Viral Pathogens of Domestic Animals and their Impact on Biology, Medicine and Agriculture

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Abstract

Domestic animals are those animals that are tamed by humans for working purpose, for food, or as pets. In addition to providing a consistent supply of food, the domestication of animals created an environment that was also favorable to the spread of disease. Viral pathogens are the microscopic organism that causes disease in vertebrates. In both industrialized and developing nations, infectious diseases of farm animals pose a danger to agriculture and can have a significant negative impact on local, regional, and even global levels. Infectious diseases are serious dangers to animal husbandry because they affect trade, and production, and sometimes even cross species boundaries to cause zoonoses, such as bovine spongiform encephalopathy (BSE) and avian influenza. Over the past 200 years, a lot of work has been done to comprehend the pathophysiology and etiology of bacterial and viral infections that affect domestic animals. Through these investigations, new approaches to the diagnosis, management, and therapy of veterinary illnesses have been developed. Importantly, studies on veterinary pathogens have also greatly influenced our understanding of the fundamental biological functions of bacteria and viruses. Animal virus research has also contributed to discovering vaccinations. Veterinary pathogen research has occasionally transformed biology and given rise to new fields. The purpose of this chapter is to highlight the importance of viral diseases in domestic animals and how they affect agriculture, medicine and biology. Furthermore, it will emphasize how animal viruses contribute to scientific advancement and zoonotic transmission. This chapter also explains how the current understanding of pathogen biology has been greatly influenced by research on animal diseases, particularly viral diseases. Animal virology and human health are closely related, as this chapter will highlight the significance of ongoing research in this field. Research on animal viruses has also aided in the development of vaccinations for various human diseases. Additionally, some viral infections affecting agricultural animals will be described.

Keywords: Pathogens, Cattle plague, Animals, Bacteria, Virus, Infection, Vaccine, Genome.

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Introduction

The term "viral pathogenesis" refers to the process by which viruses cause illness in their host. The entirety of the ways a virus produces illness (virulence) and the host either resists or is vulnerable is the portrait of viral pathogenesis (Oldstone, 1996). The viral pathogenic mechanism includes virus implantation at the portal of entry, local replication, dissemination to disease sites (target organs) and transmission to viral shedding sites in the environment (Baron et al., 1996). Humans, animals, plants, and microbes including bacteria and archaea are all infected by viruses. Animals are frequently the intermediary hosts or natural reservoirs (hosts) for viruses that can infect humans by overcoming species barriers (viral zoonoses).

Around 10 thousand years ago, in the "fertile crescent" region of East Asia, humans started breeding what are now known as domestic animals. Domestic animals suddenly offered a steady supply of food, negating the need for man to spend time and effort hunting and gathering food (Murcia et al., 2009). The Neolithic "agricultural revolution" saw the expansion of domestication over Asia, Europe, and North Africa. This was a major discovery in human history and was essential to the formation of the majority of contemporary societies. One of the main sources of protein for a sizable section of the global population nowadays is domestic animals. But generally speaking, domestic animal species are raised more densely than those of their native counterparts in comparatively tiny (and typically constrained) settings. In the industrialized nations of today, when contemporary intensive farming sometimes gathers hundreds of animals in one place, this is especially true. Therefore, diseases like viruses and bacteria have had many chances to spread and take root in new populations as a result of domestication. Furthermore, the trading of agricultural animals both domestically and internationally contributes to the spread of contagious illnesses (Murcia et al., 2009).

Infectious diseases can result in significant harm at the local, regional, or even global level, making them one of the biggest challenges to animal husbandry today. Abortions caused by bacteria or viruses, for instance, can have a major impact on a cattle farm's calves' output. On the other hand, animal diseases can sometimes pose a threat to a nation's economy by directly affecting the efficiency of production and indirectly affecting the global commerce in animals and products generated from them. Domestic animal diseases have an impact on both animal productivity and the commerce of animals, but they can also occasionally spread to people and result in zoonoses. The avian influenza subtype H5N1 is an example of a zoonosis that poses a significant risk of pandemic and has been shown to cause fatalities. Consuming tainted food can expose people to BSE, which is a prion disease that mostly impacts cattle. Millions of pounds were also estimated as the economic damages resulting from the BSE incident that occurred in the United Kingdom during the 1990s. Not all zoonoses are found in producing animals; for example, the human immunodeficiency virus (HIV), which causes AIDS, is spread from African primates to humans through cross-species contact (Murcia et al., 2009). To highlight the significance of viral pathogens on domestic animals and to study their impact on biology, medicine, and agriculture.

Animal Disease Studies and Its Impact on Medicine and Pathogen Biology

Numerous scientific advances and changes in biological perspectives have resulted from research on farm animal diseases. Up to the eighteenth century, cattle plague, often known as rinderpest, decimated livestock throughout Europe for hundreds of years. The effects of the cattle plague were so severe during the previous century that Pope Clement XI sent his doctor, Giovanni Maria Lancisi, instructions to create ways to prevent the sickness (Taylor, 2005). One of Lancisi's suggestions was to kill any sick or suspicious animals and then bury them in lime. The hygienic methods that we use today to prevent the transmission of diseases the need for quarantine, restrictions on movement of animals, and the killing of afflicted animals are strikingly similar to those that Lancisi developed (Bodjo et al., 2024).

Rinderpest is linked to other significant scientific discoveries. During a rinderpest outbreak in 1768, Geert Reinders, a self-taught Dutch farmer, was initially the first to understand the idea of "maternal immunity" and to observe that cattle who had already suffered from the natural illness (or minor symptoms) were immune to disease and infection in the future. This finding was released long before Jenner's seminal cowpox research as an extra measure to combat the disease, the clinical thermometer was ingeniously created to detect fever in animals that were thought to be rinderpest-affected (Spinage, 2012).

Some diseases that only directly affect humans have an indirect connection to domestic animals. The etiologic agent of smallpox, variola virus (VARV), has unknown origins, however it is thought to have originated from an ancestor poxvirus that afflicted animals in the initial agricultural colonies in Africa or Asia remarkably. The father of the smallpox vaccine is Edward Jenner, a country doctor from Berkeley, Gloucester, England. Jenner noted in 1796 that cowpox, when applied topically, protected against smallpox (Breman, 2021). It was shown that cowpox infection was protected against smallpox since variolated people often developed a moderate form of the illness (Ochmann et al., 2018). A new era in medicine began with this procedure. Vaccination as a means of preventing smallpox and later other infectious diseases was quickly adopted, despite early opposition to Jenner's techniques. Pasteur created the first attenuated vaccine to prevent chicken cholera, which is caused by Pasteurella multocida. He also created vaccinations to prevent rabies and anthrax, two deadly zoonoses. The creation of a TB vaccine was associated with the success of the smallpox vaccine. Robert Koch later discovered that Mycobacterium bovis, the causative agent of bovine tuberculosis, could be distinguished from Mycobacterium tuberculosis, the causative agent of human tuberculosis. Bovine tuberculosis was originally identified in 1854 the idea that the same approach that worked for smallpox could be used to create an effective vaccination for TB in humans resulted from this. Early attempts to use newly identified strains of M. bovis, however, failed since they were just as virulent as M. tuberculosis. The development of the M. bovis BCG (Bacille Calmette-Guérin) vaccine strain by veterinarian Camille Guérin and physician Albert Calmette demonstrated the veterinary role in creating an effective TB vaccine. This strain, which took more than 13 years to create and was eventually suitable for use in 1921, was highly passaged and had very little pathogenicity. More than 200 years after Jenner's groundbreaking research, vaccination remains our most effective defense against infectious diseases that affect both domestic animals as well as humans(Murcia et al., 2009)

Rotaviruses, are the primary cause of diarrhea in infants and children worldwide, and in developing nations specifically, offer an intriguing example of viruses discovered in animals before being discovered in humans. Rotaviruses were linked to diarrhea in calves long before this link was discovered in humans (Palmarini, 2007).

In the early 20th-century, research on chicken viruses produced important findings that ultimately revealed the genetic basis of cancer. In those early investigations, cell-free filtrates were used to transfer malignancies to animals. Peyton Rous demonstrated that viral etiology was also seen in chicken sarcomas in 1911, while Olaf Bang and Vilhelm Ellerman found that chicken erythroleukemia was brought on by a virus in 1908 (Murcia et al., 2009). Unfortunately, at the time, leukemias were not recognized as cancer, and chickens were not thought to be a suitable animal model for studying human diseases, thus those studies did not get the recognition they merited. To measure the RSV-Rous sarcoma virus (a virus that Rous identified) in tissue culture, Harry Rubin and Howard Temin created the focus assay in the 1950s. Because it showed the relationship between a single cell's biological activity and that of an infectious viral particle, this assay completely changed the way that RSV is studied. It was later discovered that RSV had an "oncogene," or cell-derived gene, that was adequate to cause cell transformation. This was a significant finding since it demonstrated that the "secret" of cancer was contained in the cell's DNA. Thus, research on chicken viruses led to the discovery of the genetic basis of cancer. Being both the first tyrosinekinase and the first oncogene to be identified, the RSV oncogene, v-src, had a significant impact and helped establish whole fields like signal transduction (Murcia et al., 2009).

The public is most likely most familiar with OPA (Ovine Pulmonary Adenocarcinoma), sheep's other slow disease, because it was responsible for the death of Dolly, the first nuclear- transferred cloned mammal. Jaagsiekte sheep retrovirus (JSRV), the retrovirus that causes OPA, is the only oncogenic retrovirus (is generally the only oncogenic virus) that has been shown to have a structural protein (the envelope of the virus) that acts as a dominant oncogene both in vivo and in vitro (Caporale et al., 2006). Fundamental research on the biological roles of endogenous retroviruses in the evolution of mammals was also spurred by the JSRV/OPA paradigm. Ancient remnants of

retrovirus infections that are firmly incorporated into the genomes of all animal species are known as endogenous retroviruses. Studies on JSRV-related sheep endogenous retroviruses showed in vivo that these viruses can be essential for host placentation and conceptus formation (Dunlap et al., 2006).

Research on the papillomaviruses of dogs, cattle, and rabbits has given researchers the theoretical foundation for identifying human papillomaviruses as the causative agents of certain cutaneous cancers and the vast majority of cervical malignancies (Gissmann et al., 1984). The evidence of principle obtained in the development of vaccines against animal papillomaviruses is the foundation for the current, widely reported vaccine against human papillomavirus (Palmarini, 2007).

Another significant source of zoonosis is animal viruses. Considering that 75% of human illnesses are thought to be zoonotic in the roots, the recent zoonotic cases of Hendra and Nipah virus, and most importantly avian influenza are just a few examples of infectious agents that can spread from animals to humans without prior "warning" (Taylor et al., 2001).

Major Farm Animal Viral Illnesses

Foot and Mouth Disease (FMD)

Out of the most fearsome illnesses affecting agricultural animals is most likely FMD. A highly contagious disease, foot-and-mouth disease (FMD) affects animals with cloven hooves, such as cattle, pigs, sheep, goats, and several wild species (Diaz-San Segundo et al., 2017). Fever, inappetence, lameness, and the development of vesicular lesions in the mouth, feet, nares, and teats are hallmarks of the disease (Arzt et al., 2014).

Foot and mouth disease is caused by the foot-and-mouth disease virus (FMDV), which belongs to the Picornaviridae family of the Aphthovirus genus. It is a tiny, icosahedral, non-enveloped, single-stranded RNA virus with a diameter of 26 nm (Admassu et al., 2015) and has seven different serotypes of FMDV (Foot and Mouth Disease Virus), including O, A, C, Asia-1, and South African Territories (SAT-) 1-3, as well as other subtypes because of the virus's rapid rate of mutation. Large regions of Africa and Asia are endemic to FMD; however, Europe, North America, and Australia can keep their free status without vaccination due to stringent regulations on the entry of animals and agricultural products. By carrying out massive vaccination campaigns and surveillance, South American nations have made significant investments in FMD control in recent years, moving closer to the goal of FMD elimination. The majority of nations follow the World Organization for Animal Health's Terrestrial Code in addition to the direct effects on animals and associated industries (Diaz-San Segundo et al., 2017). Following the conclusion of these outbreaks, no new cases of FMD have been reported in America. There is variation in the distribution of FMDV serotypes in endemic areas. Only three serotypes (O, A, and C) have ever been recorded in South America, while reports from Asian countries have focused on four serotypes (O, A, C, and Asia-1) and six of the seven serotypes (O, A, C, and SAT 1-3) have been found in Africa. Even though FMDV serotype C has traditionally been found throughout the world, no outbreak has involved it since 2004 (Knight-Jones et al., 2016). Cattle that have successfully recovered from the infection and those that are FMDV carriers have identical serological profiles (Eschbaumer et al., 2016). Therefore, employing a specialized sputum cup (probang) to recover infectious viruses from oropharyngeal fluid and scrapings is the standard method for identifying carriers (Stenfeldt et al., 2016). However, probang sampling's ability to identify persistently infected cattle among previously exposed animals is not dependable for identifying FMDV carriers after an outbreak. Despite ongoing debate on the epidemiological significance of the FMDV carrier state in cattle, the presence of a protracted subclinical phase of infection has had a significant impact on current disease control strategies (SUTMOLLER & CASAS OLASCOAGA, 2002).

FMD is a serious risk to sheep. Although it can be challenging to identify clinical symptoms in this species, they also develop foot-andmouth lesions and viremia. Furthermore, some infected animals may not exhibit any clinical symptoms. Because of this, sheep were crucial to the 2001 outbreak in the UK, helping to spread the illness before it was identified clinically. A humoral response is quickly developed in animals that are infected or vaccinated. Serotype-specific protection against reinfection or, in the case of vaccination, against infection is provided by high quantities of neutralizing antibodies that target the exterior structural proteins. Following the acute stage of FMD, sheep, goats, and cattle may continue to be infected for a varied amount of time without showing any symptoms. Vaccinated animals may have a similar situation following infection. The reason these animals are considered "carriers" is that, even in the presence of large levels of neutralizing antibodies, infectious viruses can be readily identified in pharyngeal scrapings, suggesting that they could be important in an outbreak scenario. According to standard definitions, a carrier is an animal that can be used to isolate a live virus 28 days after infection. African cattle and buffalo can carry the virus for up to three years and five years, respectively, however, the duration of the carrier state period varies. Pigs have not been reported to exhibit the carrier condition, but sheep and goats have (up to 9 months and 4 months, respectively) (Murcia et al., 2009).

Control of FMD in ruminant species is made more difficult by the prevalence of a subclinical chronic infection known as the FMDV carrier state (Stenfeldt et al., 2016). Animals classified as FMDV carriers are those who release infectious viruses in their oropharyngeal fluid (OPF) more than 28 days after infection (Kompasa et al.). Recent research, however, indicates that the difference between calves who recover from FMDV infection and those who continue to suffer from it happens before the already established threshold. Particular areas and specialized epithelial cells of the bovine nasopharynx or related lymphoid tissue have been identified as permanent FMDV sites (Stenfeldt et al., 2016).

Viral isolation and identification are necessary for the diagnosis of FMD in a nation free of the illness. Fast and precise diagnostic assays for FMDV are required; these tests should be able to distinguish between vaccinated and infected animals as well as identify animals that are permanently infected. New vaccines are needed for control, and they are presently being created and evaluated. To identify the best control measures to implement in the wide range of situations that may arise during an FMD outbreak, accurate epidemiological models are also required (Murcia et al., 2009). Figure 1 shows the symptoms of FMD (Foot and Mouth Disease) in animals.

Fig. 1: Foot and Mouth Disease.



Salivation associated with vesicles in mouth





Vesicles on tongue and oral cavity



Vesicles on limb

Ruptured vesicle found on tongue

Rinderpest

One of the most dreaded diseases affecting cattle is rinderpest, also known as cattle plague. It is categorized as one of the transboundary animal illnesses that can spread quickly and have severely adverse consequences. In vulnerable herds, the mortality rate might reach 100%, which can have major socioeconomic impacts (Tounkara & Nwankpa, 2017). The Rinderpest virus belongs to the Paramyxovirinae subfamily of the genus Morbillivirus, and family Paramyxoviridae. The viral genome, which is around 15.8 kb in size and is composed of single-stranded, nonsegmented, negatively polarized RNA, envelops the viral particles. Cattle, sheep, goats, and water buffaloes are among the susceptible domestic animals. The disease also naturally occurs in a variety of wild animals, including giraffes, antelopes, deer, hippopotamuses, eland, kudus, and wildebeest (Furuse et al., 2010).

Clinical symptoms usually manifest 3–5 days after infection, and in susceptible groups, morbidity and mortality rates can reach 100% (mortality is lower, about 50%, in African indigenous breeds). There are three stages to the disease's clinical manifestation. Hyperthermia occurs quickly during the prodromal phase, which is followed by the mucosal phase, which is characterized by anorexia, depression, and mucopurulent discharges from the eyes and nose. Severe hemorrhagic diarrhea, dehydration, and death are the hallmarks of the disease's terminal stage (affected animals often die 6–12 days after symptoms start). The tonsils and nearby lymph nodes undergo replication after the infection is first started in the upper respiratory tract, typically through the nasal entrance. The virus then uses lymph and blood to propagate to additional lymphatic tissues. Following this stage, rinderpest can be easily found in the lungs, digestive tract, and all of the aforementioned organs. Necrosis and erosions brought on by viral replication in the nasal mucosa are similar to the clinical manifestations seen during the disease's mucosal phase. Viral multiplication that destroys lymphoid organs causes severe immunodeficiency and opportunistic infections. The virus replicates in the gut mucosa, resulting in the bloody diarrhea seen in the last stages of rinderpest. Through direct contact with aerosol droplets made from secretions from the throat, nose, and conjunctiva, infected animals spread the disease. Additionally, the virus is excreted in milk, urine, and feces. The virus's thermolability makes indirect transmission unlikely (Murcia et al., 2009).

Although the OIE has not yet publicly recognized this, it is currently believed that rinderpest may have been eradicated worldwide. The Global Rinderpest Eradication Program (GREP), which was started in 1993 by the Food and Agriculture Organization (FAO) with assistance from UNICEF and other government organizations, marked the beginning of this tremendous accomplishment. Since rinderpest had already been eliminated in Europe and had never been developed in the Americas, this initiative combined genetic and seroepidemiological research with widespread immunization in Asia and Africa. Serosurveillance studies indicate that this once-feared disease may no longer exist, and immunization has been discontinued. If successful, eradicating rinderpest would likely be the greatest significant achievement in veterinary medicine's history (Murcia et al., 2009). Figure 2 shows the symptoms of rinderpest.

Influenza

The influenza virus is a member of the Orthomyxoviridae family of enveloped viruses. Based on antigen variations in their matrix protein and nucleoprotein, influenza viruses A (alpha), B (beta), C (gamma), and D (delta) are the four genera that infect vertebrates (Nuwarda et al., 2021). The virus that causes the most serious respiratory illness or mortality is by far type A. It may potentially trigger a global pandemic and the start of a fresh influenza outbreak. Human seasonal flu is also caused by influenza B viruses. The seasonal flu shots contain the two influenza B lineages that are currently in circulation, B/Yamagata and B/Victoria (Klimov et al., 2012). In contrast, influenza D viruses have been shown to infect cattle and sheep but have not been linked to human illness. Influenza C viruses typically induce minor symptoms and are not known to cause an epidemic (Asha & Kumar, 2019). Influenza A viruses are classified into subtypes

according to two proteins found on their surface: neuraminidase (N) and hemagglutinin (H). There are 11 distinct neuraminidase subtypes (H1 through H18 and N1 through N11, respectively) and 18 distinct hemagglutinin subtypes. Although over 130 influenza A subtype combinations have been found in nature, mostly in wild birds, there may be many more due to the tendency of the virus to "reassort." Influenza viruses exchange gene segments through a process known as reassortment. When two influenza viruses simultaneously infect a host, they may reassort their genetic makeup (Mandel, 2020).



Fig. 2: Symptoms of Rinderpest

Oral mucosa.

numerous small gingival erosions

Aerosol infections, or rather large droplets (>5 µm) produced, especially while coughing or sneezing, are thought to be the primary way that influenza viruses spread (Murcia et al., 2009). These droplets reach the mucosae by contact at close range. However, other articles have also proposed that transmission could be caused by so-called droplet cores, which are smaller (less than 5 µm) and have the ability to stay in the air for longer (aerogenic transmission). Furthermore, direct contact with virus-contaminated surfaces and subsequent mouth-nose contact might spread the infection. The viruses multiply in the laryngeal and nasal mucosae after infection. As the illness worsens, this replication also impacts the lower airways (Blümel et al., 2008).

There is strong evidence that humans can contract avian influenza viruses (AIVs) from birds through zoonotic transmission. The most prevalent AIVs in humans are many H7 and H5 strains, which can occasionally result in mild and asymptomatic infections but frequently cause severe illness (Khuntirat et al., 2011). As demonstrated by routine serological surveillance for H5 and H7 in people, exposure to diseased or deceased birds is the primary cause of AIV infections in humans (Sikkema et al., 2016).

The World Health Organization (WHO) coordinates several influenza centers where epidemiological, antigenic, and genetic data are produced and evaluated, ensuring that influenza viruses are continuously monitored on a global scale (Murcia et al., 2009).

Conclusion

Research on veterinary infections over the years has been crucial in understanding the biology of bacteria and viruses. Investigation of farm animal pathogens led to the discovery of new human infections and laid the groundwork for entirely new fields. The economics of both developed and developing countries, as well as agricultural and animal health, are still greatly impacted by viral and bacterial diseases of domestic animals, despite the last 200 years of scientific and technological progress. Environmental and climatic changes may have an impact on how different animal species interact with humans and with one another. These alterations may favor the reemergence of old infections or the emergence of new ones. For this reason, funding veterinary pathogen research and surveillance is crucial to preserving and improving the health of both humans and animals.

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