

Dynamics of Animal Pathogens

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Introduction:

The intricate interplay between animals and the viruses they host is a fascinating ballet that has significant effects on ecosystem stability as well as human health (Marchesini & De Sanctis, 2021). Animal pathogens, which include bacteria, fungi, viruses, and parasites, have a substantial impact on wildlife populations, livestock productivity, and human health. It is essential to comprehend the dynamics of these viruses, including how they adapt, spread, and engage with their hosts, to protect animal health and stop disease outbreaks. Explores the many variables that control the distribution and effects of animal diseases, providing an in-depth look at this complicated realm. The ways in which variables such as environmental influences influence disease dynamics, host vulnerability, and the existence of intermediary hosts (vectors) Look at the ongoing evolutionary arms race between diseases and their hosts, in which both parties constantly modify their strategies to get past the protections of the other. By comprehending these processes, we can develop effective solutions for disease control. This chapter will cover the significance of comprehending pathogen dynamics, transmission dynamics, host-pathogen interaction, evolutionary dynamics, immunization programs, enhanced biosecurity protocols, and focused interventions to break the cycle of transmission. All ecosystems naturally contain pathogens. Co-evolutionary responses that lessen the infections' severity or increase the host's capacity to fend off or recover from infection are the outcome of their long-term connection with their vertebrate hosts (Shillcock, 2022). Human-induced environmental changes frequently disrupt these natural pathogen-host connections, often resulting in unfavorable outcomes. Pathogens have been present on Earth since the beginning of time, and many of them have caused serious illness and death in people. Many of the illnesses that these agents induce are known to spread between different animal species as well as between animals and people. Smallpox is one such disease that exemplifies this, having developed from infections that were circulating in wildlife. Wildlife serves as a host or vector for around 70% of all newly discovered infectious diseases that affect humans (Tomassone et al., 2018). The presence of various hosts, vectors, or infectious agents in complex biological systems is a common factor contributing to the establishment of infectious illnesses. This can impede control and mitigation efforts aimed at specific hosts of management. Even though infections can affect multiple hosts, complicated interactions between the agents co-infecting the same host can still affect pathology, transmission, and virulence. HIV is one example of this, as it has favored the reemergence of drug-resistant forms of tuberculosis, and helminthiasis, like hookworm, can worsen the effects of malaria (de las Heras, 2011). In addition, ecological shifts can occasionally spur evolution and alter the intricate interactions between diseases, hosts, and environments, which will ultimately favor transmission. Changes in temperature or environment can also affect the biogeographic distribution of animal pathogen hosts and vectors, leading to the invasion (or re-invasion) of diseases that had previously been eradicated. Epidemiological investigations can only identify the source of infection in cases of localized illness outbreaks. In some cases, this can be done by identifying the contaminated

vegetable source contaminated coleslaw, or by determining the source of infection through infected manure used for fertilization. Another method of transmission is inhaling aerosolized excreta from infected animals. For example, spelunkers who explore bat-infested caverns contaminated with *Histoplasma capsulatum* spores may develop "cave disease," or there may be occasional cases of hantavirus pulmonary disease from inadvertently inhaling dust-borne rat excreta. Infected animal excretions can potentially spread disease by contaminating drinking or bathing water or by unintentionally exposing skin to puddles of rat urine, which can lead to leptospirosis (Tanga et al., 2022). A common way for animal viruses to infect humans is by intermediary transfer via vectors. Humans are typically incidental hosts and do not play a critical role in the parasite or pathogen's life cycle. Since ancient times, human societies have been plagued by vector-transmitted zoonoses, which will likely continue to do so in the future. Humans were plagued with Chagas disease as early as 9000 years ago, which was spread by the "kissing bug" (triatomine). *Trypanosoma cruzi*, the causal parasite, was identified in 1909 and is present in at least 150 species of domestic and wild animals. Paleoparasitologists have also found *T. cruzi* DNA in human mummies from prehistoric times. A common way for animal viruses to infect humans is by intermediary transfer via vectors. Humans are typically incidental hosts and do not play a critical role in the parasite or pathogen's life cycle. Since ancient times, human societies have been plagued by vector-transmitted zoonoses, which will likely continue to do so in the future.

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A well-established (and constantly expanding) set of theories is used by mathematical models of the population dynamics of infectious diseases to provide condensed representations of epidemiological systems (Karpatne et al., 2022). Most importantly, the central processes of epidemic dissemination and the important demographic groups are explicitly represented by dynamic models. Unlike chronic disorders like cancer or heart disease, infectious diseases are uncommon in that the population's overall health affects the likelihood of infection in addition to an individual's particular risk factors. This causes a population's subgroups to interact non-linearly, which can produce complicated and perhaps illogical epidemic behavior. Groups of people within the host population are categorized as "susceptible" to infection, "infected" and able to spread the disease, or "recovered" and immune to reinfection in the basic susceptible-infected-recovered

(SIR) paradigm. Transmission of infection to recent cases is driven by contacts between susceptible and infectious individuals. Although crude, this model reproduces the classical epidemic curve and has been remarkably successful in elucidating fundamental principles; including the “tipping point” threshold for epidemics to take off if is greater than 1, and the potential to achieve “herd immunity” through vaccination programs. Because of the emphasis on mechanism, dynamical models can address questions outside the scope of statistical and geospatial analyses. Modelers can conduct "what if" experiments by changing parameter values or reformulating mechanisms to investigate issues that are impractical or unethical to investigate in the real world. Through the use of cross-scale synthesis, researchers can also extract important features of epidemics, such as shifts in the value of the "effective" reproductive number (R_e) in response to the implementation of control measures or the depletion of susceptible host populations. Rabies transmission models have anticipated the disease's geographic spread, influenced vaccination policies, and offered biological understanding (Layan et al., 2021).

Models were used to assess the transmissibility of the SARS coronavirus (SARS-CoV) and to improve strategies for infection management and case isolation used to contain the outbreak after it first surfaced. Unlike the last influenza pandemic in 1968, when models were utterly ignored, dynamical models are now crucial for anticipating and combating pandemic influenza strains (Méthot & Alizon, 2015). For instance, school closures were instituted in American cities hit by the new H1N1 influenza, sometimes known as the "swine flu," in the spring of 2009 and have been recognized as a crucial control tool early on in the pandemic's propagation. Travel restrictions are pointless when a pathogen is already spreading within a region, as demonstrated by models of both SARS and influenza. As disease-dynamic models can integrate and analyze several complicated processes at the same time while accounting for the uncertainty inherent in animal diseases, they are an effective way to provide information for management decisions (Hill et al., 2022). In order to inform disease management and modeling at the interface of domestic animals and wildlife, we describe here the paths and processes of disease introduction and transmission. Managing diseases that can spread from domestic animals to wildlife poses unique challenges (Shapiro et al., 2022).

Importance of understanding the dynamics of the animal pathogen:

Understanding pathogen dynamics is crucial in various aspects of public health, epidemiology, and medicine. Pathogens, such as viruses, bacteria, fungi, and parasites, continuously develop and adapt, posing significant challenges to human health. By studying the dynamics of these microorganisms, researchers can better comprehend their transmission, spread, evolution, and the effectiveness of interventions, leading to improved strategies for prevention, control, and treatment (Peng et al., 2020). This essay will explore the importance of understanding pathogen dynamics, focusing on the transmission dynamics, evolution, and implications for public health.

• Transmission Dynamics:

A crucial aspect of pathogen dynamics involves comprehending the mechanisms through which pathogens move from one host to another. Various pathogens employ different modes of transmission, including direct contact, airborne transmission, ingestion of contaminated substances, vector-borne transmission, and vertical transmission from mother to child (Ganter, 2015). Analyzing transmission dynamics aids in pinpointing the primary routes of transmission and devising targeted interventions to halt the spread of infections. For instance, in the context of respiratory viruses such as influenza and COVID-19, grasping the dynamics of droplet transmission is vital for implementing efficient methods of preventing infections, such as wearing masks, physically separating oneself, and improving indoor ventilation (Yashavarddhan et al., 2023). Likewise, for vector-borne diseases like malaria and dengue fever, understanding the dynamics of vector populations and their interactions

with human hosts is crucial for crafting strategies for vector control such as indoor residual spraying and insecticide-treated bed nets (Mack, 2016).

• **Evolutionary Dynamics:**

Pathogens continually undergo evolutionary shifts fueled by factors such as host immunity, environmental alterations, and the introduction of antimicrobial treatments. Evolutionary dynamics significantly influence the virulence, transmission capabilities, and resistance patterns of pathogens (Andersson et al., 2020). Analyzing the evolutionary patterns of pathogens enables researchers to monitor shifts in their genetic composition over time and predict future trends in disease emergence and dissemination. For example, the swift development of antibiotic resistance in bacteria poses a grave threat to global public health. By comprehending the mechanisms behind antibiotic resistance and tracking the evolutionary paths of resistant strains, scientists can devise strategies to safeguard the effectiveness of existing antibiotics and identify novel antimicrobial agents (Muteeb et al., 2023).

• **Implications for Public Health:**

Policy and practice in public health are significantly impacted by our growing understanding of pathogen dynamics. It helps decision-makers use resources wisely and make evidence-based choices about disease surveillance, outbreak response, immunization campaigns, and more (Montibeller, 2022). Researchers can estimate the possible effects of interventions and evaluate their cost-effectiveness in managing infectious diseases by combining mathematical models with empirical data. Furthermore, knowledge of pathogen dynamics is crucial for responding to and preparing for pandemics. The importance of prompt and well-coordinated action to monitor the spread of newly emerging infectious diseases, produce vaccines, therapies, and diagnostic tools, and implement non-pharmaceutical interventions to reduce transmission has been brought to light by the COVID-19 pandemic (Chen et al., 2023). Plans for pandemic preparedness in the future can be guided by the insightful information gained from the COVID-19 pandemic. These include early detection and containment of novel viruses and improving the capacity of health systems to respond to epidemics.

To sum up, successful prevention, control, and treatment of infectious diseases depend on an understanding of pathogen dynamics. By clarifying the mechanisms of pathogen transmission and their evolutionary patterns, scientists can create focused interventions, foresee obstacles in the future, and influence public health policy and practice. It is imperative to maintain funding for pathogen dynamics research to ensure the security of global health and lessen the effects of infectious disease outbreaks.

• **Transmission Dynamics of Animal Pathogen:**

Infectious illnesses sometimes referred to as transmissible or communicable diseases, are brought on by the presence and dissemination of pathogenic biological organisms, or pathogens, within a single host organism (Sarmah et al., 2018). Bacteria, fungi, viruses, protozoa, multicellular parasites, and prions are examples of pathogens that cause disease. Since the pathogen inhibits infectious breakouts when it is absent, they are the main causes of disease epidemics. The host is the organism that a pathogen infects (Pontier et al., 2009). Pathogens cause disease in the human host by interfering with vital physiological activities or inducing immunological responses. Based on how frequently they occur, infectious diseases can be divided into four categories: endemic (constantly present in a population), pandemic (global epidemic), sporadic (occurring sporadically), and epidemic (a sudden rise of cases in a localized place within a short time frame).

Modes of Transmission

Humans can contract infectious organisms from animals in a number of ways. Animals can transmit infectious agents to humans in a number of ways, including direct contact with live

animals or their corpses, indirect contact through animal products like milk or eggs, intermediate transmission through vectors (mosquitoes, mites, ticks, etc.), and remote contact through exposure to contaminated waters, soil, or air. Diseases can spread through direct contact with animals or carcasses in a number of ways, but the two most common are by oral ingestion (foodborne zoonoses) and accidental pet handling without proper hand sanitization. Animal bites, scratches, or mucosal contact with contaminated fluids can very rarely spread disease, as in the cases of rabies and animal-related wound infections (Tsikalas et al., 2023). Animal infections can also be contracted by inhaling droplets of contaminated secretions. This is thought to have happened in China, where local epidemics of avian influenza were caused by exposure to sick ducks or fowls in open marketplaces. Anthrax infections can occasionally be brought on by inhaling microbiological spores or contaminating torn or abraded skin from contact with tainted animal hide. Animal excretions are frequently the source of animal infectious diseases that are not suspected, and in the rare instances when they are, the source is typically not found (Schantz., 1991).

• **Animal Disease via the Food Chain**

The global incidence of foodborne infectious infections is notoriously difficult to assess, even in countries with extensive surveillance. In developing nations, where healthcare infrastructure and facilities are weak and foodborne zoonoses are the most common worldwide, estimating foodborne illnesses is much more challenging (Godwin et al., 2022). It is estimated that a significant portion of animal pathogens and at least one-third of foodborne diseases affect people worldwide annually. According to earlier estimates from the Centers for Disease Control and Prevention [CDC] in 2011, there may be more than 48 million cases of foodborne disease annually, with at least 9.4 million episodes of illness being caused by 31 main pathogens acquired in the US. According to Clemmons et al. (2021), animal-derived infections that are commonly transmitted through food are assumed to be the cause of 30% of all newly found infectious disorders during the preceding 60 years. There are over 250 different types of foodborne illnesses, with the majority caused by chemicals and poisons and the remainder by transmissible microorganisms such as viruses, bacteria, prions, and parasites.

• **Bacterial Foodborne Zoonoses:**

In the US and the EU, *Campylobacter* sp. and *Salmonella* Sp. are the two most prevalent domestically acquired bacterial foodborne zoonoses. Most of the ensuing ailments are typically self-limited gastroenteritis, but infrequently, chronic side effects such as reactive arthritis/spondylitis and irritable bowel syndrome might occur. In the natural environment, these bacteria are widely dispersed and often become established in the intestines of wild and domestic animals, such as sheep, cattle, poultry, and pigs. The 10 pathogen-food combinations included in recent US research that ranked the illness burden of food source infections included five pathogens: *Campylobacter*, *Salmonella*, norovirus, *Listeria monocytogenes*, and *T. gondii*. The researchers included five pathogens in their recent US research that ranked the illness burden of food source infections: *Campylobacter*, *Salmonella*, norovirus, *Listeria monocytogenes*, and *T. gondii*. Mostly produced by lysogenic bacteriophages inserted into chromosomes to encode the genes for six or more STXs, strong cytotoxins referred to as "shiga toxins" (STXs) or "verotoxins" are produced (Lucchesi et al., 2023). These bacteriophages are primarily found in zoonotic pathogenic *E. coli*. STX1 or STX2 is the cause of the majority of STEC diseases. Due to the bacteria's resistance to stomach acid and low infectious dosage (10–100 colony-forming units), STEC spreads easily. Goats, sheep, and cattle are the main STEC hosts, however, other species may also harbor the infection. The most frequent source of foodborne illness is *Vibrio parahaemolyticus*, which primarily manifests as self-limited gastroenteritis. *Vibrios* are naturally occurring commensals in marine and estuarine saltwater. Seldom is *Vibrio vulnificus* foodborne, however, it is linked to septicemia and soft tissue infections. Q-fever and brucellosis are two other bacterial foodborne zoonoses that are more prevalent in the Mediterranean region and poor nations than they are in North America (Asante et al., 2019). The continued presence of these infections in these areas can mostly be attributed to uncontrolled animal husbandry. Different bacterial foodborne zones are summarized in Table 1.

Table 1. Bacterial foodborne zones (Asante et al., 2019).

Microbes	Distribution	Animals	Frequency
<i>Salmonella spp.</i>	Worldwide	"Poultry, cattle, rabbits, sheep, pigs, and pets"	>1 million/year in US
<i>Campylobacter spp.</i>	Worldwide	Pets, livestock, pigs, sheep, bunnies, and poultry	>1 million annually in the US
<i>E. coli—STEC</i>	Worldwide	sheep, goats, and cattle	>265,600 annually in the US
<i>Listeria monocytogenes</i>	Globally/worldwide	Ruminants, Cattle	>16,000 annually in the US
<i>Yersinia enterocolitica</i>	Worldwide	Farm animals, including pigs	N/A
<i>Vibrio spp.</i>			
<i>Vibrio parahaemolyticus</i>	"Eastern Coast US, Southeast Asia"	oysters, Sea crabs	N/A
<i>B. mellitensis</i>	Mediterranean, worldwide	Sheep & goats	N/A
<i>Bacillus suis</i>	Asia, Africa, S. America	Pigs, cattle	N/A
<i>Brucella abortus</i>	Western Europe	Cattle	500,000/year
<i>Mycobacteria bovis</i>	Worldwide	Cattle, buffaloes	N/A
<i>Coxiella burnetii</i>	"Worldwide except New Zealand"	Sheep, goats	N/A

• Vector-Borne Zoonoses:

Worldwide zoonotic disease transmission from companion animals is mostly dependent on vectors. The major worldwide vectors of companion animal zoonoses are listed in the table. In this category, visceral leishmaniosis is the most important illness globally. It is caused by *Leishmania infantum* [*L. chagasi*] and is transmitted by sandflies from the primary reservoir of domestic dogs. There are several countries in southern Europe, South and Central America, northern Africa, and Asia where the disease is prevalent, and a significant number of dogs in these areas are affected (Vilas-Boas et al., 2024). The WHO estimated in 2007 that there were around 12 million HIV-positive individuals globally, with 2 million new cases reported annually. Additionally, individuals living with HIV had a higher chance of developing serious illness. Because pets are traveling across borders more frequently, controlling leishmaniosis in endemic places is extremely difficult, and spreading the disease to non-endemic areas is quite concerning. The implementation of control measures in Brazil involved serological testing of dogs and the culling of positive animals. Additionally, the commercial vaccine Leishmune, when administered to dogs, led to a drop in the prevalence of both human and canine leishmaniosis due to a reduced rate of transmission (França-Silva et al., 2023). Cat scratch disease is the zoonotic infection caused by the *Bartonella* bacteria that is most commonly found. Although it is found throughout the world, temperate regions with indoor pets seem to have higher populations of it. Even though they don't show any symptoms, cats can harbor a lot of human *Bartonella henselae*, *clarridgeiae*, and *Koehlerae* infections (França-Silva et al., 2023). Cat scratch disease primarily affects youngsters and is spread by infected flea excrement that kittens scrape with their claws. Therefore, it is a vector-borne infection that is spread by fleas

from cats that have bacteremia to humans and other cats. Fever and localized lymphadenopathy are the typical symptoms of the infection; however, in rare cases, more serious side effects such as encephalitis, granulomatous hepatitis, retinitis, choroiditis, arthritis, and osteomyelitis might appear. Cats in impoverished nations often have a 27% seropositivity rate for *Bartonella* and a 10% bacteremia rate. Regarding increasing transmission and diseases in human societies, there are a number of tick-borne illnesses that are common to companion animals as well as humans. These include tick-borne encephalitis, which is widespread in Europe and Northwestern Asia, borreliosis [Lyme disease], ehrlichiosis, babesiosis, rickettsiosis, anaplasmosis, Q-fever, and tularemia. Only a small number of these illnesses, nevertheless, have been proven to be spread by pet interaction. Pets (dogs and cats) may help humans become exposed to diseases including ehrlichiosis, babesiosis, anaplasmosis, and Lyme disease that is transmitted through outdoor activities, even though the diseases' natural hosts are black-legged deer ticks. In endemic areas, having a dog raises the risk of rickettsiosis infection in people due to the spread of the disease by dog ticks (Stanley & Rhodes, 2021). In many US states, Rocky Mountain spotted fever (RMSF) is endemic; nevertheless, it is more common in the mid-south Atlantic states and the west-south-central region than in the Rocky Mountain states. Northern South America (Brazil and Columbia) and Central America (Mexico, Costa Rica, and Panama) also have it. Therefore, there is little chance that owning a pet will increase a person's risk of developing these illnesses. Different parasitic food borne pathogens are summarized in Table 2.

Table 2. Parasitic foodborne pathogens (Stanley & Rhodes, 2021).

Microbes	Distribution	Animals	Frequency
<i>Clonorchis sinensis</i>	35 million worldwide	pigs, Freshwater fish, rats	Asia
<i>Toxoplasma gondii</i>	Worldwide	cats, sheep, pigs, and rabbits	½ billion globally
<i>Opisthorchis sp.</i>	SE. Asia, SE. Europe, Northern, Thailand, Siberia,	Cats, Canines, fish from freshwater	Variable
<i>Fasciola hepatica</i>	Globally, elevated figures in Asia, Northern Europe, South America, and the Nile Delta.	Domestic and wild ruminants	N/A, variable
<i>Diphyllobothrium latum</i> [fish tapeworm]	China, America Baltic region, Northern Japan, N. hemisphere,	Freshwater fish	N/A
<i>Taenia solium</i> [pork tapeworm]	Southeast Asia, Africa, Central America, South America, and Eastern Europe	Undercooked pork, Pigs	Not at all
<i>Taenia saginata</i> [beef tapeworm]	Worldwide, SE. Asia, high in E. Africa, China, cosmopolitan	Cattle, rarely in Beef, deer	4 million global
<i>Paragonimus westermani</i> [lung fluke]	South and Central America, Asia. Africa.	Pigs, crabs, Freshwater shellfish	20 million globally
<i>Angiostrongylus cantonensis</i>	Southern US, Australia, India, SE. Asia, Caribbean	rats—lung worm, crab fish Freshwater crabs,	N/A
<i>Visceral cysticercosis</i>	SE. Asia, Africa, South and Eastern Europe, South and Central America.	Fecal-oral route	10–20% of the population in endemic areas
<i>Gnathostoma spinigerum</i> [Gnathostomiasis]	Japan, France, Spain, rarely in the US, Cosmopolitan, Netherlands	cats, snails, dogs, Freshwater fish, frogs, chickens	N/A
<i>Anisakis simplex</i> [Herring worm]	Australia, Central America, SE. Asia,	squids, Sea—fish, marine mammals	N/A

Factors influencing transmission rates:

The effects of industrialization and community growth to accommodate the world population increase are examples of human-related issues. The ecology of wildlife is impacted by the development of new roads, homes, towns, and farms, which results in the removal of forests (Fong & Fong, 2017). Furthermore, changes in farming and food chain practices, increased hunting and pet ownership, ecotourism, and the growth of the culinary industry all contribute to human encroachment on animal ecology. The exposure of humans to animals and wildlife can be impacted by political regime shifts, armed conflicts, starvation, mass migration, lax border restrictions, and the collapse of public health infrastructure. Moreover, malnourishment and inadequate nutrition typically leave a population particularly vulnerable to a range of illnesses, including infections that are either directly or indirectly spread by animals.

Genetic variability, selection pressures for the development of increased microbial resistance and virulence, and changes in the ecosystem and biodiversity all have an impact on pathogen-related factors. These changes can also have an impact on the composition and quantity of the local fauna, which can lead to an increase in the number of vectors and disease reservoirs/hosts. In recent times, there has been a growing concern regarding climatic and environmental variables. This is because abnormal changes in the climate pattern in the north and south hemispheres due to global climate change might impact the life cycles of host vectors and affect the fauna and ecology of these animals.

Host-Pathogen interaction:

The symbiotic relationship between hosts and their microbiota is a complex network that influences host physiology, immunomodulation, and overall health. A variety of factors influence this dynamic connection, including dietary components, microbiota-derived metabolites, and a wide spectrum of antimicrobial drugs (Kogut et al., 2020). By acting as a physical barrier, the maternal-fetal interface protects the developing fetus from dangerous diseases and medications that are present in the mother's bloodstream. Nonetheless, certain infectious agents, including viruses, have the potential to penetrate this protective barrier by exploiting their small size or replicating within maternal and fetus placenta cells. Notable instances include *T. gondii*, *N. caninum*, *Brucella abortus*, and *Chlamydia abortus*, among other contributing factors, inducing tissue damage and boosting the likelihood of abortion (Pastor-Fernández et al., 2021). Newborn calves must make a number of difficult adjustments in their early years as they adapt to a new, highly pathogen-filled environment. They have to learn to control their body temperature on their own, go from eating through the umbilical cord to drinking milk from bottles or buckets, and change from having a pre-ruminant digestive system to a ruminant digestive system. The calf experiences an immense amount of stress as a result of these numerous changes, which frequently put its immune system to the test in the first three weeks of life. At the same time, dangerous pathogens such as coronavirus, *Cryptosporidium* spp., and enterotoxigenic *Escherichia coli* (ETEC) colonize the digestive tract during this critical time, highlighting the transition from passive immunity derived from colostrum to the development of active immunity (Osorio, 2020). In order to start replication, the virus transfers its genetic material into the host cell. To accomplish this, the viral capsid fuses with the phagosome of the host cell or the viral or cellular machinery creates pores in the capsid (Kellermann, Scharte, & Hensel, 2021). During this sequence, pathogen-associated molecular patterns (PAMPs) contained in the virus are selectively engaged with by pattern recognition receptors (PRRs), which help the host immune system recognize the virus. This recognition event triggered a sequence of innate immune responses, leading to the release of interferons and cytokines as well as the mobilization of immune cells (Rajput & Thakur, 2023). As innate immune cells, NK cells have the amazing ability to respond quickly and destroy cells that a virus has altered or infected without the need for prior sensitization (Mikelez-Alonso et al., 2021). Even though NK cells are innate immune cells, they can exhibit characteristics similar to the adaptive immune response. Like T cells, NK cells

express antigen-specific receptors, go through clonal proliferation when they come into contact with pathogens and mature into self-tolerance. Additionally, they are able to produce long-lasting memory cells that self-renew continuously and provide powerful effector responses against pathogens that they have already encountered (Sharrock & Sun, 2020). The outcome of this virus-host interaction relies on a number of variables related to either the virus or the host (Correa et al., 2021). These outcomes could result in the virus being eliminated by the host's immune system, the virus evading the host's immune system, or acute, chronic, persistent, or latent infections established (Hoffman et al., 2020). Research suggests that viruses with a high rate of mutation have an advantage when it comes to evolving, surviving, and evading the host's immune response. The host range of the virus may also change as a result of these modifications (Tenthorey et al., 2022). Prebiotics and phytonutrients are particularly important dietary components for enhancing immunity and fortifying chickens against disease (Islam et al., 2022). Furthermore, during the past 10 years, a great deal of research has been done on the supplementation of yeast-derived products with the goal of improving innate immunity. The foundation for investigating nutrigenomic strategies to advance the profitability and well-being of chicken production. As of right now, 10 TLR (Toll-like receptor) genes in chickens have been fully characterized. Variations in TLR sequences affect how the recognition patterns of Pathogen-Associated Molecular Patterns (PAMPs), thereby altering the host's defenses against pathogenic diseases. TLR polymorphism has significant potential as a genetic marker in selective breeding programs meant to enhance chicken breeds (Rehman et al., 2021). Globally, gastrointestinal nematodes (GIN) provide significant threats to sheep health and the economy. *Haemonchus contortus*, *Nematodirus battus*, *Teladorsagia circumcincta*, and several species of *Trichostrongylus* (such as *T. colubriformis* and *T. vitrinus*) are the primary GIN that harm sheep. These parasites are usually spread by the fecal-oral route, wherein infectious larvae grow in the abomasum or small intestine, causing severe mucosal damage and inciting the host's immune system to become inflamed (Smith et al., 2021). Additionally, sheep can serve as hosts for enteric pathogens of significant worldwide importance, including *Salmonella enterica* and *Escherichia coli* (STEC), which produce Shiga toxin (van den Brom et al., 2020). Furthermore, due to their physiological, genetic, and immunological resemblances to human virus outbreaks, pigs are becoming more and more popular in xenotransplantation and as models for human diseases and conditions. In addition to causing disease transmission and fatalities, these epidemics force the culling of swine herds, which results in significant economic losses (Marrana, 2022). Forecasting newly emerging infectious diseases (EIDs) in pigs and people is a major issue. Viral dynamics are heavily driven by selection mechanisms, leading to fast variations in viral landscapes, even if viral zoonoses are scarce in humans in comparison to the enormous viral diversity seen in the animal kingdom. In an EID scenario, the introduction of a novel host can act as a new found viral reservoir, allowing the virus to spread to other vulnerable species. For example, the SARS-CoV-2 transmission chain started with horseshoe bats, moved to an unidentified mammalian intermediate, later to humans, then to minks, and back to humans (Glud et al., 2021).

Evolutionary Dynamics of Animal Pathogen

Because metagenomics offers a more comprehensive viewpoint, it has greatly increased our understanding of the diversity of the animal virome. Animal viruses are currently classified into 5 out of 6 realms, 5 out of 10 kingdoms, 11 out of 17 phyla, 26 out of 39 classes, 36 out of 59 orders, and 99 out of 189 families according to the most recent update to the International Committee on Taxonomy of Viruses (ICTV) classification system, which was released in July 2021. The great diversity of animal viruses is brought to light by this new classification scheme, underscoring the significance of metagenomics in revealing this diversity (Walker et al., 2021). One intriguing finding from metagenomics studies of animal viromes is that, in line with their large species diversity, invertebrates usually contain a much greater diversity and ample of viruses than vertebrates. Specifically, a thorough metagenomics study of invertebrates has revealed new viral lineages and families, as well as those that were previously thought to be unique to vertebrates. These investigations have also demonstrated that invertebrate viruses exhibit a broad variety of

novel genome structures, demonstrating that viral genome evolution is more flexible and dynamic than previously thought (Harvey & Holmes, 2022). Meanwhile, a variety of stressors, such as the scarcity of vital nutrients, frequently confront free-living bacteria in the environment (Marmion et al., 2022). A host that can provide a stable and nutrient-rich habitat through an autotrophic or heterotrophic lifestyle is one of the many strategies that bacteria can use to lessen or avoid environmental stressors. It may be significantly more advantageous for a variety of bacteria to evolve chemotaxis abilities and adaptations that make it easier for them to colonize a host because carbon and nitrogen are scarce in the environment. Novel bacterial traits and behaviors that improve the bacteria's capacity to thrive in an environment associated with their host could emerge as a result of this selective pressure (Wiesmann et al., 2023). Both commensal and pathogenic organisms possess a variety of adaptations that improve their capacity to exploit resources. For example, they can secrete siderophores to scavenge iron or form biofilms to secure a space. However, because they involve harming the host directly, pathogens have evolved unique mechanisms to obtain resources that are unavailable to commensals (McLaren & Callahan, 2020). Microbes use a combination of active and passive interference strategies to outcompete one another. Frequently harboring prophage capable of initiating viral outbreaks and possessing mechanisms to release toxins into the surroundings or target cells, these organisms are equipped with defensive tools to eliminate rival organisms. Because of these adaptations, microbes can more successfully compete for resources and ensure their survival in a variety of ecological niches (Brüssow, 2021; Hernandez et al., 2020). Secreting chemicals that interfere with competitors' biofilms or cell-to-cell communication are two more active interference tactics. In addition to being widely utilized by pathogens, these mechanisms are also frequently employed by commensals against them. These tactics help organisms better exploit resources in a variety of ecological niches by impeding the growth and survival of their competitors (Kern et al., 2021).

- **Genetic variation and adaption in pathogens**

Genetic variation has largely influenced the evolution of animals and plants resulting from microbial acquisition (Ma et al., 2022; Perreau & Moran, 2022). In contrast to mutations, which result in minor alterations to preexisting genomes, the holobiont gains hundreds of new functional gene sets in a single step in acquiring a microbe. Microbes play a crucial role in the evolution of life forms by supplying a diverse array of genetic material that can be integrated into the host's genome. They existed on Earth for two billion one hundred million years before animals and plants appeared (Rosenberg, 2022). The concept of holobiont recognizes the interdependence of the host and its associated microbiome, emphasizing their co-evolutionary relationship. It views these entities as a single, cohesive entity. This viewpoint encourages a broader understanding of inheritance and the quick evolution of organisms as a result of the inheritance of acquired characteristics (Huitzil et al., 2023). It is therefore advisable to consider that these animal and plant holobionts obtained their genetic materials in the form of microbes. The next processes dictated and implemented were the mutations and selection processes, both in the microbe and the host for optimized performance. This process showcases how the HGT plays a critical role in the co-evolutional relationship between the host and the microbes and how the host's genetic makeup is shaped (Zilber-Rosenberg & Rosenberg, 2021). Research is currently being done to determine how much host genetics affect the gut microbiota. But an increasing amount of research from studies on a variety of animal species, including humans, mice, chickens, cattle, and swine, indicates that host genetics may have an impact on the makeup of the gut microbiota. Since the introduction of cutting-edge technologies, like genome-wide association studies (GWAS), a great deal of correlations have been found between the abundance of commensal bacteria and the genotypes of single nucleotide polymorphisms (SNPs), which are primarily found in genes linked to immune disease and host metabolic syndrome. These results demonstrate the intricate relationship between gut microbiota and host genetics, which can have implications for understanding the occurrence of various diseases (Fan et al., 2020). Despite the statistical significance of the relationship between host SNPs and individual bacterial taxa, recent studies have challenged this finding, suggesting that environmental factors may have a

more profound impact on shaping the gut microbiota than host genetics. (Cahana & Iraqi, 2020; Sanna et al., 2022). Population variation, genetic distance, age, and environmental variables may all contribute to the differences in understanding the roles of host genetics and environmental factors (De Kort et al., 2021). Furthermore, host genetic influences on the gut microbiota may be masked by the interplay between environmental variables and host genetics. To fully comprehend the intricate interactions that exist between host genetics, environmental variables, and the gut microbiota, more research is required (Cai et al., 2020).

Ticks are an obligate bloodsucking arthropod that is found all over the world. They frequently parasitize humans and other animals and act as intermediates or vectors for a diversity of infections, such as bacteria, viruses, and protozoa (Jia et al., 2022). Across many tick species, the GC content is comparably constant, *I. Persulcatus* has the lowest conserved synteny among the six tick genomes that have been sequenced, indicating a high degree of genetic divergence from other tick species. Orthologous protein sequences from six tick species, including *I. scapularis*, and two outgroup species, *P. tepidariorum*, and *C. sculpturatus*, in order to evaluate the evolutionary relationships between these species and arachnids. After constructing a maximum likelihood tree with these sequences, the evolutionary distances between the species will be calculated. In addition, using the coding sequences of 464 single-copy orthologous genes, we calculated the divergence period of these species. Identifying the genetic diversity and evolutionary links between tick species and their arachnid relatives is made possible by this analysis (Jia et al., 2020). Influenza Antigenic drift and shift cause viruses (IAVs) to exhibit a high degree of variety. The process known as "antigenic drift" refers to the slow buildup of minor genetic changes in the genome, particularly in the hemagglutinin (HA) and neuraminidase (NA) proteins, aiding influenza A viruses (IAVs) in evading host immune responses. This phenomenon is attributed, at least in part, to the limited proofreading capability of the viral RNA polymerase as shown in Figure 1 (Varghese et al., 2022).

When multiple subtypes of Influenza A virus infect a cell simultaneously, a process known as antigenic shift occurs, as shown in figure 2. This phenomenon involves a substantial change where viral segments are exchanged, leading to the emergence of new viral subtypes. Antigenic shift represents a distinct immunological event from the existing Influenza A viruses and occurs in a host lacking prior immunity.

New viral subtypes that arise via the genetic reassortment of IAVs have the potential to trigger epidemics or pandemics in humans since there is a lack of pre-existing immunity against the new antigens (Huang & Wang, 2020).

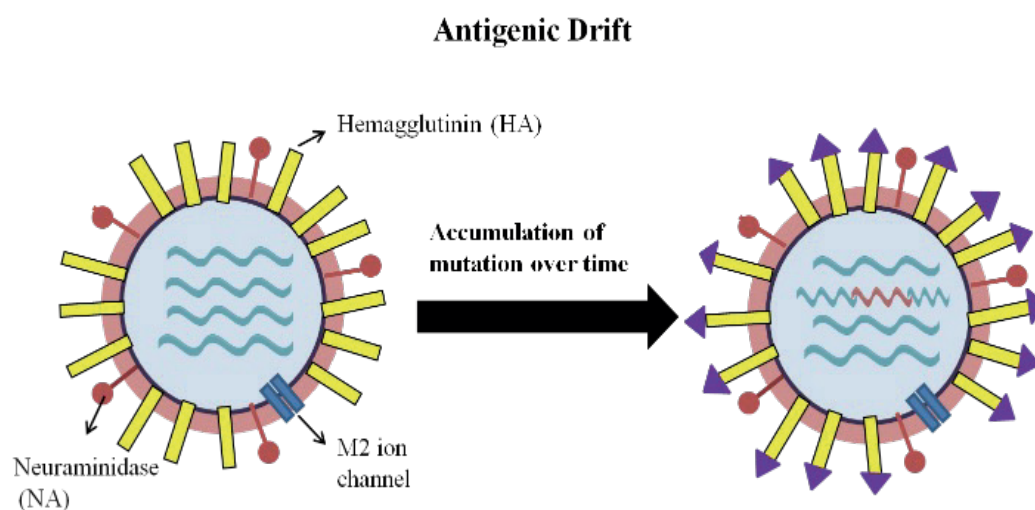


Figure 1. Antigenic drift

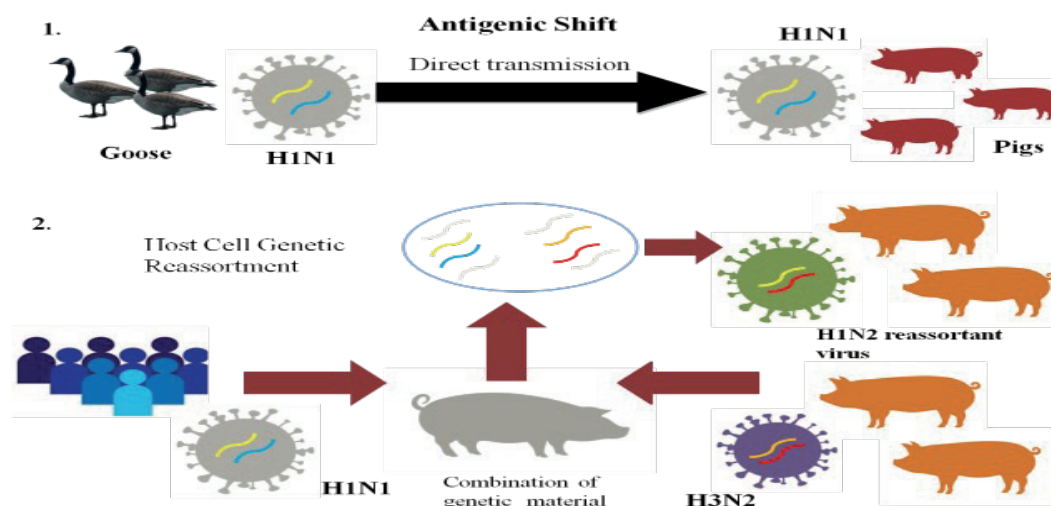


Figure 2 Antigenic shift

Disease control and management strategies

Animal disease control programs (CPs) have various advantages, including as better animal welfare and health, reducing the need for antibiotics, and increasing the safety of animal products in the event of zoonotic disease outbreaks. CPs also help to reduce direct and indirect disease losses (Hodnik et al., 2021). For ages, indigenous communities have relied on medicinal herbs as their main source of disease prevention and management for livestock. The local plants are a useful resource for illness prevention and management since the villagers are aware of their medicinal properties. Because it is easily accessible in remote locations and has the capability to cure an inclusive livestock illnesses, ethnoveterinary medicine is a highly adaptable and dynamic field that offers a more affordable option than synthetic medications (Rafique Khan et al., 2021). A few benefits of using medicinal plants to control animal disease are its affordability, convenience of usage, and little environmental effect. These plants are also a great resource for illness prevention and control since they frequently contain a variety of bioactive chemicals with antibacterial, anti-inflammatory, and immunomodulatory properties (El-Saadony et al., 2023). To effectively manage these challenges, specialized strategy plans must be developed for the prevention and control of exotic and transboundary animal diseases (TADs) (Singh, 2021). In the context of India, examples of such viral diseases include African swine fever (ASF), transmissible gastroenteritis (TGE), and swine vesicular disease in pigs, as well as Rift Valley fever, African horse sickness (AHS), West Nile fever, Eastern equine encephalomyelitis (EEE), Western equine encephalomyelitis (WEE), and Venezuelan equine encephalomyelitis (VEE). Furthermore, prion diseases such as bovine spongiform encephalopathy (BSE) and scrapie, Nipah virus, Hendra virus, SARS coronavirus, and FMD virus types 'C', 'SAT I', 'SAT II', and 'SAT III' are serious issues that need for focused prevention and control measures. Because of the distinctive dangers and challenges posed by each of these illnesses, specific strategies that are adapted to their particular traits and possible effects on agriculture, public health, and animal health are required. Through individualized strategic plans, nations can better protect their livestock, agricultural sectors, and overall biosecurity by tackling these illnesses (Yadav et al., 2020).

- **Vaccination and immunization programs**

With vaccinations available for over four hundred diseases affecting fish, birds, and mammals, vaccination is an essential approach to treating infectious diseases in livestock. Vaccines are particularly important to the livestock production businesses because they help prevent diseases like Marek's disease in poultry, Porcine Reproductive and Respiratory Syndrome (PRRS) in pigs, and

Foot-and-Mouth Disease (FMD) in cattle, sheep, goats, and pigs. Vaccinations improve livestock strength against disease by lowering or eliminating the dangerous effects of infections on their health, survival, and production. Essentially, vaccinations are essential to maintaining the health and welfare of animals, which in turn ensures the livestock sector's feasibility and profitability. Lumpy Skin disease (LSD) can be effectively controlled when there is a regional commitment to coordinate efforts aimed at limiting its spread, as demonstrated by the Balkans' successful eradication of the disease. These precautions consist of vaccinations, vaccine campaigns, trade and limited action for cattle, a feasible stamping-out program, decontamination, and vector control. The experience of the Balkans shows that eradicating LSD on a regional level is difficult but possible (Tuppurainen et al., 2021).

Vaccines containing *Clostridium novyi* can be used to help prevent economic losses in animals in cases of black disease, but controlling fascioliasis is just as crucial to the overall control strategy. Vaccination is the most effective way to stop the spread of LSD in both endemic and newly affected places. In both locations where the disease is already common and in areas where outbreaks have recently occurred, immunization is the major method of preventing the spread of LSD. The effectiveness of LSD control depends on the vaccination approach chosen, and there are differences in the value, cost, safety, and response of the vaccines that are now on the market (Ahmed, Yehia, & Ahmed, 2022; Caravedo & Cabada, 2020). To minimize the risk of an LSD outbreak, it is essential to implement biosecurity measures, enhance tracing and surveillance, conduct awareness campaigns, and administer inactivated vaccines. Since LSD is a transboundary disease, its constant appearance and reemergence in different nations raises serious concerns for animal health (Tuppurainen et al., 2021). It is crucial to maintain stringent control and prevention methods to prevent the spread of LSD, as outbreaks can have severe consequences for both animal health and the economy. *Lactobacillus casei* cells have been used to synthesize and produce ETX, a non-toxic mutant vaccine (toxoid). A vaccine made up of a bacterial suspension that expresses the recombinant protein has shown promise as an effective candidate for preventing enterotoxaemia in mice (Alimolaei, Golchin, & Baluch-Akbari, 2021). A wide range of clostridial toxoid, bacterin-toxoid, or whole culture vaccines protect against a variety of diseases worldwide animals. However, successfully arousing the host's immune system is a substantial problem in the forming of an ideal vaccination. The generation of mutants by the identification of clostridial target genes and the production of DNA vaccines are recent developments in the field of clostridial vaccines. Additionally, animal immune responses can be enhanced by novel vaccination formulations that contain suitable adjuvants, especially for toxoid vaccines. These advancements in vaccine technology have the potential to significantly improve the effectiveness of clostridial vaccines and provide better protection for animals against various diseases (Abdolmohammadi Khiav & Zahmatkesh, 2021). Canine coronavirus vaccines offer protection to young puppies, even though the disease itself is typically mild and tends to resolve on its own without intervention. In contrast, feline coronavirus infections can manifest as either mild symptoms or progress to a severe, potentially fatal immune-mediated condition known as feline infectious peritonitis. As a result, the goal of vaccinating domestic cats is to incite a protective immunological response without inducing an immune-mediated disease. Vaccines targeting bovine coronavirus are extensively utilized in cattle populations to guard against enteric and respiratory ailments in young calves (Tizard, 2020). Different vaccines used against pathogens are given in Table 3.

Table 3. Vaccines Against Various Pathogens in Different Species (Tizard, 2020).

Species	Pathogen	Vaccines	Types	References
<i>Salmonid</i>	Infectious Hematopoietic Necrosis	Apex IHN®	DNA vaccines	(Marsella et al., 2022)
<i>Canine</i>	Canine distemper virus	Recombitek® CDV	Viral vector (canarypox)	(Gong et al., 2020)
	Leishmania	Leish-Tech®	Recombinant protein	(Yasmin et al., 2022)
	Borrelia burgdorferi	Vanguard® cr Lyme	Chimeric Protein	(Izac et al., 2020)
	Leishmania	Lentifend®	Chimeric Protein	(Aida et al., 2021)
<i>Feline</i>	Feline Leukemia virus	PureVax® Recombinant FeLV	Viral vector (canarypox)	(Tizard, 2021)
<i>Equine</i>	West Nile Virus	ALVAC® -WNC	Viral vector (canarypox)	(Vrba et al., 2020)
	Classical swine fever virus	Suvaxyn® CSF Marker	Chimeric viral vector (BVDV)	(Li et al., 2022)
<i>Swine</i>	A.pleuropneumoniae	Porcilis® APP	Subunit	(Hugo Dunlop, 2021)
	Porcine Circovirus Type 2	Ingelvac CircoFLEX®	Subunit (BEVS)	(Madapong et al., 2022)
	Porcine Circovirus Type 2	Circumvent® PCV-M G2	Subunit (BEVS)	(Aida et al., 2021)
<i>Rabbits</i>	Rabbit hemorrhagic disease virus	Novibac® Myxo-RHD	Chimeric viral vector (myxoma virus)	(Mears, 2022)
<i>Bovine</i>	Bovine Herpesvirus-1	Bovilis® IBR Marker Live	DIVA vaccines/marker vaccines	(Petrini et al., 2021)
	Foot and Mouth Disease	Adt. A24 FMD	DIVA vaccines/marker vaccines	(Singh et al., 2024).

• Surveillance and early detection methods

The most effective strategy for managing AKAV (Akabane virus) involves vaccinating susceptible animals before the onset of the disease season. In Japan, a live attenuated virus vaccine has been used, while in Australia, Japan, and Korea, an inactivated virus vaccine suitable for emergency vaccination of pregnant animals has been employed. Additionally, implementing vector control measures like safeguarding breeding areas from flies, using insect repellents, and administering pesticide treatments can also be beneficial in controlling the spread of the virus.

Output-focused standards specify the desired outcomes of surveillance, rather than specifying the specific activities that must be carried out, as is the case with input-based surveillance. When applied correctly, output-based techniques can produce surveillance standards that are uniform and cross-nationally comparable. This can result in disease control programs (CPs) that are customized for each country, taking into account their specific risk factors, such as herd density, contact structure, and disease occurrence. This may result in CPs that are socially acceptable, financially feasible, and optimally designed. Because of this, output-based management can increase the security of the animal trade while enabling nations to select the best control strategies by their particular epidemiological conditions (Costa et al., 2020). The fundamental guidelines for disease management, which involve providing therapy to impacted individuals, immunizing healthy individuals and animals, restricting

animal mobility, managing animal populations, and executing test-and-cull tactics (for illnesses like anthrax, glanders, and Rift Valley fever), can likewise be utilized in the handling of zoonotic diseases (Rao & Sharma, 2023). (Rao & Sharma, 2023). It is essential to decontaminate infected materials to minimize the risk of contracting new infections (Pandey et al., 2020). Appropriate disposal of terminated pregnancies can help reduce the frequency of brucellosis. Maintaining cleanliness and utilizing protective equipment like gloves, masks, lab coats, helmets, and goggles is critical. When suitable, comprehensive disinfection of polluted materials and locations should be carried out to aid in preventing the spread of diseases such as brucellosis, salmonellosis, and tuberculosis. Addressing emerging and re-emerging zoonotic diseases necessitates collaborative and interdisciplinary efforts. Efficient monitoring depends on well-supplied laboratories, sufficient diagnostic capacities, skilled staff, and adequate funding (Rahman et al., 2020). To effectively handle extremely dangerous transboundary disease agents, BSL III and BSL IV facilities are essential to guarantee biosafety, biosecurity, and biocontainment (Brake et al., 2020).

It is essential to put into practice strict zoo hygiene protocols, such as isolating new arrivals, controlling rodents and disease-carrying insects, cleaning and disinfecting animal enclosures and the entire facility, disposing of waste properly, and managing the remains of deceased animals, to successfully regulate and restrict the spread of newly identified infectious diseases and diseases that can spread across borders between countries (Collett et al., 2020; Gongal et al., 2022).

Prompt, fast, and exact disease reporting based on diagnostic tests approved by the World Organization for Animal Health (OIE) is crucial for early identification and reaction to pathogens, stopping further transmission. To fight new foreign diseases, it is suggested to set up standard operating protocols (SOPs) and technical instructions, together with defined decision-making levels, sufficient financing, and legal backing (Yadav et al., 2020). Starting bat surveys in a specific location is vital, but it is equally important to monitor other animals living in the same natural environment either at the same time or shortly after, including possible hosts for cross-species disease transmission events (Ruiz-Aravena et al., 2022). Integrating the sampling of diverse animal categories and assessing anthropological and human behavioral hazards must be an essential component of the planning and execution stage (Saylors et al., 2021). It is essential to prioritize communities and consider societal and cultural issues in studies to ensure comprehensive surveillance (Bedson et al., 2021). Initially, monitoring at predetermined locations can provide a rough approximation of animal host species (including both bats and non-bats), host movement behaviors, and viral release. This data can guide strategic choices for establishing prolonged monitoring at suitable locations.

Using concise genetic material sequences from an updated test aids in identifying variety and tracing changes in virus excretion patterns within populations over time, whether seasonally or based on a predetermined timetable (e.g., monthly). This method allows for the observation of both the presence and variety of coronaviruses among bats and other animals or pets sampled, while also collecting ecological information to explore factors impacting viral survival. Additionally, this data can offer a fundamental assessment of the risk linked to potential transmission opportunities (Geldenhuys et al., 2021).

Spatial and temporal dynamics of animal's pathogen

• Spatial distribution patterns of pathogens

Communal resting, a phenomenon where organisms gather during their dormant hours, is observed across a multitude of species, encompassing primates, bats, birds, and even invertebrates. This behavior, also known as colonial roosting or aggregation during rest, is prevalent among an array of fauna, showcasing the diversity of this natural occurrence (Stuart et al., 2023). These social gatherings can vary in size, ranging from small groups like tent-making bats and some loosely colonial seabirds to large assemblies of hundreds or even thousands of individuals, observed in colonial seabirds, pre-murmuration roosts of European starlings, cave-roosting bats, and social bees.

The patterns of communal roosting play a significant role in infectious diseases, as the frequency of interactions can impact the likelihood of infection and the spread of pathogens. The clustering behavior within communal species has been shown to facilitate the transmission of various pathogens, such as the fungal agent responsible for white-nose syndrome in bats (*Pseudogymnoascus destructans*), phocine distemper virus in harbor seals, and West Nile virus in American crows and robins (Lunn et al., 2021). Examining the extent of spatial correlation can provide insights into how parasites disperse across landscapes and explain their modes of transmission (Turner et al., 2021). For instance, spatial correlation observed over significant distances may indicate the impact of key climatic factors, whereas proximity-based spatial correlation suggests a localized infection process. Similar investigations into wildlife diseases can help identify transmission pathways and inform disease management strategies. If scientists find that a zoonotic illness shows significant spatial connection within its animal host population, this could lead to the deployment of widely spread sampling locations to reveal environmental factors. Furthermore, the size and range of spatial connections carry consequences for the wider theoretical understanding of disease spread dynamics. The intensity and range of spatial connection are probably shaped by the traits of the hosts and pathogens in question. Pathogens that can survive in the environment for extended periods are likely to be more affected by environmental variations compared to those transmitted directly. Moreover, highly mobile creatures such as large predators or migrating bats may effectively spread pathogens throughout the environment, reducing spatial correlation (Albery et al., 2022). The movement of animals is a significant factor in the spread of the porcine reproductive and respiratory syndrome virus (PRRSV) between farms (Sanchez et al., 2023). In the United States, the swine industry is characterized by a highly interconnected network of pig movements between farms due to the vertical integration of the sector. Piglets are transported from breeding facilities to growing operations (such as nurseries, finishing units, and wean-to-finish farms) and then to slaughter, with ownership maintained throughout the production process. These movements frequently cover long distances, ranging from several hundred to thousands of kilometers, rendering the US pork industry vulnerable to outbreaks of infectious diseases. The relocation of animals is a critical risk factor for the occurrence of PRRSV (Porcine Reproductive and Respiratory Syndrome Virus), and a farm's position within the broader movement network is associated with its susceptibility to the disease. The industry's structure, which involves the transportation of pigs across vast geographical areas, facilitates the rapid spread of pathogens, posing a significant challenge to disease control and prevention efforts (VanderWaal et al., 2020).

Although climatic and meteorological factors are implicated in the appearance of certain vector-borne zoonotic illnesses (VBZDs), they are not the most frequently cited reasons. Instead, changes in land utilization are the most frequently cited factor contributing to the emergence of vector-borne and zoonotic diseases (VBZD), accounting for 26% of all VBZD illnesses. The second-largest category is unspecified or unknown drivers of emergence (14%), followed by international trade and commerce (11%), emphasizing the impact of globalization in bringing people, vectors, and pathogens into closer contact. Environmental factors, including climate and weather patterns, are the fourth leading contributor to the emergence of vector-borne and zoonotic diseases (VBZDs), accounting for 10% of the identified VBZDs examined in this research (Swei et al., 2020).

• **Temporal dynamics of disease outbreaks (seasonality, epidemical cycle)**

There are several ways in which infectious illnesses in cattle can spread. Livestock trading is one of the primary routes of transmission. The movement of livestock is especially significant because contagious animals can spread disease over great distances between locations. Therefore, when a highly contagious disease like classical swine fever breaks out, substantial trade restrictions are put in place (Cochran et al., 2023). However, the disease can spread freely through trade before the first case is discovered. This unlimited trading phase, which can last for weeks or months, is known as the "high-risk period". Among the largest pig sectors in the world is found in Germany. Germany was the third-largest pork producer in the world in 2011–2013, behind China and the

United States. Germany produces about 4.5 million tons of pork meat annually. An estimated 7 billion euros are gained in manufacturing value annually. It has been demonstrated that trading in sick pigs was the most common source of infection in subsequent outbreaks for the classical swine fever epidemics that occurred in Germany in the 1990s. Many diverse parties can be involved in the trade-related transmission of an infectious disease, such as farmers, slaughterhouses, or traders. Diverse interactions between hosts are a major element in the unequal transmission of pathogens, as infectious people can contribute to new infections in diverse ways (Arthur et al., 2017). Individual differences in behavior and other characteristics, as well as shifts in the general patterns of interaction throughout time and space, all contribute to variations in contact rates. Epidemiology is one of the fastest-growing applications of network theory. In order to understand and model contact patterns, network theory has been applied frequently. Characterizing contact networks in community contexts, like homes, schools, or hospitals, has been important recently in order to discover therapies for diseases requiring intimate touch and to forecast transmission patterns with high accuracy. There may be geographical "hotspots" for the spread of illness in confined spaces, and establishing the contact network is essential to the success of control initiatives. Rainfall, humidity, and temperature are examples of environmental factors that can either directly or indirectly affect how animal infections spread (Bett et al., 2017). For instance, warm and humid conditions may favor the survival and reproduction of certain pathogens or their vectors, leading to increased transmission rates. Similar to this, modifications to land use or habitat layout can have an impact on disease dynamics by changing the abundance and distribution of host species. Contact networks have been utilized in farm animal farming contexts to characterize vast spatial scales within or between nations in the transfer of diseases from farm to farm. Animal movement databases are utilized to create connections between farms.

Since the seminal work of Kermack and McKendrick (1927) (Guckenheimer and Holmes 1983; Strogatz 2018), much epidemiological modeling has been grounded in evaluations of deterministic, nonlinear dynamical systems. These studies have mostly focused on determining the stability of attractors, or the singular solutions to which all trajectories eventually converge, such as chaotic attractors, equilibria, or limit cycles (Schwartz and Smith 1983; Diekmann and Heesterbeek 2000; Brauer et al. 2019). The management outcomes have generally significantly improved as a result of these temporally nuanced techniques. Every node's infection risk must be evaluated in order to put effective disease control and surveillance mechanisms into place. So-called centrality measures have been defined for this aim. Among these centrality measures is the range mentioned above. The degree of a node is the most basic centrality metric, and it is simply computed by counting the number of neighbors (Krnec & Škrekovski, 2020). A member of the Flavivirus genus of the Flaviviridae family of viruses, the virus that causes West Nile virus (WNV). People have been found to contract WNV from mosquito bites. Before the mid-1990s, it was a rare illness that was originally discovered in Uganda, East Africa, in 1937. Romania saw the first significant WNV outbreak in 1996. Since then, WNV has spread around the world, becoming endemic in Asia, Africa, the Middle East, West Asia, Europe, and North America. WNV spread over all 48 of the US's continental states between 1999 and 2005, starting in New York State. WNV initially occurred in the United States in 1999 (Nash et al. 2001). By 2003, WNV had proliferated to seven Canadian provinces after being discovered for the first time in Ontario and Quebec in 2001. In humans, WNV can result in neurological illness and even death. 5674 WNV human cases were recorded in the US in 2012 alone (CDC 2013a), with 92% of cases resulting in sickness at the site and 5% (286) deaths. The primary vector of WNV, female mosquitoes, is responsible for most human transmissions. In nature, WNV is spread through a cycle that involves mosquito-bird transmission. The main WNV reservoir is birds. More than 17 native bird species in North America are known to be WNV carriers. The mosquito species that transmit WNV differ depending on the region. The most common species in the Midwest and West are *Culex quinquefasciatus* and *Culex tarsalis*, but the most common species on the east coast of North America is *Culex pipiens* (Hayes et al. 2005). It can infect horses, humans, and other mammals. The virus enters a mosquito's circulation when

it bites an infected bird. An infected mosquito, which permits the virus to infect the bloodstream and seriously sickens the victim bites a human or animal. Twenty percent or so of those infected with WNV go on to get West Nile fever. For birds and mammals, influenza (often referred to as the flu) is a common respiratory illness brought on by RNA (ribonucleic acid) viruses. Numerous influenza A viruses have their natural hosts in wild aquatic birds. Airborne influenza is spread by breathing. When someone with the virus coughs or sneezes, virus-laden droplets enter the air and can be breathed in by another person, exposing them to the infection. Hands infected with the virus can also transmit the virus. Additionally, direct touch with virus-containing bird droppings or nasal secretions as well as contact with infected surfaces can spread influenza.

Table 4. Temporal dynamics of diseases

Disease	Cause/symptoms	Animals	Distribution	Transmission	Seasonality	frequency	Reference
Japanese Encephalitis sero-complex	Encephalitis, meningitis, or meningo-encephalitis	Humans, horses, and several species of birds	Worldwide, highest in Uganda in East Africa, Africa, North America, Romania, Europe, West Asia, and the United States	Vector borne, mosquito-bird transmission Culex pipiens, Culex tarsalis. Culex quinquefasciatus	Starts in summer & continues to fall (Mid-April to November)	2,205 cases reported each year	Mencattelli, G., et.al. (2023).
Avian and Human Influenza	Depression, appetite loss, stop-laying eggs, anxious symptoms, swelling and blue staining of wattles and combs from blood circulation disruption, coughing, sneezing, and diarrhea	Wild birds, poultry, and occasionally people	Africa, North America, the Middle East, and Asia	Exposure to saliva, mucous, or feces from infected birds	Between December and February	3–5 million cases severe illness and about 250,000–500,000 deaths each year.	Huang, M. L., Wu, H. D. I., & Chao, D. Y. (2023).

Disease	Cause/symptoms	Animals	Distribution	Transmission	Seasonality	frequency	Reference
Schistosomiasis	Liver enlargement, kidney damage and bladder and ureteric fibrosis	Cattle, sheep, goats, primates, rodents & humans	Africa, the Middle East, the Caribbean, China, Indonesia, the Philippines, Brazil, Venezuela, and Suriname, as well as Corsica, France	Through snails	Rainfall		Léger, E., et.al. (2020).
Brucellosis	Oozing skin sores in horses ("fistulous withers"), mastitis and lameness in goats, and arthritis in cows and pigs.	Goat, pigs, horses, sheep cattle & buffaloes	West Asia, India, the Middle East, Southern Europe, and Latin America have the highest prevalence of brucellosis, followed by the Mediterranean basin, the Middle East, Central Asia, China, the Indian subcontinent, sub-Saharan Africa, and portions of Mexico, Central America, and South America.	Through contact with infected birthing tissues and fluids (e.g., placenta, aborted fetuses, fetal fluids, vaginal discharges), direct contact with infected animals.	Spring and summer seasons, which are the livestock's offspring seasons	500,000 cases annually	Khosnood S, et.al. (2022)

Disease	Cause/symptoms	Animals	Distribution	Transmission	Seasonality	frequency	Reference
Anthrax	high fever, muscle tremors difficult breathing, depression and sometimes swelling	domestic and wild herbivores as well as most mammals and several bird species	all over the world except Antarctica	Ingestion	rainfall leading to prolonged droughts and diminished hydrological regimes	20,000 to 100,000 cases annually	Stears, K., et.al. (2021).
Foot-and-mouth disease (FMD)	A decrease in milk production, a fever, depression, hypersalivation, appetite loss, weight loss, growth retardation, and blisters (or vesicles) on the nose, tongue, or lips, inside the oral cavity, between the toes, above the hooves, on the teats, and at pressure points on the skin	Pigs, sheep, goats, cattle, and other ruminants with cloven hooves	A few regions of South America, much of Africa, the Middle East, and several regions of Asia	Direct contact with infected animals or indirect contact with secretions or excretions (including semen and milk) from infected animals or by mechanical vectors (people, horses, dogs, cats, birds, vehicles) or air movement over land or water	Rainy season and the cold and dry season (and not in January in the middle of the rainy season)		Guerrini, L., et.al. (2019)

Conclusion:

The movement of pathogens by human activity to new areas or species, known as "pathogen pollution," poses a significant threat to both human and animal health in our interconnected world. Invasive alien species (IAS) refer to organisms like animals, plants, fungi, or microorganisms that humans have introduced to environments beyond their natural habitats. Once established, these species can disrupt local ecosystems through rapid reproduction, extensive dispersal, and adaptability to new environments. This often results in the displacement of native species and contributes to global biodiversity loss. In addition to their impact on biodiversity and economies, these translocated species can also facilitate the spread of diseases in the areas they invade (Chinchio et al., 2020). These dangerous biohazardous pathogens, like extremely virulent avian flu, hoof and mouth ailment, and brucellosis, possess the potential to greatly influence both affluent and impoverished nations, impacting animal well-being, financial stability, food protection, and public welfare

(Roth & Sandbulte, 2021). The capacity of foodborne pathogens to transfer between animals and humans, along with their capability to generate toxins leading to illnesses or fatalities, is significant enough to acknowledge the gravity of the issue (Abebe et al., 2020). Microscopic pathogens have the potential to induce illness by ingesting animal products tainted with microorganisms or their toxins (Gallo et al., 2020).

Pathogen adaptation during immunization initiatives has been noted in instances where vaccines fail to suppress pathogen populations below communicable thresholds or do not elicit protection against various antigens (Day et al., 2022). For example, oral poliovirus immunization has demonstrated a return to natural virulence as a result of adaptation, underscoring the complexities of vaccine development (Layman et al., 2021).

The possible advantageous impacts of immunization on antigenically changeable pathogens include decelerating antigenic evolution by augmenting immunity and diminishing the overall frequency or population size of the pathogen (Wen et al., 2022). The historical evolutionary progression of canine distemper virus (CDV) has resulted in occurrences of CD in immunized animals, raising doubts about the efficacy of existing vaccines. The development of CDV has been influenced by selective forces and the co-evolution of codon sites within H gene sequences, where specific residues in the H protein play a vital role in host cell penetration. These findings are instrumental in shaping investigations into vaccines and potential treatment targets (Wang et al., 2023).

Temporal dynamics of disease outbreaks can be influenced by factors such as seasonality, climate, host behavior, and pathogen characteristics (Semakula et al., 2023). Geospatial and chronological analysis tools, such as geographic information systems (GIS), spatial statistics, time-series analysis, and mathematical modeling, have been employed to investigate the dynamics of COVID-19 disease infection and dissemination. Integrating spatial and temporal analysis can offer a more holistic comprehension of the dynamics of pathogens and disease outbreaks (Cuadros et al., 2020; Owusu et al., 2022).

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