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ABSTRACT

Zoonotic respiratory illnesses have played a significant role in shaping human history and continue to pose global health challenges by crossing over from animals to humans. This abstract investigates the historical significance of diseases and the current dangers they pose, with a focus on specific examples and their consequences. Throughout history, respiratory pandemics that have caused widespread devastation have been triggered by infectious agents originating from various animal sources. The 1918 Spanish Flu, which originated from an H1N1 influenza A virus with mixed avian and swine origins, serves as a notable illustration of the effects of zoonotic respiratory illnesses. Tuberculosis, caused by a bacterial infection, has demonstrated the ability to cross from cattle to humans, showing zoonotic potential with *Mycobacterium bovis*. New dangers in the current world consist of illnesses such as MERS and Avian Influenza. MERS, which is caused by a type of coronavirus, has been connected to dromedary camels, emphasizing the ongoing danger of animals passing diseases to humans. Constantly looming threats, avian flu variants such as H5N1 and H7N9 originate from wild birds as their natural hosts. The effects of zoonotic respiratory diseases are displayed through the COVID-19 pandemic, which is a result of the SARS-CoV-2 virus. Bats are thought to be the original source of the virus, and it is likely passed on to other animals before reaching humans. Confronting these difficulties requires a comprehensive and collaborative strategy. The integration of human, animal, and environmental health is essential for effective surveillance and mitigation strategies, known as the One Health approach. Effective collaboration on a global scale, sharing of data, and comprehending the factors involved in the transmission of zoonotic diseases are essential for preventing and managing these illnesses. In light of continued challenges with respiratory diseases that can be transmitted from animals to humans, it is essential to take a proactive and multidisciplinary approach to safeguard human health from these changing dangers.

Keyword: Zoonotic Respiratory Diseases; Historic Impact; Emerging Threats; Pandemics; One Health Approach

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INTRODUCTION

Zoonotic respiratory diseases are illnesses caused by microorganisms found in animals that can be transferred to humans via the respiratory system. Due to their potential to produce pandemics and global health catastrophes, such as COVID-19, these diseases have escalated in significance recently. The transmission of these diseases is often facilitated by modern transportation systems, cross-border trade, and increased human encroachment into natural habitats, leading to massive contact with wildlife (Chomel 2014, McFarlane 2015, Hassell et al. 2021). Various pathogens, including viruses, bacteria, and fungi, are responsible for causing zoonotic respiratory diseases. COVID-19, SARS, MERS, and avian influenza are the most common zoonotic respiratory diseases. The COVID-19-causing SARS-CoV-2 virus is assumed to have emerged in bats and spread to humans, potentially via an intermediate animal host. Similarly, coronaviruses causing SARS and MERS are also thought to have originated from bats and spread to humans via the carriers like civets and camels, respectively (Contini et al. 2020). The influenza viruses that cause bird flu, also known identified as avian influenza, are mostly found in birds. Humans can get the disease by coming into contact with infected domestic or wild birds (Peiris et al. 2016).

Many routes exist for spreading zoonotic respiratory disorders, including physical contact with sick animals or their waste, intake of infected animal products, and inhaling particles carrying the pathogen. For instance, when an infected individual talks, sneezes or cough, COVID-19 spreads by respiratory droplets. Another person may inhale these droplets and become infected. Some zoonotic respiratory diseases can also spread by touching contaminated surfaces like door handles or utensils or touching bodily secretions from contaminated persons or animals (Karesh and Noble 2009, Rehman et al. 2009). Zoonotic respiratory diseases can present with a range of symptoms, although they typically involve fever, irritable throat, cough, body pains and difficulty breathing. In certain situations, the disease can escalate to more chronic disorders, such as acute respiratory distress syndrome (ARDS), pneumonia, and even death. Early diagnosis and treatment are vital in preventing the spread of zoonotic respiratory diseases and minimizing the severity of symptoms. Treatment options may include antiviral medications, antibiotics, and supportive care to manage symptoms. Vaccines may also be available for certain zoonotic respiratory diseases, such as avian influenza (Warwick and Corning 2013, Rahman et al. 2020). The summary of various respiratory zoonotic diseases is enlisted in Table 1.

Prevention measures for zoonotic respiratory diseases include avoiding contact with infected animals, practicing good hygiene such as hand washing and wearing masks, and following food safety guidelines when handling animal products. To prevent the spread of these diseases, public health officials may take measures like imposing travel restrictions or implementing quarantine protocols. Ongoing surveillance and research into these illnesses are vital to comprehend their origins, pattern of transmission and possible treatment (Bender and Shulman 2004, Rahman et al. 2020, Ziarati et al. 2022). Zoonotic respiratory diseases impose a major threat to global public health and require a collaborative, multidisciplinary approach to prevention and treatment. Early identification, quick intervention, and continuous surveillance and research work are all part of the effort to prevent and manage these illnesses. More investment in public health infrastructure and research, as well as a better knowledge of the processes that contribute to the genesis and spread of zoonotic infection, are necessary to avoid future outbreaks and preserve public health (Nantima et al. 2019, Milbank and Vira 2022).

2. HISTORICAL PERSPECTIVE OF ZOONOTIC RESPIRATORY DISEASES

Zoonotic Respiratory illnesses have caused some of the most catastrophic global pandemics in history, leading to a crucial impact on mortality rates worldwide. With an estimated one-third of the planet's population affected and at least 50 million documented deaths, the 1918 influenza outbreak ranks

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Table 1: Summary of Zoonotic Respiratory Diseases: Causative Agent, Animal-Host Species, Mortality Rate, and Global Prevalence.

Disease	Causative Agent	Animal-Host Species	Mortality Rate	Global Prevalence
Anthrax	<i>Bacillus anthracis</i> bacterium (Omodo et al. 2023)	Cattle, sheep, goats (Omodo et al. 2023)	45-80% (Stratilo et al. 2020)	Africa: (Romero-Alvarez et al. 2020) Asia: (Sushma et al. 2021) Europe: (Sushma et al. 2021) Middle East: (Dogany and Metan 2009) North America: (Jernigan et al. 2002)
Avian influenza	<i>Influenza A virus</i> (Mosaad et al. 2023)	Chickens Turkeys Wild waterfowls (Mosaad et al. 2023)	60% (Camphuy sen et al. 2022)	Asia: (Sims et al. 2005) Europe: (Atkinson et al. 2006) Africa: (Brown 2010) North America: (Pasick et al. 2012)
Bovine tuberculosis	<i>Mycobacterium bovis</i> bacterium (Abrantes and Vieira-Pinto 2023)	Cattle animals (sheep, goats) Domesticated animals (cats, dogs) Wild animals (deer, bison, badger) (Kasir et al. 2023)	16% (Nakayiza, Walekhwa et al. 2022)	Africa: (Ayele et al. 2004) Europe: (Yahyaoui-Azami et al. 2017) North America: (Yahyaoui-Azami et al. 2017) South America: (Arnot and Michel 2020)
Brucellosis	<i>Brucella</i> bacterium (Jokar et al. 2023)	Cattle animals (sheep, goats, pigs, cows) Domesticated animals (dogs) (Jokar et al. 2023)	<5% (services 2004)	Africa: (Ducrottoy et al. 2017) Asia: (Thimm 2013) Middle East: (Musallam et al. 2016) Central & South-east Europe: (Taleski et al. 2002)
Camelpox	<i>Camelpox virus</i> (Gieryńska et al. 2023)	Camels (Gieryńska et al. 2023)	28% (Jezek et al. 1983)	Middle East: (Balamurugan et al. 2013) North Africa: (Zhgunissov et al. 2021) Central Asia: (Afonso et al. 2002) South Asia: (Venkatesan et al. 2018) East Africa: (Kriz 1982)
Hantavirus pulmonary syndrome	<i>Hantavirus</i> (Sundar et al. 2023)	Rats Mice (Avižiniienė et al. 2023)	30-40% (Thorp et al. 2023)	North and South America: (Hjelle and Glass 2000) Europe: (Vaheri et al. 2013) Asia: (Kruger et al. 2015) Africa: (Witkowski et al. 2014)
Hendra virus infection	<i>Hendra virus</i> (Tomori and Oluwayelu 2023)	Horses Flying foxes (fruit bats) (Wang et al. 2023)	50-100% (Marsh and Wang 2012)	Australia: (Field et al. 2010)
Middle east respiratory syndrome	<i>MERS coronavirus (MERS-CoV)</i> (Azhar et al. 2019)	Camels (Azhar et al. 2019)	20% (Park et al. 2018)	Middle East: (Memish et al. 2014) Europe: (Zumla et al. 2015) Asia: (Hui et al. 2015) South Korea: (Cowling et al. 2015)
Monkeypox	<i>Monkeypox virus</i> (McCollum and Damon 2014)	Rats Monkeys (El Eid et al. 2022)	1-10% (Parker and Buller 2013)	Central & West Africa: (Pastula and Tyler 2022)
Nipah virus infection	<i>Nipah virus</i> (Shariff 2019)	Flying foxes (fruit bats) Pigs (Soman et al. 2020)	40-90% (Alam 2022)	South East Asia: (Hossain et al. 2008)

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Pasteurellosis	<i>Pasteurella multocida bacterium</i> (Register and Brockmeier 2019)	Cattle animals (sheep, goat) Domesticated animals (cat, dog) Wild animals (rabbits, rodents) (Mohamed and Abdelsalam 2008)	<10% (Reinsch et al. 2008)	North America: (Snyder and Credille 2020) Asia: (Brickell et al. 1998) Europe: (Magariños et al. 1996) Africa: (Miller 2001)
Plague	<i>Yersinia pestis</i> (Kool and Weinstein 2005)	Rats Mice Squirrels (Smiley 2008)	≥90% (Pechous et al. 2016)	Central Asia: (Tsuzuki et al. 2017) Africa: (Duncan and Scott 2005) Europe: (Bramanti et al. 2019)
Psittacosis	<i>Chlamydia psittaci</i> (Stewardson and Grayson 2010)	Parrots Cockatiels Parakeets Pigeons Poultry (Jorgensen 1997)	<1% (Chu et al. 2019)	North and South America: (Chu et al. 2019) Asia: (Matsui et al. 2008) Australia: (Elliot 2001) Europe: (Rehn et al. 2013)
Q fever	<i>Coxiella burnetii bacterium</i> (Woldehiwet 2004)	Cattle animals (sheep, goats) (Hirschmann 2019)	1-2% (Parker et al. 2006)	Australia: (Sloan-Gardner et al. 2017) Europe: (Georgiev et al. 2013)
Severe acute respiratory syndrome	<i>SARS coronavirus (SARS-CoV)</i> (Lam et al. 2003)	Bats Civet cats (da Costa et al. 2020)	10% (Anderson et al. 2004)	Asia: (Curley and Thomas 2004) Europe: (Worobey et al. 2020) Australia: (Rockett et al. 2020) North America: (Worobey et al. 2020) South America: (Poterico and Mestanza 2020) South Africa: (Pulliam et al. 2022)
Swine flu	<i>Influenza A virus</i> (Perez-Padilla et al. 2009)	Pigs (Parmar et al. 2011)	2-20% (Singh and Sood 2012)	North America: (Sinha 2009) East & South-east Asia: (Trevenec et al. 2011) Europe: (Klemm et al. 2016) Africa: (Butler 2009) Australia: (Webb and Seppelt 2009)
Pneumonic tularemia	<i>Francisella tularensis Bacterium</i> (Reed et al. 2011)	Domesticated animals (cats, dogs) Wild animals (rabbits, rodents, squirrels, beavers) (Matyas et al. 2007)	30% (Penn and Edwards 2019)	North America: (Matyas et al. 2007) Europe: (Maurin and Gyuranecz 2016) Asia: (Matyas et al. 2007)

among the worst pandemics in history. The source of the 1918 influenza virus is unclear, although it is hypothesized to have been patented in birds before spreading to humans, potentially through a middle host like pigs. The 1918 influenza affected many young adults, with an estimated 99% of deaths occurring in people under 65. The severity of the pandemic worsened by the close living conditions of soldiers in World War I, which facilitated the speedy spread of the disease (Morens and Fauci 2007, Short et al. 2018). The Severe Acute Respiratory Syndrome (SARS-2003) outbreak resulted in a considerable upsurge in mortality. The virus, alleged to started in bats and spread to people through civet cats in China, is to blame for the SARS pandemic. The outbreak resulted in 8,096 confirmed cases and a total of 774 deaths in 26 countries, with a mortality rate of approximately 10% (Matus et al. 2023,

McGarity-Palmer et al. 2023). Similarly, the 2012 Middle East Respiratory Syndrome (MERS) pandemic had a mortality impact. The coronavirus that causes MERS; originated from camels before infecting humans. The outbreak resulted in 2,494 cases and 858 deaths across 27 countries, with a mortality rate of approximately 34% (Alsaadi et al. 2023, Mohapatra et al. 2023). Recently, the COVID-19 pandemic has been having a significant impact on mortality rates over the world. As of March 2023, there were around 590 million confirmed illnesses and nearly 14 million fatalities worldwide. Before infecting humans, the coronavirus that causes COVID-19 was first appeared in bats, maybe via an intermediary host like pangolins. The mortality rate of COVID-19 varies depending on age, underlying health conditions, and access to medical care. Overall, the estimated global mortality rate is approximately 2%, with higher rates among older adults and those with underlying health conditions (Haruna et al. 2023, Qureshi et al. 2023).

Studying zoonotic respiratory diseases is an imperative study of literature because of the increasing risk posed by these types of infections. With the increase in human activities that bring people and animals into closer contact, such as deforestation, urbanization, and wildlife trade, the risk of diseases jumping from animals to humans is more substantial than ever. Zoonotic respiratory infections, especially avian influenza, MERS, and SARS, are potent to cause devastating outbreaks and pandemics, as evidenced by the current COVID-19 pandemic. By investigating zoonotic respiratory diseases at the animal-human interface, we can better understand the transmission mechanisms, risk factors, and prevention strategies for these diseases, ultimately helping to reduce their impact on human and animal health. This chapter also incorporates policies and practices that aim to promote more sustainable and responsible interfaces between humans and animals, thus mitigating the threats of future zoonotic disease outbreaks.

2.1. ANTHRAX

Anthrax is a disease that affects animals but can potentially infect people. It is caused by the bacteria *Bacillus anthracis*. Meanwhile, the disease is typically contracted by contact with diseased animals, their waste products or soil polluted with the bacteria's spores and is classified as a zoonotic illness. *Bacillus anthracis* produces spores that can remain viable in the environment and animal products for many years. The spores can live in hostile conditions because of their excellent heat, chemical, and radiation resistance (Omodo et al. 2023). Anthrax contracts by inhaling, ingesting, or exposure to the spores. Anthrax spreads to people through contact with diseased animals or animal yields, including meat, hides, and wool. Inhalation anthrax can occur when spores are inhaled, usually from contaminated animal products or soil. Cutaneous anthrax can occur when spores enter through a cut or abrasion in the skin. Gastrointestinal anthrax can occur when spores are ingested, usually through contaminated meat (Chanda et al. 2023). Flu-like symptoms, including fever, muscle cramps and fatigue are typical symptoms of inhalation anthrax, followed by respiratory distress and shock. A raised, itchy lump that turns into a pain-free ulcer, encircled by a black region of dead tissue, resulted from cutaneous anthrax. Gastrointestinal anthrax can induce nausea, abdominal pain, vomiting and bloody diarrhea (Pradhan and karanth 2023).

Anthrax significantly impacted human history and was responsible for several deadly outbreaks. One of the most well-known outbreaks occurred in the late 19th century in Scotland, where a herd of sheep caused the death of several hundred people. More recently, in 2001, an epidemic in the US, believed to be a bioterrorism attack, resulted in 22 cases and 5 deaths (Parker Jr 2023). The utilization of anthrax as a bioweapon by terrorist organizations or rogue nations, which results in widespread disease and fear, is one of the biggest concerns. The likelihood of a bioterrorism assault might rise, resulting from the

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development of artificial genetic and biological engineering that could make it simpler to manufacture and alter more deadly or drug-resistant anthrax strains. Antibiotic resistance is a different danger that makes treating anthrax infections more difficult. In areas with weak veterinary and public health infrastructure, natural epidemics can happen when people come in contact with diseased animals or their products. The spread of infectious illnesses can mitigate by tracking and researching anthrax, creating new vaccinations and treatments, upgrading the infrastructure of public health and fostering more international collaboration (Doganay and Demiraslan 2015).

2.2. AVIAN INFLUENZA (BIRD FLU)

Influenza A causes avian influenza is a viral pathogen. The disease is commonly referred to as bird flu as it affects birds. It is infectious and it can rarely transfer to people resulting in fatal respiratory infections (Mosaad et al. 2023). Avian influenza is an illness caused by *Influenza A* strain that mainly infects birds. Avian influenza viruses have different subtypes, with the H5N1 genotype being the most well-known for having the ability to sicken humans severely (Qureshi et al.). Direct contact with diseased birds, their excrement, or ambient surfaces contaminated with the virus can result in the human transmission of avian influenza. The virus can also be contracted through the consumption of undercooked or raw infected poultry products, such as eggs or meat (Ntakiyisumba et al. 2023, Saifur et al. 2023). The symptoms of avian influenza in humans can vary, but typically include cough, fever, irritable throat, body aches and in severe cases respiratory distress, pneumonia, and even death. The severity of the symptoms can depend on the age and overall health of the individual (Debnath et al. 2023).

Historically, avian influenza has instigated several deadly outbreaks in birds and humans. In 1997, one of the most widely recognized avian influenza outbreaks happened in Hong Kong, infecting 18 individuals with the H5N1 subtype and resulting in six fatalities. Since then, there have been numerous additional outbreaks of avian influenza, with the H5N1 and H7N9 subtypes causing the most distress due to their potential to cause severe illness in humans. Avian influenza continues to represent a hazard to both humans and animals. The possibility that the virus would mutate and spread quickly amongst people, causing a global pandemic, is one of the key threats (Shi et al. 2023). The virus's ability to spread to domestic poultry and other animals due to its persistence in wild bird populations is another danger. Moreover, infections may become difficult to cure if the virus develops resistance to antiviral drugs. The likelihood of the virus spreading to new areas is further increased by the continued commerce and travel of live animals and their byproducts worldwide. Firm monitoring and early warning systems, enhancing biosecurity precautions, raising public awareness, and investing in the development of efficient vaccines and antiviral drugs are all essential for reducing these new dangers (Palese 2004, Watanabe et al. 2012).

2.3. BOVINE TUBERCULOSIS

Bovine tuberculosis, also known as TB or cattle TB, is a chronic bacterial infection primarily affecting cattle, but can also infect other domesticated animals and wildlife. It may also be transmitted to others by eating contaminated food or having close contact with sick animals, which can result in life-threatening respiratory conditions (Abrantes and Viera-Pinto 2023). The bacterial agent that causes bovine TB is *Mycobacterium bovis*. The bacteria primarily affects the lungs and can spread to other organs of the infected animal, leading to chronic illness (Kasir et al. 2023). Transmission of the bacterium typically occurs through direct contact with sick animals or by the intake of infected food and water. Humans can contract bovine tuberculosis through inhalation of airborne bacteria or consuming

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contaminated meat and dairy products (Collard 2023). The symptoms of bovine tuberculosis in cattle can vary but typically include chronic cough, loss of weight and decreased milk production. The symptoms in people might range from moderate respiratory disorders to severe pneumonia (Ramanujam and Palaniyandi 2023).

Bovine tuberculosis has had a significant impact on human history, causing a high mortality rate during the industrial revolution in Europe and parts of North America due to the consumption of contaminated milk. In the early 20th century, bovine tuberculosis was considered a significant public health threat, leading to the development of control programs aimed at eradicating the disease in livestock (Perea et al. 2023). The main concern is the infection growing among cow herds, which might result in large financial losses for the agriculture sector. Furthermore, there is fear that consuming infected animal products might spread bovine TB to people and cause life-threatening sickness. Another serious hazard is the development of drug-resistant strains of the bacteria that causes bovine TB because they make treatment more challenging. Controlling the illness is further made difficult by the disease's transmission between animals and cattle, especially in regions where both species interact closely. Implementing efficient control and preventative measures, such as routine testing and the killing of diseased animals, immunization programs, and public awareness campaigns on the responsible handling and use of animal products is crucial to addressing these rising dangers (Olea-Popelka et al. 2004, De la Rua-Domenech et al. 2006, Miller and Sweeny 2010).

2.4. BRUCELLOSIS

The genus *Brucella* is the source of the bacterial illness known as brucellosis. Although it mostly affects cattle including cows, sheep, and goats, it may also infect people by contact with infected animals or eating infected food, which can result in a fatal sickness (Jokar et al. 2023). The *Brucella* bacterium, which mostly affects livestock's reproductive system, is the cause of brucellosis. Four *Brucella* species may infect people: *B. suis*, *B. canis*, *B. melitensis*, and *B. abortus* (Rangel-Ortega et al. 2023). Direct contact with infected animals, eating unpasteurized meat and dairy or undercooked food can all spread brucellosis to people. It can also be spread via inhaling contaminated air or accidental exposure to contaminated materials, such as laboratory samples (Koyun et al. 2023). The symptoms of brucellosis in humans can vary but typically include fever, fatigue, joint pain, muscle aches, and headache. It can cause long-term effects including arthritis, cardiac issues, and chronic weariness in extreme situations (Koyun et al. 2023).

The public's health was significantly impacted by brucellosis throughout history. In the early 20th century, it was a leading cause of occupational disease among abattoir workers and farmers. The development of effective vaccination programs and control measures has significantly reduced the incidence of brucellosis in developed countries (Al Zahrani et al. 2023). There are various new risks posed by *Brucella* to human and animal health. The main concern is that people will get the illness from infected animals like cattle, goats, and sheep and then pass it on to themselves by consuming the animal products. The rise of *Brucella* strains that are resistant to medications is another major concern since it makes the illness more challenging to cure (Ducrotoy et al. 2014). The likelihood of the illness spreading to new areas is further increased by the worldwide movement of people and animals. However, because *Brucella* can spread widely and generate concern, its potential as a bioweapon is an increasing problem. Implementing efficient control and prevention measures, such as routine screening and elimination of infected animals, vaccination campaigns, public awareness campaigns on safe practices and consumption of animal products, and monitoring drug resistance patterns in *Brucella* strains, is crucial to combat these emerging threats (Olsen et al. 2018, Harpreet et al. 2019).

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2.5. CAMELPOX

A virus called *Camelpox* affects humans, but camels are the central targets. The Orthopoxvirus genus of viruses, which causes camelpox, is most common in the Middle East, Central Asia, and North Africa, where camel herding is common (Gieryńska et al. 2023). This disease is related to other diseases such as cowpox and smallpox (Anuradha et al. 2023, Sepehrinezhad et al. 2023). Continuous contact with diseased camels, eating raw meat or milk that has been tainted and inhalation of infected aerosols are all ways that the disease can be passed from camels to people. In addition, camelpox can also be transmitted through exposure to contaminated materials such as bedding or equipment, or insect bites. In humans, camelpox usually manifests as a mild, self-limiting disease, with symptoms including fever, rash, and vesicular lesions on the skin. Camelpox has the potential to root severe ailments in humans, with complications that may include pneumonia, meningitis, and septicemia (Thakur et al. 2023).

There is inadequate information available regarding the historical impermanence angle of camelpox in humans. However, outbreaks of camelpox have been reported in regions where camel husbandry is prevalent, with sporadic cases occurring among people who come into contact with infected camels or contaminated materials (Gieryńska et al. 2023). To summarize, the present rising threat status of camelpox is unknown. While not currently seen as a serious hazard to public health, constant monitoring and control are required due to the virus's propensity for breakouts and its future use in bioterrorism. Camelpox is classified as a moderate danger to public health and safety by the World Health Organization. To combat this potential hazard, regular monitoring of camel habitats, vaccination programs, and public education campaigns on managing and consuming animal products are critical measures in lowering the risks connected with camelpox. In tackling new hazards posed by infectious illnesses like camelpox, it is critical to stay alarmed and proactive (Balamurugan et al. 2013, Dahiya et al. 2016).

2.6. HANTAVIRUS PULMONARY SYNDROME

Hantavirus pulmonary syndrome (HPS) is a respiratory disorder that is rare but serious and is caused by exposure to *Hantavirus*. Hantavirus pulmonary syndrome was first identified in the US in 1993, and since then, it has been reported in several other countries in the Americas (Sundar et al. 2023). Hantaviruses can be identified in the faeces, saliva, and urine of infected rodents like deer mice and rice rats, which are responsible for causing the syndrome (Avižinienė et al. 2023). Infected rodents or their droppings are the main sources of disease transmission to people. Direct engagement with a sick person's body fluids or blood can potentially spread the virus but this is very rare (Alshammari 2023). Symptoms of HPS typically include fever, muscle aches, and fatigue, followed by coughing and breathlessness. In some cases, the disease can progress rapidly to severe respiratory distress and can be fatal in up to 40% of cases (Pattiyakumbura et al. 2023).

There have been several outbreaks in the Americas since HPS was originally discovered in 1993, with the majority of cases being reported in the US. With a fatality rate between 30% and 40%, HPS has always had a high mortality outlook (Fullerton et al. 2023). Public health is still threatened by the disease, particularly in areas where rodents harbour the virus. The danger of HPS outbreaks may potentially rise due to the introduction of new virus strains or modifications in the behavior of rodent populations. The existing COVID-19 pandemic has also highlighted the potential for newly developing infectious illnesses to spread quickly and result in severe morbidity and mortality. To counter this possible hazard, continuing rodent population tracking, public education campaigns on proper rodent handling and sanitation, and research into vaccinations and therapies are necessary. It is critical to stay alert and

antagonistic in dealing with emerging and re-emerging infectious disease risks such as HPS (Barui et al. 2022).

2.7. HENDRA VIRUS INFECTION

The *Hendra virus* is responsible for causing a rare and fatal zoonotic illness known as Hendra virus infection. The virus was first identified in 1994 in Australia and has since been responsible for a small number of human and equine deaths. The *Measles virus* and the *Mumps virus* are both members of the family Paramyxoviridae, which contains the virus (Tomori and Oluwayelu 2023). The virus is believed to be primarily transferred to humans through nearby contact with sick horses, which are considered to be the natural host for the virus. It is thought that flying foxes, a type of fruit bat, serve as the reservoir for the virus, and can transmit it to horses through contact with their urine or other bodily fluids. It is thought that exposure to body fluids from infected animals, such as saliva, nasal secretions, or blood, can cause the Hendra virus to spread from horses to people. The spread of the virus is extremely rare from one person to another (Wang et al. 2023). Symptoms of Hendra virus infection are alike to those of other respiratory illnesses and may comprise fever, headache, muscle aches, and coughing. Patients may encounter progressively severe symptoms as the illness worsens, including organ failure, encephalitis, and pneumonia (Becker et al. 2023, Wang et al. 2023).

Since the first outbreak of the Hendra virus in 1994, few cases of the disease were reported in Australia. The historical mortality perspective for Hendra virus infection is relatively high, with a mortality rate of approximately 50%. Moreover, the equine industry can suffer significant economic losses due to the disease, as infected horses may need to be put down to avoid further transmission of the virus. Taking necessary precautions to prevent exposure to the Hendra virus is crucial, especially for those who work with horses or in areas with fruit bats. Wearing protective clothing and practicing good hygiene can help minimize the risk of infection (Becker et al. 2023, Sachan et al. 2023).

2.8. MIDDLE EAST RESPIRATORY SYNDROME (MERS)

The highly contagious viral respiratory disorder termed Middle East respiratory syndrome (MERS) is primarily caused by the *Middle east respiratory syndrome coronavirus* (MERS-CoV). Since the virus was initially discovered in Saudi Arabia in 2012, numerous other nations, mostly in the Middle East, have reported many cases of this disease (Azhar et al. 2019). Humans can get the virus by getting into continuous contact with sick animals or by breathing in respiratory secretions from infected individuals. The virus is believed to have its origins in bats and is transmitted to humans primarily through camels. MERS can also spread through human-to-human transmission, particularly among individuals who have close contact with infected individuals, such as healthcare workers who are attending to MERS patients (Control and Prevention 2016). Fever, breathlessness and cough are the major symptoms which can progress to severe respiratory illness, pneumonia, and even death. MERS is thought to have a death rate of about 35% and those who have underlying conditions including diabetes, chronic lung disease, and immunosuppression are more susceptible to dying from it (Control and Prevention 2014).

Since its emergence in 2012, several episodes of MERS have been recorded, primarily in the Middle East, but also other regions such as South Korea. South Korea experienced the greatest MERS epidemic outside of the Middle East in 2015, where over 180 cases were reported, resulting in 36 fatalities (Kim and Kim 2018, Salamatbakhsh et al. 2019). MERS remains an emerging infectious disease with potential hazards, although there is no confirmed active outbreak. One of the major problems is the disease's lack of effective treatment, with no specialized antiviral medicine available. The virus's ability to spread is

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also a concern, as MERS-CoV is conveyed through intimate contact with infected people or their respiratory secretions. Moreover, camels are thought to be the virus's principal reservoir, and continuing surveillance of the virus in animals is required to understand the danger of transmission to humans. Lastly, MERS-CoV, like other viruses, can modify and adapt to new hosts, which might affect how the virus spreads and the degree of sickness it causes. To address the rising hazards associated with MERS, continuing research, surveillance, and planning are required (Lee and Hsueh 2020).

2.9. MONKEYPOX

Monkeypox is a viral disease that is relatively rare and mostly affects primates and people living in Central and West Africa. Monkeypox is induced by the *Monkeypox virus*, which is closely linked to the virus that causes smallpox (McCollum and Damon 2014). Direct exposure to infected animals or their body fluids, including blood, faeces, and respiratory secretions, is the main way in which the virus is transferred. Continuous exposure or nearby contact with infected body secretions can lead to transmission of the virus in the human population. The respiratory droplets from an infected person can also transmit the disease to others (El Eid et al. 2022). Monkeypox symptoms are comparable to smallpox symptoms but less severe. The disease usually begins with a fever, headache, muscle aches, and exhaustion, followed by skin irritation involving the whole body. Lesions progress to become fluid-filled and then scab over and fall off after a few weeks (Kannan et al. 2022).

Monkeypox is a rare disease, and outbreaks are infrequent. In 1958, the emergence of a pox-like disease was reported in monkeys that were being used for research, leading to the identification of what is now known as monkeypox. Later, in 1970, the disease was identified in humans. However, since 2003, there have been several outbreaks in Central and West African countries, including Nigeria, the Democratic Republic of Congo, and Cameroon. In the United States, there have been a few isolated cases of people who have travelled from Africa or had close contact with infected animals. The fatality rate from monkeypox ranges from 1% to 10%, with younger age groups being more frequently affected (Parker and Buller 2013). Monkeypox is a growing concern to people due to a variety of circumstances. When humans continue to intrude on natural ecosystems and come into touch with animals harbouring the virus, the chance of transmission from animals to humans grows. Recent outbreaks of monkeypox in other regions of Africa have also extended beyond their initial locations, and there is a danger of human-to-human transmission, particularly in hospital settings. Furthermore, the lack of a particular treatment or vaccination for monkeypox might make it difficult to control outbreaks and manage individual patients. As a result, more study and monitoring are required to better understand and manage the hazards associated with monkeypox, as well as to generate effective strategies to prevent the virus's spread (Modgil et al., Wani and Kumar 2022).

2.10. NIPAH VIRUS INFECTION

The zoonotic disease, *Nipah virus* (NiV) can have serious effects on both human and animal nervous systems and respiratory systems. The virus was discovered in 1998 after an encephalitis and respiratory sickness outbreak among Malaysian pig farmers and employees at slaughterhouses. The virus is named after the Malaysian town of Sungai Nipah, where the first epidemic occurred (Nor et al. 2000, Shariff 2019). The virus naturally infects fruit bats of the Pteropodidae family, sometimes referred to as flying foxes. Humans can contract the virus by coming into touch with infected bats, eating contaminated fruits, or drinking raw date palm sap. Person-to-person transmission can also occur, particularly in healthcare settings (Soman et al. 2020). NiV infection in humans can cause symptoms that vary from

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mild or moderate respiratory disease to severe encephalitis with convulsions and coma. In some cases, neurological symptoms such as dizziness, confusion, and disorientation may precede respiratory symptoms (Hossain et al. 2008).

Since the first outbreak in Malaysia, there have been several more outbreaks of the NiV infection in both India and Bangladesh, with the majority of infections occurring in rural areas where bats and infected date palm sap are common (Hossain et al. 2008, Plowright et al. 2019). Mortality rates vary depending on the outbreak and population affected and ranges from 40-90%. NiV infection has no particular therapy or vaccination. Although it is largely spread by animals to humans, the Nipah virus continues to pose a serious threat to human health. Throughout the years, there have been various outbreaks in South and Southeast Asia, with the most recent taking place in India in 2018. As humans continue to expand their populations and encroach upon natural habitats, there is an increased likelihood of exposure to the virus. Furthermore, the Nipah virus can cause severe illness in humans, including encephalitis and respiratory illness, making it a public health concern, highlighting the need for continued surveillance and preparedness to address this emerging threat (Alam 2022).

2.11. PASTEURELLOSIS

Pasteurellosis is a bacterial infection caused by the *Pasteurella multocida* bacterium. The most common way to contract the infection is through animal bites, especially from dogs and cats, but also from other animals such as rabbits, rodents, and farm animals (Register and Brockmeier 2019). Pasteurellosis is more common in individuals who work with animals, such as veterinarians, animal handlers, and farmers. The bacteria move in the body through a skin incision or wound caused by an animal bite or scratch. In some cases, it can also be transmitted through respiratory droplets when an infected animal sneezes or coughs. Symptoms caused by the bacteria vary based on the strength of the infection and the person's immune response. Common symptoms include swelling, redness, and pain at the site of the bite or scratch, fever, chills, swollen lymph nodes, and difficulty breathing (Mohamed and Abdelsalam 2008).

Historically, pasteurellosis has been documented as a significant public health concern in individuals who work with animals, particularly those who handle cats and dogs. In the United States, it is assessed that about 10-15% of all domestic animal bites are caused by *Pasteurella* species (Toranzo et al. 1991). In severe cases, pasteurellosis can lead to sepsis, meningitis, and other life-threatening complications (George et al. 2008). Pasteurellosis is an uncommon but rapidly spreading bacterial illness with devastating repercussions for human health. The rising abundance of domestic animals in human civilization has raised the potential of microbial exposure, notably through dog and cat bites and scratches. Pasteurellosis poses a substantial public health problem due to limited treatment options and the rise of antibiotic-resistant bacteria. As human connections with domestic animals grow, it is critical to emphasize continuous research, surveillance, and preventative strategies to minimize the prevalence of this disease and improve outcomes for individuals who are affected. By increasing public knowledge of this rising issue, we can fight to reduce the risk of Pasteurellosis and ensure a healthier future for both humans and animals (Wilson and Ho 2013).

2.12. PLAGUE

The bacterium *Yersinia pestis* causes respiratory plague, a severe and possibly lethal contagious disease. This disease is primarily associated with bubonic and septicemic plagues, but it can also manifest as a respiratory illness, known as pneumonic plague (Kool and Weinstein 2005). Respiratory plague is the

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dangerous infectious form of the illness, since it may be passed from person to person via the air, resulting in extensive outbreaks. The bacterium is primarily found in rodents and their fleas, which serve as the primary reservoirs for the disease (Smiley 2008). When infected fleas bite humans, they can transmit the bacterium, leading to a bubonic or septicemic plague. Inhaling aerosolized droplets or dust infected with *Y. pestis* can also cause respiratory plague. The disease can also spread through direct exposure to infected body fluids, such as blood or pus, or by touching contaminated surfaces (Kool and Weinstein 2005). The symptoms of respiratory plague usually appear within 1-3 days of exposure and include headache, chills, fever weakness, cough, chest pain, and breathlessness. The illness can rapidly progress, leading to severe pneumonia, septic shock, and death if left untreated. Pneumonic plague is often fatal if not treated promptly, with a mortality rate of 90% or higher (Pechous et al. 2016).

Many pandemics throughout history, notably the 14th-century “Black Death”, which killed an estimated 25 million people in Europe, have been attributed to the respiratory plague. Pneumonic plague cases have recently been recorded in several international locations, including China, Mongolia, and also the Democratic Republic of the Congo. In 2017, a pneumonic plague outbreak in Madagascar resulted in over 2,300 cases and more than 200 deaths (Duncan and Scott 2005, Tsuzuki et al. 2017). Plague is a serious increasing danger to human health due to a variety of variables, including the growth of antibiotic-resistant strains, changes in global climatic patterns and human behaviour, and the possibility for purposeful release as a bioweapon. Continuous efforts to improve monitoring and readiness, find novel treatment options, and raise knowledge of the disease's risk factors are critical to reducing the danger of a broad epidemic. With potentially serious repercussions, prioritizing research and public health measures to ensure that we are prepared to confront this rising issue and safeguard the health and safety of people globally (Ditchburn and Hodgkins 2019).

2.13. PSITTACOSIS

Psittacosis, often known as parrot fever, is a respiratory condition brought on by the *Chlamydia psittaci* bacteria. The disease can affect both humans and birds, particularly parrots, pigeons, and doves, which serve as reservoir hosts (Stewardson and Grayson 2010). Transmission occurs through inhalation of the bacterium from infected bird faeces, feathers, and respiratory secretions. Individuals who are regularly in contact with birds, such as those who work in pet stores and poultry facilities, and those that are passionate about birds are more likely to become infected (Jorgensen 1997). Psittacosis can cause a range of symptoms in humans, varying in severity from mild to severe, including chills, fever, cough, headache, muscle aches and breathlessness. The infection can lead to pneumonia and even death in extreme circumstances. Psittacosis is often underdiagnosed, as it can mimic symptoms of other respiratory illnesses (Branley et al. 2014).

Historically, psittacosis outbreaks have been reported in various countries, including the United States, Japan and Australia. One notable outbreak occurred in 1929 when hundreds of people in the United States became sick after attending a parrot show (Ramsay 2003). Although uncommon, psittacosis represents a rising hazard to human health due to various causes. For starters, the condition can be difficult to identify, with symptoms ranging from minor to severe, such as fever, headache, muscle pains, and cough. Misdiagnosis or delayed identification can result in consequences such as pneumonia and even death. The growing popularity of exotic pets, such as parrots, has increased human exposure to the virus, especially among bird handlers and pet owners. Lastly, the rise of antibiotic-resistant virus strains poses a substantial public health problem, decreasing the effectiveness of standard treatment methods. Considering the potential for severe effects and limited treatment options, continued research, surveillance, and preventative measures are critical to minimizing the risk of psittacosis and maintaining

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the health and safety of both humans and animals. We can lower the danger of psittacosis by raising knowledge of the disease's risk factors and implementing appropriate pet-keeping practices (Weston et al. 2022).

2.14. Q FEVER

The disease was originally mentioned as "query fever" because of the unknown nature of its cause, but it was later renamed "Q fever". Humans who have Q fever may develop acute or chronic illnesses which are most commonly contracted by inhaling the bacteria. Q fever is found worldwide and can affect people of all ages (Woldehiwet 2004). The bacterium that causes Q fever, *Coxiella burnetii*, is frequently found in livestock and poultry such as cows, goats, and sheep. The bacteria can be found in their milk, urine, animal waste and other bodily fluids (Tissot-Dupont and Raoult 2008, Hirschmann 2019). The bacteria can be transmitted through exposure to infected animals, ingestion of contaminated milk, or breathing in a contaminated environment. The Q fever infection is mostly spread through inhalation of bacteria-contaminated particles, including dust or soil. Those who interact with livestock, such as vets, farmers, and abattoir workers, are more likely to get the illness (Gwida et al. 2012, Hirschmann 2019). Q fever can cause a range of symptoms that vary in severity and duration. Sweating, fever, headaches, and fatigue are the most typical symptoms. Additional symptoms may include cough, chest pain, and shortness of breath. The symptoms can last for several weeks to several months. Q fever can lead to severe impediments, such as pneumonia, hepatitis, and endocarditis, in some cases (Parker et al. 2006, Honarmand 2012).

The first recorded instances of Q fever in humans were identified in Australia during the 1930s. Since then, outbreaks of Q fever have appeared in many countries around the world, including the United States, Europe, and Australia. In the past, Q fever was commonly linked with exposure to infected animals in the workplace and outbreaks were often linked to the processing of animal products. While Q fever is generally considered a mild illness, severe cases can occur, and fatalities have been reported. In recent years, epidemics have been associated with exposure to infected soil and dust, emphasizing the relevance of environmental variables in disease transmission (McDade and Marrie 1990).

2.15. SEVERE ACUTE RESPIRATORY SYNDROME (SARS)

Coronavirus causes respiratory infections, including severe acute respiratory syndrome (SARS). The disease emerged in southern China in November 2002 and spread to other countries, leading to a global outbreak in 2003. SARS can result in severe respiratory distress, leading to conditions such as acute respiratory distress syndrome (ARDS) and pneumonia, and has a high mortality rate (Lam et al. 2003). The virus was transmitted from bats to people via an intermediate host, according to some theories, possibly civet cats or other mammals. The virus is highly infectious and can spread rapidly through close contact with infected individuals (da costa et al. 2020). Respiratory droplets from infected individuals are the primary mode of transmission for SARS. SARS can spread by contaminated droplets in the air from infected individuals as well as through contact with contaminated surfaces or objects. The infection usually takes from two to seven days to incubate, but it can take as long as ten days (Al Huraimel et al. 2020, da costa et al. 2020). The symptoms of SARS are similar to those of the flu and include fever, cough, and shortness of breath. Some patients may also experience body pain, headaches, and diarrhea (Grant et al. 2020).

The outbreak of SARS during the period of 2002-2003 was a major public health emergency, with 8,098 cases and 774 fatalities recorded across 26 nations. SARS is estimated to have a 10% mortality rate. The

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outbreak was contained through widespread public health measures, including quarantine, travel restrictions, and infection control measures. Since then, there have been no identified cases of SARS reported globally (Anderson et al. 2004). The persisting COVID-19 pandemic produced by the SARS-CoV-2 virus continues to be an ongoing cause of danger. Even though the virus has been circulating for over a year, new varieties are constantly emerging, some of which may be more transmissible or resistant to current vaccinations. These mutations have the potential to cause fresh waves of infections, undermining global efforts to manage the epidemic. Furthermore, there is supporting evidence that long-term health issues, known as chronic COVID, may impact a considerable number of COVID-19 survivors. These effects, which can vary from weariness and trouble concentrating to more serious respiratory and cardiovascular disorders, may have far-reaching consequences for world health even after the epidemic has passed (Gilbert 2020).

2.16. SWINE FLU (H1N1 INFLUENZA)

A strain of the *Influenza A* virus causes swine flu, commonly referred to as H1N1 influenza. The disease first emerged in Mexico in 2009 and rapidly spread to become a global pandemic. The genetic makeup of the H1N1 virus includes elements of the swine, avian, and human influenza viruses, making it very contagious and capable of causing severe illness. It is called "swine flu" because the virus originated in pigs (Perez-Padilla et al. 2009). The virus can mutate and spread from pigs to humans and then spread in the environment affecting human communities. As a result of respiratory droplets inhaled when an infected person sneezes or coughs, the flu can also be spread from person to person. Another way to catch the virus is to come into contact with it before touching your lips, nose, or eyes (Parmar et al. 2011, Kawanpure et al. 2014). Swine flu symptoms include fever, cough, hoarseness, body aches, malaise, chills, headache, diarrhea, and vomiting, which are similar to seasonal influenza symptoms. Acute respiratory distress syndrome (ARDS), pneumonia, and even death can result from swine flu in extreme instances (Brand et al. 2013).

The swine flu pandemic that occurred between 2009 and 2010 was the first worldwide pandemic in more than four decades. An estimated 1.4 billion individuals were affected by the virus globally and in June 2009, it is declared a pandemic by the World Health Organization (WHO). The pandemic concluded in August 2010, with over 18,000 deaths related to swine flu complications reported. The majority of deaths occurred in the Americas and Southeast Asia. After the 2009 pandemic, swine flu became a seasonal flu virus and vaccines were developed to prevent its spread. While the number of fatalities from swine flu is normally low, certain populations, such as youngsters, pregnant women, and individuals with underlying health issues, may be more vulnerable to severe consequences (Wheaton et al. 2012, Beckman et al. 2013).

2.17. PNEUMONIC TULAREMIA

Pneumonic Tularemia is an infrequent infection caused by *Francisella tularensis*, a bacterium also referred to as rabbit fever. Although pneumonic tularemia is rare, it is considered a potential bioterrorism agent due to its high virulence and ability to be aerosolized (Reed et al. 2011). This bacterial pathogen can survive in the soil for a longer period, it can also colonize in water as well as in the corpses of dead animals. There are four subspecies of the bacterium, each with different levels of virulence. Types A and B are the most dangerous and are frequently prevalent in North America, while Type B may be found throughout Asia as well as Europe. The bacteria is resilient to several popular disinfectants and may live in a variety of environmental conditions (Hepburn and Simpson 2008). Pneumonic Tularemia is spread by direct contact with infected animals such as rabbits, rats, and deer,

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tick bites, or aspiration of contaminated dust or aerosols. It can also be transmitted through the consumption of contaminated water or food. In rare cases, tularemia can also be transmitted from person to person through direct contact with infected body fluids or inhalation of aerosolized bacteria (Matyas et al. 2007). Pneumonic tularemia symptoms often appear 3 to 5 days following bacterial contact. The disease can manifest itself in many ways depending on how it is spread. Symptoms include fever, chills, exhaustion, spastic muscles, headache, and respiratory symptoms such as coughing, chest discomfort, and shortness of breath. If left untreated, tularemia can be lethal, with a death rate of up to 30% for the pulmonary manifestation of the disease (Penn and Edwards 2019).

Being an uncommon condition, pneumonic tularemia has a fluctuating incidence. Since this was first detected in rabbits in Tulare County, California, in 1911. In the United States, the disease is most commonly reported in rural areas of the western and midwestern states. Referring to the Centers for Disease Control and Prevention (CDC), 230 cases of tularemia were reported in the United States in 2019 (Kwit et al. 2019). Historically, the disease has been associated with outbreaks among soldiers and other military personnel and has been used as a biological weapon in the past. The most current outburst of tularemia occurred in Sweden in 2019, where more than 30 cases were reported among hares and humans (Dryselius et al. 2019, Kwit et al. 2019).

3. CONCLUSION

The impact of zoonotic respiratory diseases on global mortality rates cannot be overstated. From the Spanish Flu pandemic in 1918 to the more recent outbreaks of SARS, MERS, and COVID-19, these diseases have caused significant morbidity and mortality, disrupted the economies, and had led to widespread social and political upheaval. The rapid spread of these diseases highlights the importance of global cooperation and investment in research and response efforts to address emerging threats. To prevent future outbreaks, it is crucial to improve surveillance and early detection systems for zoonotic diseases, particularly in areas where high-risk human-animal contact occurs, such as in wet markets and slaughterhouses. We also need to promote responsible practices in animal agriculture and wildlife trade, such as implementing biosecurity measures and regulating the transport and trade of live animals. Additionally, investing in the development of vaccines and antivirals, as well as supporting research into the genetic makeup and transmission patterns of zoonotic diseases, can help us better prepare for and respond to future outbreaks.

Furthermore, we need to prioritize the equitable distribution of healthcare resources and access to vaccines in the face of future outbreaks. The current COVID-19 pandemic has highlighted the unequal distribution of healthcare resources worldwide, as many low-income countries have struggled to obtain vaccines and other critical resources. Ensuring that healthcare resources and vaccines are distributed fairly can help mitigate the impact of future outbreaks and prevent the further spread of disease. In conclusion, zoonotic respiratory diseases had a major impact on global health and mortality rates throughout history. To prevent and control these diseases, we must remain vigilant and invest in research and response efforts, improve surveillance and early detection systems, promote responsible practices in animal agriculture and wildlife trade, and prioritize equitable access to healthcare resources and vaccines. By taking these steps, we can help mitigate the impact of future outbreaks and safeguard public health.

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