



Zoonotic : Emerging and Reemerging Viral Diseases in Indonesia

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Abstract

Zoonoses are diseases that have claimed millions of lives in both humans and animals. This disease can be transferred from infected animals to humans or vice versa. It has been reported that 75% of zoonotic diseases are emerging. This paper aims to describe various types of emerging and reemerging zoonotic diseases that occur in Indonesia and abroad. Data collection is done online through several websites including the Office International des Epizooties, World Health Organization and the Ministry of Health of the Republic of Indonesia in collaboration with published research reports related to zoonotic diseases. Various disease data were found, both emerging and reemerging. The zoonotic diseases that are endemic and have been reported include COVID-19, avian influenza, swine influenza, dengue, chikungunya, hepatitis E, and rabies. All these diseases occur in Indonesia and throughout the world. Based on the description above, it can be concluded that various types of emerging and reemerging zoonotic diseases occur in Indonesia.

Keywords: Zoonoses, emerging, reemerging, virus, disease

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Introduction

Zoonoses are diseases that are transmitted by infected animals to humans or vice versa. As many as 60% of diseases in humans are zoonotic diseases and about 75% are emerging diseases that have attacked humans in the last three decades (Ministry of Health, 2021). Various emerging and reemerging diseases that can be transmitted from animals to humans have been widely reported. According to a report from OIE (2021), that more than half of emerging diseases detected internationally since 1940 are zoonotic, and since 1960 the relative frequency of detection of emerging and zoonotic diseases has increased. Zoonotic diseases that have been identified since 1918 until now include influenza virus infection and corona virus, added a reference (Choi, 2021).

Emerging disease is a disease that has just occurred and is identified in a certain area. While

reemerging disease is a disease that has occurred but has been reported again with increasing cases. Emerging and reemerging diseases caused by viral and zoonotic infections that have been reported in several countries include SARS, dengue virus, hepatitis E virus, swine influenza, avian influenza and chikungunya virus (Jaijyan et al., 2018). The country of Indonesia has experienced cases of emerging and emerging disease outbreaks. The cases of emerging diseases that have been reported in Indonesia are the Covid-19 pandemic by the SARS-CoV-2 virus and the avian influenza outbreak.

According to the results of a survey conducted by LIPI in 2020, public knowledge of zoonotic diseases is still low. Meanwhile, most of the emerging and reemerging diseases that have the potential to become epidemics and pandemics originate from zoonotic diseases, so knowledge and awareness are needed to anticipate and prevent zoonotic diseases. In addition, the importance of the role of educational institutions related to disease and animal health and human health as a source of information in the prevention and control of zoonotic diseases. Therefore, the purpose of writing this scientific article is as a source of information for stakeholders in the prevention and control of zoonotic diseases for the wider community.

Materials and Methods

Data on zoonotic and reemerging diseases will be taken according to disease case reports from the World Animal Health Organization (Office Internationale des Epizooties/OIE), the World Health Organization (WHO), the Ministry of Health of the Republic of Indonesia (Kemenkes RI) and the Directorate General of Livestock and Animal Health (Directorate General of PKH) in collaboration with related research reports that have been published.

Results and Discussion

Various types of zoonotic diseases have been reported to be epidemic in the last two decades. These zoonotic diseases have had an impact on animal and human health as well as economic disturbances both nationally and internationally. Generally, zoonotic diseases are caused by acute viral infections (Robb, 2021). The zoonotic diseases caused by emerging and reemerging viruses are described below.

Covid-19

Coronavirus is an RNA virus with a particle size of 120-160 nm. This virus mainly infects animals, including bats and camels. Before the Covid-19 outbreak, there were 6 types of coronavirus that could infect humans, namely alphacoronavirus 229E, alphacoronavirus NL63, betacoronavirus OC43, betacoronavirus HKU1, Severe Acute Respiratory Illness Coronavirus (SARS-CoV), and Middle East Respiratory Syndrome Coronavirus (MERS-CoV). The coronavirus that causes Covid-19 is included in the betacoronavirus genus. The results of phylogenetic analysis show that this virus belongs to the same subgenus as the coronavirus that caused the Severe Acute Respiratory Illness (SARS) outbreak in 2002-2004, namely Sarbecovirus. On this basis, the International Committee on Taxonomy of Viruses proposed the name SARS-CoV-2 (Susilo et al., 2020).

The first Covid-19 disease was reported in Indonesia on March 2, 2020, with two cases. Data on March 31, 2020 showed that there were 1,528 confirmed cases and 136 deaths. The Covid-19 mortality rate in Indonesia is 8.9%, this figure is the highest in Southeast Asia. As of March 30, 2020, there were 693,224 cases and 33,106 deaths worldwide. Europe and North America have become the epicenter of the Covid-19 pandemic, with cases and deaths already surpassing China. The United States ranked first with the most Covid-19 cases with the addition of 19,332 new cases on March 30, 2020, followed by Spain with 6,549

new cases. Italy has the highest mortality rate in the world, at 11.3% (Susilo et al., 2020).

Avian Influenza

Avian influenza is a disease that attacks poultry. This disease is caused by type A influenza virus from the family Orthomyxoviridae, namely strain H5N1. The virus that initially only attacks birds, but a few years ago this virus caused many deaths in humans in Asia. In late 2003 to early 2004, outbreaks of bird flu caused by the H5N1 virus had spread to several Southeast Asian countries, including Indonesia. Based on data from the WHO until December 10, 2013 the total cases of avian influenza in humans amounted to 648 cases with 384 deaths, all of which occurred in 15 countries. While in Indonesia alone there were 195 cases with 163 people died (Sarah, 2019).

The spread of this disease through the air and contact with contaminated objects. The spread of avian influenza is acute which can cause rapid death in poultry and humans. Due to the ferocity of this disease outbreak, the government also needs to quickly take preventive measures so that bird flu does not continue to cause new victims and its spread can be minimized. Collaborating with WHO is one of the paths taken by the Government of Indonesia. Some of the preventive measures include keeping farms at a distance from residential areas, mass culling of infected poultry groups, the use of disinfectants and antiseptics (Sarah, 2019).

Swine Influenza

The virus that causes swine influenza comes from the family Orthomyxoviridae strain H1N1. This virus is often the cause of epidemics and pandemics that affect human health. Influenza pandemic strain H1N1 was first reported in 1918 (Swine influenza) and caused a pandemic in the following years, namely 1957 known as the Asian flu pandemic, 1968 known as Hong Kong flu and 1977 known as Russian flu until 2009 known pandemic influenza A H1N1. Influenza type A viruses are highly variable, suggesting that continuous antigenic variation is a major cause of epidemics and pandemics. Surface glycoprotein antigens undergo two main types of antigenic variation, for example, antigenic shift and antigenic drift. Antigenic shift is the result of major changes in one or both of the surface antigens [haemagglutinin (HA) and neuraminidase (NA)] and sometimes causes a pandemic. Three mechanisms may operate in antigenic shift, leading to the emergence of pandemic influenza strains, eg genetic re-assortment, direct transfer from avian/mammal host to humans and viral recycling. While antigenic drift occurs due to small changes in HA or NA and often causes epidemics (Mourya et al., 2019).

Humans can be infected with this virus from several subtypes, namely A(H1N1), A(H1N2) and A(H3N2). Human infection is mainly acquired through direct contact with infected animals or a contaminated environment. The risk factors for this disease are when humans come into direct contact with infected pigs or visit sites where pigs are exhibited, in addition some limited human-to-human transmission has occurred. Other viral infections in humans can cause illness ranging from mild upper respiratory tract infections (fever and cough), early and rapidly developing sputum production to severe pneumonia, sepsis with shock, acute respiratory distress syndrome, and even death. Conjunctivitis, gastrointestinal symptoms, encephalitis and encephalopathy have also been reported to varying degrees depending on the subtype (WHO, 2018). There were 151,700-575,400 people worldwide died from infection with the virus (H1N1) during the first year the virus was circulating. Globally, 80% of virus (H1N1)pdm09-related deaths are estimated to occur in people younger than 65 years (CDC, 2019).

Outbreaks of swine flu have been reported in several parts of the world. In the Americas, swine flu was first reported in the north and midwestern United States in 1918. However, the virus could only be isolated in pigs in 1930. The classic European swine influenza virus was first isolated during an outbreak in northern Italy in 1976. According to surveillance conducted in 2006 and 2007, swine flu has caused acute respiratory distress in pigs in Belgium, England, Italy, France and Spain. Human swine flu infection caused by subtypes H1N1 and H3N2 was reported in Italy in 1993. A surveillance serology in Japan showed that swine flu subtype H1N1 has occurred in Asia since 1977. In Southern China, isolation of the subtype H1N1 swine flu virus was carried out in 1993. In Indonesia, H1N1 influenza (2009 pandemic strain) was reported in April 2009. The virus was detected in a pig abattoir in Jakarta province and in a pig farm on Bulan island, in the Riau Islands province, in 2009. Indonesia's 2009 swine flu epidemic was responsible for responsible for 1,005 confirmed cases and five deaths (Nurhayati et al., 2020).

Dengue

Dengue fever is a common viral disease that causes 50 million cases annually in more than 100 countries in the tropics and subtropics. Dengue virus (DENV) belongs to the flavivirus genus and family Flaviviridae. Dengue fever is considered the second largest disease after mosquito-borne malaria. Most dengue virus infections are asymptomatic, but a small number of cases of dengue hemorrhagic fever are dengue shock syndrome (DSS) which is characterized by circulatory collapse. Dengue virus is a positive sense single-stranded RNA virus with 11 kb genome. The dengue virus has four different antigens and serotypes named DENV 1-4. The dengue virus is transmitted to humans through the bite of the *Aedes aegypti* mosquito. Symptoms of dengue virus infection are mostly asymptomatic so it is very difficult to predict the first dengue infection in humans. According to the Chinese medical encyclopedia, the first dengue infection probably dates back to 992 AD. It is very difficult to predict the place of origin of the dengue virus, but several studies have shown this virus may have originated in Africa because many mosquito-borne diseases occur there and often infect primates. . Another study predicts that the dengue virus originated in Asia. In the late 19th century to early 20th century, this virus spread to tropical and subtropical countries (Jaijyan et al., 2018).

The first dengue virus outbreak was reported in 1953/1954 in Manila and the second outbreak occurred in 1958 in Bangkok. Sudden outbreaks of dengue fever occurred in China from 1978-2008 resulting in more than 600,000 cases and about 475 deaths overall. Occurring in America, DENV expanded its geographic reach and came back in North America via Texas and Florida in America. The DENV epidemic was limited by (the control of DENV started in 1947 by the Pan America Health Organization (PAHO). This organization focused on eradicating the *Aedes aegypti* mosquito from Central and South America. The PAHO program was discontinued in the 1970s and the *Aedes aegypti* population increased again which led to an increase cases of DENV. In 2009 the first DENV outbreak occurred in florida more than 70 years out of 16 reported DENV cases. In 2010, DENV caused infection in 66 people in Florida and thereafter reported several cases of dengue virus infection, according to the CDC report in 2013 there were 4 cases of dengue virus infection in Hawaii, in 2011 there were 2 cases in Florida and in 2012. After that In 2013 there were 20 cases of dengue fever in Florida and 3 cases in Texas. Recently, according to a newspapers a total of 80 cases of dengue fever have been reported in the United States and its territories in 2017. This indicates that DENV increases its geographic reach and could cause a pandemic in the near future (Jaijyan et al., 2018).

Chikungunya

The chikungunya virus is estimated to have occurred during 2014-2016 and caused more than 14,000 deaths, mainly among the elderly. Chikungunya virus (CHIKV) is an arbovirus, a member of the Alphavirus genus in the family *Togaviridae*. This virus is a positive strand RNA virus. Chikungunya virus was isolated for the first time in the Mokande plateau between Tanzania and Mozambique, in the Eastern Democratic Republic of the Congo in 1958. Since then, outbreaks of chikungunya have been documented in South Africa and Zimbabwe in 1956-1977, Democratic Republic of the Congo, Zambia, Senegal, Uganda, Nigeria, Angola and the Central African Republic in 1958-2000 and Equatorial Guinea in 2002. The chikungunya virus was introduced in Asia at two different times. The first expansion in Asia corresponds to early differences in the Asian genotype of ECSA (east/central/south african), which has diverged from the West African genotype. Chikungunya was first reported in Asia, particularly in Thailand in 1958 and early 1960. The second Asian expansion was associated with the emergence of the ECSA A226V mutant, also known as the Indian ocean lineage (IOL) lineage, which evolved from the ECSA genotype in Kenya in 2004. (Anggraeni et al., 2021).

Chikungunya outbreaks in Indonesia occurred in around 24 areas from 2001-2003. Then in 2009 and 2010, outbreaks of chikungunya broke out in Western and Central Indonesia, and cases increased from around 3,000 per year to 83,000 and 52,000 cases per year, respectively. After 2010, detected cases fell to 3,000 per year (Arif et al., 2020). The number of chikungunya cases in Indonesia was 5,042 cases in 2019. Deaths due to chikungunya have not been reported to date. Provinces that have reported chikungunya outbreaks include North Sumatra, West Java, Central Java, Bali, West Kalimantan. Purbalingga Regency is one of 17 regencies in Central Java which is an endemic area of chikungunya. The number of chikungunya cases in Purbalingga Regency in 2020 was reported as 116 cases, increasing to 512 cases until April 2021 (Pramestuti et al., 2021).

Re-emerging chikungunya virus showed higher affinity for *Aedes albopictus* and more precisely a change in the extrinsic incubation period to become more infectious and lethal after additional mutations in Kerala, India. This virus spread east to the entire continent of Southeast Asia. Currently, the ECSA-IOL genotype is circulating in many Asian countries (Anggraeni et al., 2021).

Hepatitis E

Hepatitis is caused by hepatitis E virus (HEV) which has a reservoir host, namely mice. It is estimated that HEV infection in humans worldwide annually includes 3 million cases with 70,000 deaths. The case fatality rate (CFR) due to HEV infection in adolescents and adults ranges from 0.5 to 3% while in pregnant women it can reach 30% (Mulyono et al., 2019). Meanwhile, WHO estimates that hepatitis E caused around 44,000 deaths in 2015 (accounting for 3.3% of deaths due to hepatitis virus. In Indonesia, HEV was first recognized among communities located along forest rivers in West Kalimantan (Bornea), with the outbreak (>2500 cases) which occurred in 1987. The second outbreak occurred in 1991 (>1500 cases) in a nearby area (Sedyaningsih-Mamahit et al., 2002).

This virus has at least 4 different types: genotypes 1, 2, 3 and 4. Genotypes 1 and 2 are found only in humans. Genotypes 3 and 4 circulate in several animals including pigs, wild boars and deer without causing any disease, and occasionally infect humans. The virus is shed in the feces of an infected person and enters the human body through the intestines. It is transmitted mainly through contaminated drinking water. The infection usually clears

up on its own and clears up in 2-6 weeks. Sometimes a serious illness known as fulminant hepatitis (acute liver failure) develops, which can be fatal (WHO, 2021).

The incubation period after exposure to HEV ranges from 2 to 10 weeks, with an average of 5 to 6 weeks. An infected person sheds the virus from a few days before to 3-4 weeks after the onset of the disease. In areas of high disease endemicity, symptomatic infection is most common in young adults aged 15-40 years. In these areas, although infection occurs in children, it often goes undiagnosed because they usually have no symptoms or only mild disease without jaundice (WHO, 2021).

Rabies

Rabies is a deadly disease that is transmitted from animals to humans and attacks the central nervous system. Dogs are the main source of transmission of rabies to humans through saliva containing the rabies virus. About 99% of human deaths infected with rabies are caused by dog bites. Losses incurred in areas infected with rabies include death and reduced productivity of exposed humans and livestock, high costs of investigation and control, and high costs of post-exposure treatment (Hidayati et al., 2019).

Currently, cases of disease transmission from animals to humans are still a serious threat to public health. One of the diseases of animal origin that are still dangerous for humans is rabies. Approximately 55,000 people die each year from rabies, and 45% are from Southeast Asia. Rabies in Indonesia has spread in 25 provinces until 2017. Based on data from the Directorate General of Disease Prevention and Control (P2P) of the Directorate for Control of Zoonotic Vector Infectious Diseases, in 2017 cases of death due to rabies (Lyssa virus) decreased by around 27.12%. Cases of Rabies Contagious Animal Bites (GHPR) in 2016 only decreased by 19.44% to 64,774 reports. The number of rabies-free provinces as of 2017 was 9 provinces, namely 5 historically free provinces (Papua, West Papua, Bangka Belitung, Riau Islands, and West Nusa Tenggara) and 4 exempted provinces (Central Java, Special Region of Yogyakarta, East Java, and DKI Jakarta). This condition requires more mature strategic planning for the 26 provinces in Indonesia which are still endemic. Rabies itself has existed in Indonesia since the 18th century (Novita, 2019).

Conclusion

Based on the description above, it can be concluded that there are several emerging and reemerging zoonotic diseases caused by viruses that are endemic in Indonesia, namely Covid-19, avian influenza, swine influenza, dengue, chikungunya, hepatitis E, and rabies.

Acknowledgments

The author would like to thank the editor-in-chief of the Indonesian Veterinary Research journal so that this journal can be published. The author also expresses his gratitude to various parties who have contributed ideas to improve the publication of this journal.

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