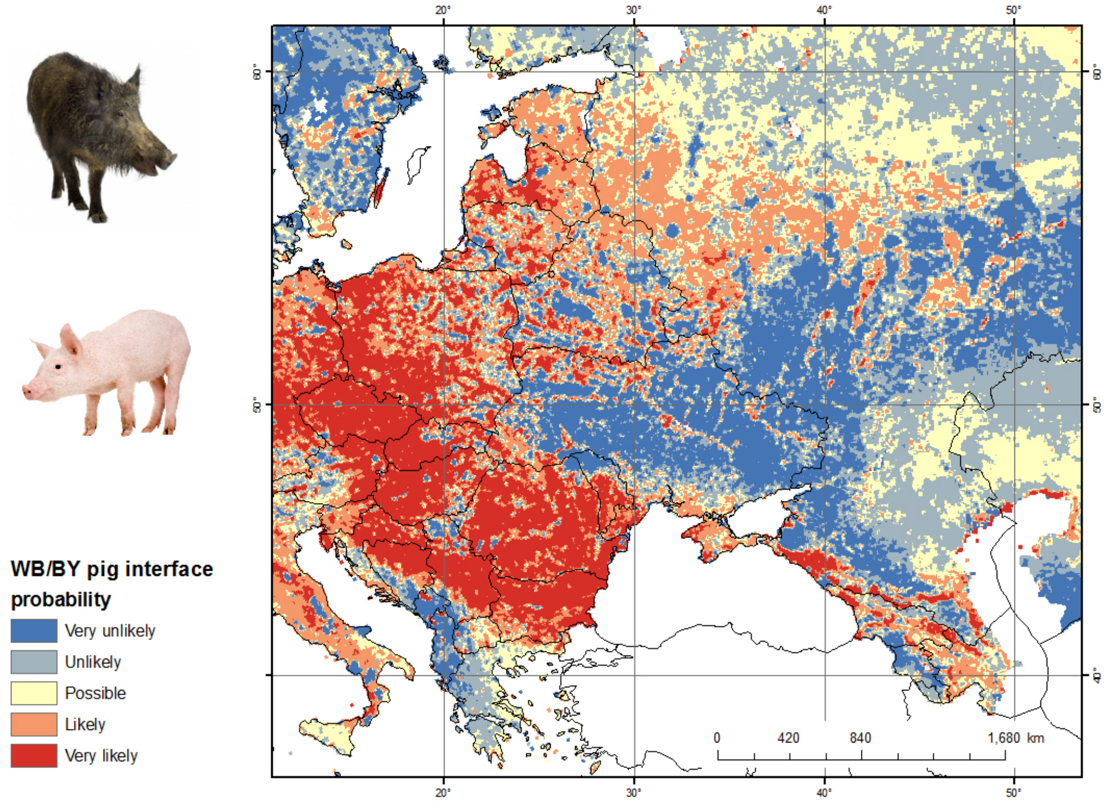
Based on the 3 equally weighted spatial variables (average annual temperature, estimated population density of wild boar and human footprint index, Figure 30) at district district-level resolution.

Note: Refer to the disclaimer on page ii for the names and boundaries used in this map.

Source: Author's own elaboration. Country boundaries based on UN Geospatial. 2023. Map of the World. In: United Nations. [Cited: 10 November 2024]. http://www.un.org/geospatial/content/map-world-1"www.un.org/geospatial/content/map-world-1

FIGURE 32

Identification of interface between populations of wild boar and domestic pigs in eastern Europe



Based on their rescaled population densities originally available as raster layers

Note: Refer to the disclaimer on page ii for the names and boundaries used in this map.

Source: **FAO/ASFORCE.** 2015. *Wild boar mapping distribution over Europe and in countries at risk based on demographic data. Technical report. Targeted research effort on African swine fever*. KBBE.2012.1.3-02. Grant Agreement #311931. Deliverable D10.5/ASFORCE Report, 2015

DATA-DRIVEN RISK MAPPING

In countries that experience ASF as a persistent problem, statistical analysis of empirically collected disease occurrence data can provide valuable insights and greatly improve understanding of the effect of risk factors in space. It is reasonable to apply a data-driven approach to the analysis of disease notifications in a country that has many such observations. The key to success with data-driven risk assessments and risk mapping is consistent disease reporting aligned with the population distribution metrics capable of providing analysis with accurate data. There can be a multitude of statistical solutions to perform empirical disease risk analysis studies and generate risk maps, but any would require a good understanding of epidemiological context and appropriate discrimination of affected epidemiological units or sub populations based on their vulnerability to the disease.

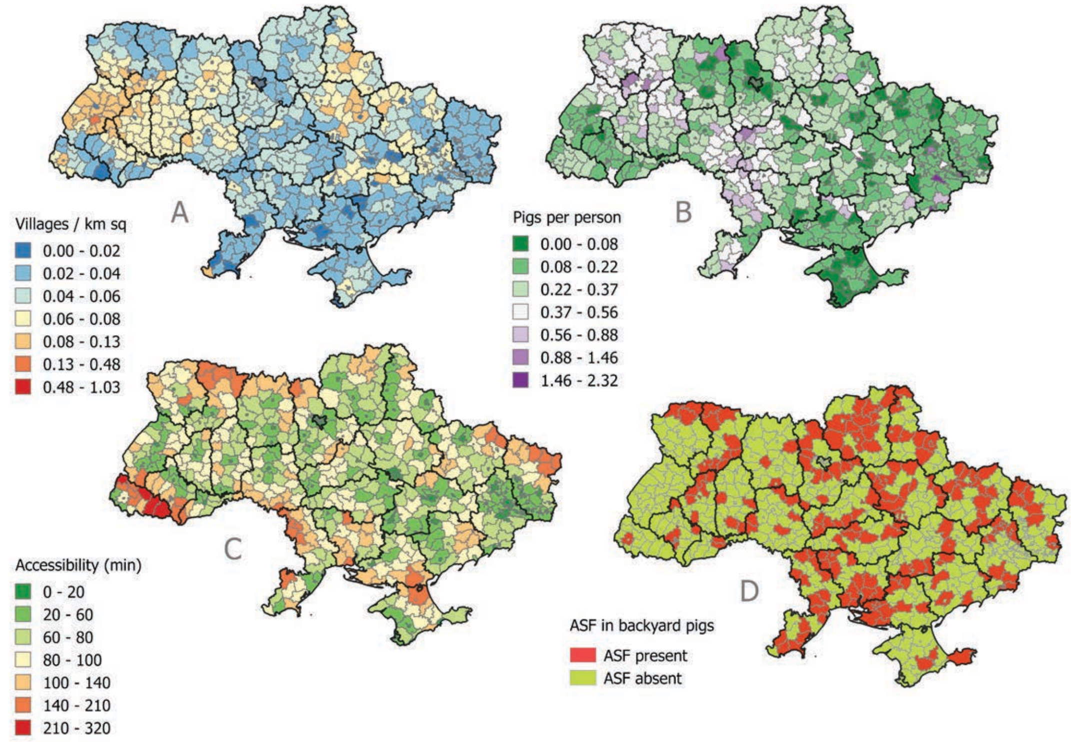
Every effort should be made to use a carefully selected subset of data for each step or branch of the analysis. Mixing up disease notifications in different subpopulations, for example, those in domestic pigs and wild boar is inappropriate and will not produce any meaningful results. Whenever large commercial farms with high biosecurity are affected, they should be treated separately from the epidemiological units with low biosecurity standards.

The arrangement of population data for calculating disease occurrence metrics, such as the attack rate, can significantly impact the value of the indicator. For example, pooling disease notifications from epidemiological units with low to non-existent biosecurity (e.g. small commercial farms and villages) into one category and using the total number of such units as a common denominator might yield one result. Alternatively, arranging the same data differently (e.g. pooling farms together and treating villages separately) can produce a significantly different numeric estimate of the attack rate. These potential effects should be carefully investigated before building any data-driven model, as they directly affect the outcomes of the analysis.

Developing, statistical testing and validation of spatially explicit disease risk models is a highly technical task which

FIGURE 33

Three arbitrarily selected potential spatial risk factors and the occurrence of African swine fever in the backyard pig production sector in Ukraine at district-level resolution



A – Average density of villages; B – Number of pigs per rural inhabitant; C – median travel time from villages to a city with 50K or more inhabitants (quantitative predictors). D - Presence and absence of ASF disease detections in the backyard sector (qualitative dependent variable).

Note: Refer to the disclaimer on page ii for the names and boundaries used in this map.

Source: Author's own elaboration. Country boundaries based on UN Geospatial. 2023. Map of the World. In: United Nations. [Cited: 10 November 2024]. http://www.un.org/geospatial/content/map-world-1"www.un.org/geospatial/content/map-world-1

requires appropriate expertise and experience. It is highly recommended to outsource such research projects to professional experts, preferably those who are experienced in animal disease risk modelling. However, even highly qualified experts and sophisticated methods cannot create a statistically robust model or produce practically applicable outcomes without carefully collected and appropriately arranged data that accurately describe disease occurrence and capture the specifics of the epidemiological context.

For this reason, one should select potential spatial risk variables with a clear epidemiological hypothesis in mind or assumptions to test, rather than including into the model too many (often irrelevant or highly collinear) variables to avoid noise and help interpretation of results. For example, the following questions to be answered as a part of the analysis of ASF occurrence in Ukraine (Figure 33, D) were selected: (A) What is the effect of the average density of villages as epidemiological units with very low biosecurity? (B) What is the effect of the number of pigs per rural inhabitant? (C) What is the effect of the average travel time from villages to the urban centre? In this example, spatial risk variables were arranged to fit the polygons of the second-level administrative division. Respectively, the disease observations in the backyard sector (the dependent variable that we may try to explain) were aggregated at the same level and using the same set of polygons in the presence/absence map (Figure 33, D). Such an aligned dataset with several explanatory variables and a dependent one can be investigated statistically and allow for answering the above questions, assessing the relative contribution of each factor (perhaps excluding irrelevant ones) and arriving at a conclusion. Then, if proven to be statistically robust, model outcomes can be made into a risk map.

There are multiple ways to statistically analyse the effect of predictor variables (risk factors) on the dependent variable (disease occurrence). The choice of the type of multivariable regression analysis should account for the type of both predictors and the dependent variable (e.g. continuous versus categorical). It is better to outsource such an analysis to competent experts in geostatistics, who could account for the peculiarities of the dataset, choose the most appropriate methodology and generate a risk map in case the statistical model selected can explain variation in disease occurrence reliably enough.

Disease risk maps are usually generated by assigning disease probability values scaled to the range from 0 (disease is likely absent) to 1 (disease is likely present) to some geographical units. Most often they come out gridded, e.g. geographical units are represented as rectangular equally sized areas (grids or rasters) but can also be originally arranged or re-aggregated to fit polygons of administrative division. Probability values over 0.5 or more towards the higher end of the range (75, 90, 95) indicate likely presence of disease. Apart from the probability value, statistical metrics such as confidence of prediction (reliability of estimate) are usually provided as modelling outputs. Both of those should be considered when geographic visualisations are produced. Sometimes, for the sake of easier interpretation and visualisation, probabilistic disease occurrence maps are simplified (reclassified) to show only the likely presence and absence of disease. Probabilistic disease occurrence maps are generated using statistical analysis of empirical disease events and therefore are as good, as is the quality of the input data.

High-resolution risk maps can be used to classify epidemiological units by the anticipated risk score and therefore prioritize them for surveillance or interventions. Risk maps that come out as aggregated estimates of risk are useful for identifying particular regions of the country that need attention or resources.

Key messages:

- A starting point in the spatial risk assessment for ASF is the classification or ranking of epidemiological units by their biosecurity levels. This helps to estimate which of them are more likely to become infected if all other conditions or risk factors are held equal. The list of epidemiological units should include both professional and backyard pig units (e.g. farms and villages).
- Every effort should be made to collect and maintain an up-to-date georeferenced pig farm register containing information on their biosecurity characteristics. All commercial pig holdings must be evaluated against formally accepted biosecurity criteria so that they can be visualized on a map as distinct biosecurity score classes.
- There are three distinct stages in the evolution of the epidemiological situation with ASF: 1) pathogen introduction (incursion, spillover) to a susceptible population or sub population; 2) epidemic spread (invasion) of a disease; and 3) endemic persistence of a pathogen.
- The risk of disease changes as the epidemiological situation worsens. It is reasonable to consider and evaluate the risk of disease at different epidemiological stages separately for each of the pig subpopulations, carefully examining their actual epidemiological role in the process based on the information coming from the field investigations.
- In spatial epidemiology, a risk factor for disease spread is a spatially explicit variable relevant to or statistically proven to increase the probability of disease event or infection persistence. Mapping risk factors is a way to qualify or quantify occurrences of certain spatial phenomena capable of affecting disease dynamics across space. With ASF, there is always an interplay of multiple risk factors.
- Mapping spatial risk factors of ASF must be done concerning specific swine sub populations (commercial, backyard and wild boar), as disease drivers and epidemiology differ between them. There is also an interplay of risks related to transmission between these subpopulations.
- The occurrence of the disease itself is an obvious risk factor for the surrounding animal population. Risk is often anticipated based on criteria as simple as proximity, accessibility or adjacency. Often this is the most practical way of defining areas at risk in the absence of any other criteria or considerations.
- Drawing radial buffer zones around cases or outbreaks, generating polygons of accessibility or classifying regions based on the distance to infected areas and some epidemiological considerations are all valid ways of spatial risk assessment strongly facilitating further disease management interventions. Using GIS is often a key to producing such primary spatial risk assessments in response to ASF emergencies.
- Analysis of live pig and product movements can be incorporated into GIS to help with spatial risk assessments. Various statistics on the characteristics of farms or other network nodes such as slaughterhouses in the value chain system can be incorporated. Pig or product movement data can be aggregated and summarized at a level of administrative division to provide a generalized picture of production or trade-related flows in the pig industry.
- Slaughterhouses and meat processing plants are important nodes in the pig value chains. They can have a critical role in the epidemiology of ASF and its spread. All slaughterhouses should be registered, described in their essential characteristics and mapped.
- Application of GIS to describe spatial patterns of pig and pork value chains and evaluate associated risks is a potent area for enhancing and improving your information system's capacity and supporting ASF management interventions and decision decision-making processes.

- Knowledge-driven risk mapping is an approach that uses pre-existing knowledge of the relative importance of risk factors for a disease. In data-deficient settings, such knowledge is organized into a GIS-assisted calculation and mapping process to predict the suitability of a geographic area for disease events.
- From the perspective of ASF epidemiology, interfaces are spatiotemporal domains where pathogen transmission between different subpopulations of pigs can be expected to occur more often than elsewhere. Such interfaces are a variation of knowledge-driven risk maps.
- Data-driven disease risk mapping utilises good quality empirical data on the distribution of disease events and tries to find a constellation of spatial variables (risk factors) that can explain the observed variation in disease metrics and thereby reliably predict the probability of disease occurrence elsewhere.
- Animal disease risk mapping is a dynamically developing area in the domain of spatial epidemiology, already significantly contributing to the management of diseases such as ASF. However, the application of these approaches requires good-quality data and the availability of spatial analysts with relevant expertise and experience.

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To date, African Swine Fever (ASF), a major challenge to sustainable pig production globally, has resulted in billions of dollars in losses in Africa, Europe and Asia. Proper response to outbreaks of this devastating disease is a key to its management. To address this, animal health authorities must have access to reliable information that can aid in complex decision-making before and during outbreaks. Geographic information system (GIS) technology is an effective and flexible tool that can strongly help competent agencies with disease management and intervention planning.

This handbook focuses on promoting the use of GIS in managing ASF and serves as a reference guide that outlines the benefits of GIS and the essential steps for effective data collection and organization. It offers practical examples of GIS in action, richly illustrating population distribution, disease occurrence mapping, and risk assessment and visualization. While avoiding complex technical details, it gives extensive guidance on preparing essential datasets and organizing them into a functional GIS. Designed as an entry-level resource, the handbook bridges basic ASF epidemiology and GIS. It is aimed at officials, animal health professionals, pig farmers, wildlife managers, hunters, GIS experts, students, and other stakeholders involved in the global prevention and control of ASF. It encourages these individuals to develop their own decision-support GIS to improve ASF management and reduce its impact both in domestic pigs and wild boar.

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