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# Review a brief history of coronaviruses in Thailand

Duncan R. Smith

Molecular Pathology Laboratory, Institute of Molecular Biosciences, Mahidol University, 25/25 Phutthamonthon Sai 4 Road, Salaya, Nakhon Pathom, 73170, Thailand

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## ABSTRACT

As with many countries around the world, Thailand is currently experiencing restrictions to daily life as a consequence of the worldwide transmission of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). SARS-CoV-2 is the third respiratory syndrome coronavirus to be introduced into Thailand, following previous importation of cases of the severe acute respiratory syndrome coronavirus (SARS) and the Middle East respiratory syndrome coronavirus (MERS). Unlike SARS and MERS, SARS-CoV-2 was able to establish local transmission in Thailand. In addition to the imported coronaviruses, Thailand has a number of endemic coronaviruses that can affect livestock and pet species, can be found in bats, as well as four human coronaviruses that are mostly associated with the common cold. This article seeks to review what is known on both the endemic and imported coronaviruses in Thailand.

## 1. Introduction

The world is currently undergoing a pandemic of historic proportions. The pandemic is driven by the spread of a novel virus, the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), which results in a range of symptoms and a disease termed Covid-19. The virus is a member of the species *Severe acute respiratory syndrome-related coronavirus*, which is a member of the genus *Betacoronavirus* of the family *Coronaviridae* (*Coronaviridae Study Group of the International Committee on Taxonomy, 2020*). At the time of finalizing this article (1st August 2020), more than 17 million people have been reported to have been infected worldwide, resulting in more than 660,000 deaths (*WHO, 2020a*). The first cases of human transmission of this virus are believed to have occurred in Wuhan, China with the first cases being reported in December 2019 (*Huang et al., 2020*). Thailand was the first country outside of China to report a case (imported) of SARS-CoV-2 infection of a visiting tourist which occurred in January 2020 (*WHO, 2020c*). Since then some 3312 cases of locally acquired and imported infection have been reported in Thailand (*WHO, 2020a*). SARS-CoV-2 is the third highly pathogenic respiratory coronavirus to have been imported by travelers to Thailand, with the prior importation of both the severe acute respiratory syndrome coronavirus (SARS; family *Coronaviridae*, genus *Betacoronavirus*, species *Severe acute respiratory syndrome-related coronavirus*) and the Middle East respiratory syndrome coronavirus (MERS; family *Coronaviridae*, genus *Betacoronavirus*, species *Middle East respiratory syndrome-related coronavirus*).

Thailand is located in Southeast Asia, and it shares borders with

Malaysia to the south, Myanmar to the west and northwest, Laos to the east and northeast and Cambodia to the southeast. The population of Thailand is just under 67 million (*Anon, 2020c*), but the country houses an additional several million migrant workers, mostly from neighboring countries (*Anon, 2019*). Importantly however, Thailand is a major tourism destination, and in 2019 slightly under 40 million people from countries around the world visited Thailand (*Anon, 2020b*). This significant population flux leaves Thailand relatively open to the importation of novel pathogenic viruses through asymptomatic, or minimally symptomatic, infectious visitors.

## 2. The coronaviridae

The family *Coronaviridae* contains 2 subfamilies, 5 genera and 46 species of virus (*Walker et al., 2019*). The first subfamily, *Letovirinae* contains only one genus (*Alphaletovirus*) which has only a single virus species (*Microhyla letovirus 1*) which infects amphibians (*Bukhari et al., 2018*). In contrast, the second subfamily, *Orthocoronavirinae*, contains the remaining 45 viral species in this family distributed in four genera (*Alphacoronavirus*, *Betacoronavirus*, *Deltacoronavirus* and *Gammacoronavirus*). The viruses in this family have a positive sense, single stranded RNA genome that can vary from 26.4–31.7 kb, making them amongst the largest RNA genomes (*Payne, 2017*). The genome is capped and polyadenylated, and possesses 5'- and 3'- untranslated regions as well as multiple open reading frames (*Payne, 2017*). Viruses in the subfamily *Orthocoronavirinae* can infect a range of birds and mammals and proposed infection routes include fomites, aerosols and oral-fecal

E-mail address: [duncan.smi@mahidol.ac.th](mailto:duncan.smi@mahidol.ac.th).

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transmission, depending upon the specific virus. While the primary reservoirs for coronaviruses are animals, some coronaviruses are zoonotic, able to establish infection in humans, resulting in human-to-human transmission, and to date seven human coronaviruses have been identified (Chen et al., 2020). Across the subfamily *Orthocoronavirinae*, the viruses primarily target respiratory and enteric epithelial cells (Holmes, 1999), consistent with their modes of transmission, and infection generally result in broadly gastrointestinal or respiratory manifestations, albeit that these manifestations may be associated with a range of other symptoms.

### 3. Endemic animal coronaviruses in Thailand

A number of both animal and human coronaviruses have been shown to circulate in Thailand. Animal coronaviruses include those of domesticated animals including livestock (cattle, pigs and chickens) and pets (cats and dogs). In addition, bats in Thailand have been shown to harbor a number of different coronaviruses. Human coronaviruses (HCoV) endemic in Thailand include HCoV-229E, HCoV-OC43, HCoV-NL63 and HCoV-HKU1.

Two coronaviruses that affect pigs in Thailand have been identified, namely Porcine epidemic diarrhea virus (PEDV; Subfamily *Orthocoronavirinae*, genus *Alphacoronavirus*, species *Porcine epidemic diarrhea virus*) and Porcine deltacoronavirus (PDCoV; Subfamily *Orthocoronavirinae*, genus *Alphacoronavirus*, species *Coronavirus HKU15*). PEDV was first discovered in 1977 after an outbreak of diarrhea affecting pigs in pig farms in Belgium, and while the virus affects pigs of all ages, mortality is higher in younger pigs and piglets (Pensaert and de Bouck, 1978). PEDV was first detected in Thailand in 1995, although the outbreak was relatively confined (Srinuntapunt et al., 1995). PEDV subsequently emerged in 2007 in pig farms in Nakhon Pathom province, a high density pig farming area in Thailand (Puranaveja et al., 2009). Since then continued circulation of PEDV has been confirmed in studies looking at samples from 2008 to 2012 (Temeeyasen et al., 2014), 2008–2015 (Stott et al., 2017) and 2011–2016 (Tuanthap et al., 2019). PDCoV was originally identified in pigs in Hong Kong in 2012 (Woo et al., 2012), and subsequently in Ohio, USA (Wang et al., 2014), South Korea (Lee and Lee, 2014) and China (Dong et al., 2015; Song et al., 2015). PDCoV was first detected in pig farms in an eastern province of Thailand in 2015 (Janetanakit et al., 2016; Lorsirigool et al., 2017), however interestingly, subsequent evolutionary analysis suggested that Thai strains, as well as those from neighboring countries were somewhat evolutionarily distinct from both the USA and China strains (Saeng-Chuto et al., 2017a, b).

Bovine coronavirus (BCoV; Subfamily *Orthocoronavirinae*, genus *Betacoronavirus*, species *Betacoronavirus 1*) was originally identified by Mebus and colleagues during trials of a vaccine for bovine rotavirus (Mebus et al., 1973a, b; Mebus et al., 1972; Stair et al., 1972). Infection of BCoV in cattle is associated with enteric diarrhoea in calves, and winter dysentery in adult cattle (Hodnik et al., 2020), and the virus can infect both wild and domesticated ruminants (Salem et al., 2020). While a role for BCoV in enteric disease is well established, the virus may also play a role in the disease bovine respiratory disease complex (Ellis, 2019). There is little data on the prevalence of this virus in Thailand. However, an early study (Aiumlamai et al., 1992) suggested the presence of antibodies to BCoV in a high proportion of bulk milk samples collected in Muaklek (Saraburi province, Thailand), while molecular confirmation of circulation of BCoV was shown with the detection of the virus by PCR in three of 25 diarrheic fecal samples collected from cattle in the central region of Thailand (Singasa et al., 2017). Given the economic importance of this virus (Hodnik et al., 2020), further surveillance is warranted.

Infectious bronchitis virus (IBV; Subfamily *Orthocoronavirinae*, genus *Gammacoronavirus*, species *Avian coronavirus*) causes the severe poultry disease infectious bronchitis (Bande et al., 2016). The disease was first observed in North Dakota USA in 1930 (Schalk and Hawn, 1931), and

the virus was first propagated in embryonating eggs in 1937 (Beaudette and Hudson, 1937), making it the first coronavirus to be cultured. Unlike porcine and bovine coronaviruses where the symptoms are predominantly enteric, IBV infection primarily manifests as a respiratory disease, although involvement of the kidneys and reproductive track can also occur (Bande et al., 2016). The virus is present worldwide and causes significant economic losses (Cavanagh, 2007). In addition, some studies have suggested that pheasants may also be susceptible to this virus (Liebing et al., 2020). In Thailand infectious bronchitis in chickens was first reported in 1962 (Chindavanig, 1962), and outbreaks have occurred continuously since that time (Antarasena et al., 1990; Munyahongse et al., 2020; Pohuang et al., 2009, 2011; Promkuntod et al., 2015; Upatoom et al., 1983) despite the use of vaccination, possibly due to strain specific vaccine breakthrough (Jordan, 2017).

Coronaviruses in Thailand can affect both cats and dogs. Dogs can harbor two unrelated coronaviruses. The first, canine coronavirus (CCoV; Subfamily *Orthocoronavirinae*, genus *Alphacoronavirus*, species *Alphacoronavirus 1*) was originally identified in 1971 during an outbreak of diarrhea in military dogs in Germany (Binn et al., 1974). Since then the distribution has been established to be worldwide (Decaro and Buonavoglia, 2008). The second canine coronavirus, canine respiratory coronavirus (CRCoV; Subfamily *Orthocoronavirinae*, genus *Betacoronavirus*, species *Betacoronavirus 1*) associated with the respiratory disease kennel cough was first identified in the United Kingdom in 2003 (Erles et al., 2003), and is also found widely distributed (Priestnall et al., 2006). Studies have shown that both CCoV (Sakulwira et al., 2003; Tingpalapong et al., 1982) and CRCoV (Piewbang et al., 2017; Pohuang et al., 2009) are circulating in Thailand. Feline infectious peritonitis (FIP) is a common disease in cats that can be fatal in kittens (Tekes and Thiel, 2016). While FIP was first described in 1963 (Holzworth, 1963), it was not until 1979 that the causative agent was determined to be a coronavirus (O'Reilly et al., 1979) originally termed feline infectious peritonitis virus, but now known as feline coronavirus (FCoV; Subfamily *Orthocoronavirinae*, genus *Alphacoronavirus*, species *Alphacoronavirus 1*), a virus belonging to the same viral species as CCoV. Infection with FCoV is believed to be generally asymptomatic or to cause only mild enteric symptoms, but in a proportion of cases of infection the virus can undergo changes to cause the more severe FIP causing biotype (Licitra et al., 2013). The first molecular evidence of the circulation of FCoV in cats in Thailand was in 2009 (Manasateinkij et al., 2009), and other studies have confirmed this observation (Techangamsuwan et al., 2012, 2013).

Bats have long been known to be a natural reservoir for many viruses. One study in the Indian Flying Fox (*Pteropus giganteus*) found evidence for 55 viruses from nine viral families (Anthony et al., 2013), and viruses known to have a natural reservoir in bats include rabies virus (family *Rhabdoviridae*, genus *Lyssavirus*, species *Rabies lyssavirus* (Pawan, 1948)), Nipah virus (family *Paramyxoviridae*, genus *Henipavirus*, species *Nipah henipavirus* (Yob et al., 2001)) and Ebola virus (family *Filoviridae*, genus *Ebolavirus*, species *Zaire ebolavirus* (Leroy et al., 2005)). The tolerance of bats to viruses possibly results from a robust interferon response, coupled with a reduced inflammatory response (Gorbunova et al., 2020). Somewhat surprisingly, the presence of coronaviruses in bats was not established until 2005 (Lau et al., 2005; Li et al., 2005) in surveys of wildlife undertaken in response to the 2003 SARS epidemic. Currently (23/7/2020), some 4460 bat coronavirus sequences from around the world have been deposited in the database of bat-associated viruses (Chen et al., 2014) with sequences originating from a number of different bat species, and at least 30 bat-associated coronaviruses have been fully sequenced (Wong et al., 2019). Importantly, bats are believed to be the original source for many coronaviruses that affect both animals and humans (Corman et al., 2018). In Thailand the first report of bat associated coronaviruses was in a study on bat guano (Wacharapluesadee et al., 2013) which detected group C coronaviruses (currently *Orthocoronavirinae*, genus *Betacoronavirus*, subgenus *Merbecovirus*). Subsequent studies by the same group identified a number of alpha- and betacoronaviruses in as many as 14 different bat species

(Wacharapluesadee et al., 2018, 2015).

#### 4. Endemic human coronaviruses in Thailand

The first human coronavirus, B814, was identified in a study of common colds amongst children in a residential boys' school undertaken between June 14, 1960, and June 13, 1961 (Kendall et al., 1962). The virus initially proved unculturable in the systems used at the time, but the virus was used to infect 3/7 volunteers (Kendall et al., 1962). Subsequent studies were able to develop an organ based tissue culture system that allowed propagation (Tyrrell and Bynoe, 1965). At about the same time a study undertaken in medical students at the University of Chicago identified five novel agents, of which four were isolated from students with mild upper respiratory disease (Hamre and Procknow, 1966). The agents isolated in this study included one designated 229E, which would later become the species type virus (Subfamily *Orthocoronavirinae*, genus *Alphacoronavirus*, species *Human coronavirus 229E*). However, it was not until the electron microscopy study of Almeida and Tyrrell (Almeida and Tyrrell, 1967) that B814, 229E and avian infectious bronchitis virus were shown to be essentially morphologically identical.

A virus belonging to a second species of human coronavirus, HCoV-OC43 (Subfamily *Orthocoronavirinae*, genus *Betacoronavirus*, species *Betacoronavirus 1*) was isolated from respiratory specimens that had originally failed to show evidence of any virus, by using a tracheal organ culture system (McIntosh et al., 1967b). The virus was subsequently adapted to growth in suckling mouse brain (McIntosh et al., 1967a), and it was shown that this virus was serologically distinct from HCoV-229E, but had a "one-way serologic relationship" with strains of mouse hepatitis virus (Subfamily *Orthocoronavirinae*, genus *Betacoronavirus*, species *Murine coronavirus*), that had been identified in by Cheever and Daniels in 1949 (Cheever and Daniels, 1949), and independently by Gledhill and Andrewes in 1951 (Gledhill and Andrewes, 1951).

Coronaviruses belonging to two more species, namely HCoV-NL63 (Subfamily *Orthocoronavirinae*, genus *Alphacoronavirus*, species *Human coronavirus NL63*) and HCoV-HKU1 ((Subfamily *Orthocoronavirinae*, genus *Betacoronavirus*, species *Human coronavirus HKU1*) were isolated in 2004 and 2005 respectively. HCoV-NL63 was first isolated by two groups almost simultaneously in the Netherlands (Fouchier et al., 2004; van der Hoek et al., 2004), and in both cases the virus was isolated from children less than a year old, while HCoV-HKU1 was first isolated in Hong Kong from a 71 year old man who had recently returned from China (Woo et al., 2005). Markedly, both HCoV-NL63 and HCoV-HKU1 were identified after the 2003 SARS outbreak. The four endemic coronaviruses are believed to be broadly distributed around the world, and they are mostly associated with the common cold, although in some cases, and particularly in immunocompromised patients, the disease can be more severe (McIntosh and Peiris, 2009).

A number of studies have shown evidence of circulation of human coronaviruses in Thailand, and all four endemic HCoVs have been shown to be present. Two studies have detected all four endemic HCoVs in patients with pneumonia (Dare et al., 2007) and in patients with respiratory infection in southern Thailand (Suwannakarn et al., 2014). Theamboonlers and colleagues (Theamboonlers et al., 2007) looked for HCoV-OC43 and HCoV-229E in 226 children with acute lower respiratory tract infections and found 8 cases of HCoV-229E and 2 cases of HCoV-OC43 as well as one co-infection. Similarly, HCoV-OC43 and HCoV-229E were detected in respiratory samples from suspected influenza cases (Wertheim et al., 2015). HCoV-OC43 was detected in US military personnel with fever and respiratory symptoms or diagnosed with pneumonia who were stationed in Thailand for the 2003 Cobra Gold military exercise (Fuller et al., 2006), and HCoV-229E has been detected in Thai military recruits with respiratory illness (Levy et al., 2015). Uncharacterized human coronaviruses have been variously detected in children with community acquired pneumonia (Pratheepamornkull et al., 2015) and in samples from patients with influenza-like

illness (Horthongkham et al., 2014). HCoVs in Thai children were also found in a large multi-center, multi-country study of respiratory viruses and influenza-like illness, and while all four endemic viruses were detected across the study, there was no country specific breakdown of coronavirus species detected (Taylor et al., 2017). Most recently, a HCoV-HKU1 virus was detected in a non-ill bat guano miner (Joyjinda et al., 2019). All of these studies support the ongoing circulation of these HCoVs, and their association with respiratory illness.

#### 5. Coronaviruses imported to Thailand

In addition to the four human endemic coronaviruses, three human coronaviruses, SARS, MERS and SARS-CoV-2 have been imported into Thailand. However, only one of these viruses, SARS-CoV-2, has established local transmission. SARS cases are believed to have first occurred in the city of Foshan, Guangdong Province, Southern China in November 2002 (Xu et al., 2004). A physician from southern China who attended a conference in Hong Kong is believed to be the index patient (Hui and Chan, 2010) for the outbreak of SARS that occurred in Hong Kong (Lee et al., 2003), as well as in other countries including Canada (Booth et al., 2003), Singapore (Hsu et al., 2003) and Vietnam (Nishiyama et al., 2008). In total, some 8096 cases and 774 deaths occurred around the world (as cited in (Shaw, 2006)). Ancestor viruses of SARS were subsequently identified in bats (Lau et al., 2005; Li et al., 2005), although it is probable that the bat SARS virus had first jumped species to palm civets before transmission to humans (Wang and Eaton, 2007). SARS was first introduced into Thailand by a World Health Organization physician (who subsequently died of his disease) who had treated a SARS patient in Vietnam, (Chaovavanich et al., 2004). By the end of the outbreak, a further 8 cases had been identified, all of which were imported, and of the nine infected people, two died (ProMed-Mail, 2003) and there were no reports of local transmission.

The first known case of MERS occurred in an elderly man who was admitted to a hospital in Jeddah, Saudi Arabia in 2012 (Zaki et al., 2012). The virus (MERS-CoV) was isolated from sputum samples of the patient, and subjected to sequencing analysis which identified the agent as a *Betacoronavirus* (Zaki et al., 2012). Some three months later, a novel coronavirus, that was subsequently shown to have high homology to the Saudi Arabian isolate, was identified in a Qatari national with a history of travel to Saudi Arabia upon his hospitalization in UK (Bermingham et al., 2012). By the end of January 2020 some 2519 laboratory-confirmed cases of MERS, including 866 associated deaths have been reported worldwide, albeit that the majority of cases (2121 cases) have occurred in Saudi Arabia (WHO, 2020b). Dromedary camels have been implicated as the main zoonotic reservoir (Elfadil et al., 2018), with African bats as the likely ancestral reservoir host for MERS-CoV (Goldstein and Weiss, 2017). MERS has been imported to Thailand three times, and again, in no case has local transmission occurred. The first case occurred in a 75-year-old Omani man who had travelled to Thailand to seek medical attention for a heart condition in June 2015 (Plipat et al., 2017; Suttha et al., 2018). Upon initial screening at a private hospital in Bangkok, the patient was diagnosed with suspected pneumonia, and given his history of recent travel from the Middle East, MERS was suspected. However, it was only in the third day of hospitalization that MERS infection was confirmed, and the patient was transferred to the Thai Ministry of Public Health designated priority hospital (Bamrasnaradura Infectious Diseases Institute, Bangkok) for MERS patients and those suspected to be infected with MERS (Plipat et al., 2017; Suttha et al., 2018). The second importation of MERS to Thailand also occurred in an elderly Omani man visiting Thailand for medical reasons in June 2016, while the third case was an 18 year old Kuwaiti man visiting Thailand for a vacation in July 2016 (Suttha et al., 2018). All three cases were treated at the Bamrasnaradura Infectious Diseases Institute, and all three survived their infection. Markedly, the case fatality rate for MERS infection is believed to be around 35 % (Guarner, 2020). As with the cases of SARS imported to Thailand, no case of local transmission of



MERS has been reported.

As noted earlier, the first case of SARS-CoV-2 infection reported outside of China occurred in January 2020 in Thailand (WHO, 2020c), and since then some 3312 cases of locally acquired and imported SARS-CoV-2 infection and 58 deaths have been reported (as of 1st August 2020; (WHO, 2020a)). Unlike both SARS and MERS, there have been a number of cases of community acquired infection. However, the fact that in 7 months only slightly over 3000 cases have been detected is quite remarkable. In dramatic contrast, the first cases of SARS-CoV-2 infection in the United Kingdom (a country of an approximately similar population size to Thailand) were detected in late January 2020 (Lillie et al., 2020), and as of 1st August 2020 the United Kingdom has reported some 303,185 infections and 46,119 deaths (as of 1st August 2020; (WHO, 2020a)). The reasons for the great discrepancy in infection rates remains unknown. However, Thailand has a long history of dealing with infectious diseases (Aungkulanon et al., 2012) and part of the strategy are the village health volunteers, or community health workers who act at a grassroots level (Kauffman and Myers, 1997) and more than one million of these volunteers were engaged in the response to SARS-CoV-2 (Anon, 2020a). In addition, the Thai government instituted a strong lockdown, with the closure of most businesses, schools and universities, as well as limits on movement between provinces. Social aspects that may have contributed to the low spread of the disease include the traditional, non-contact greeting of the “Wai” as well as a high rate of mask compliance in public.

## 6. Conclusions

Thailand has a number of endemic coronaviruses, and has seen the repeated importation of severe respiratory disease associated coronaviruses. For the endemic viruses, the coronaviruses found in bats represent a particular concern as all three severe respiratory disease associated viruses (SARS, MERS and SARS-CoV-2) are believed to have an ancestor in bats, albeit with possible transmission to other species before emerging in humans (Boni et al., 2020; Corman et al., 2018). Thus there is the potential for an endemic, severe respiratory disease associated virus to arise in Thailand. Given the large population flux in Thailand, there is always the risk of importation of viruses that have a significant risk to the Thai population. These include not only coronaviruses, but other viruses such as highly pathogenic avian influenza viruses and Ebola. On the positive side, Thailand has shown a remarkable track record in controlling disease spread when importation of a highly transmissible virus has occurred. In particular, with both SARS and MERS there was no reported transmission to healthcare workers, unlike the situation in some other countries (Suwantar and Apisantharak, 2015). While the situation in Thailand currently looks positive with no community transmission for around nine weeks (as of 1st August 2020), the easing of restrictions on businesses, travel and education will need to be carefully monitored.

## Author statement

Duncan R. Smith is the sole author, and no other person contributed to the review. The author has no conflict of interest.

## Declaration of Competing Interest

None.

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## References

- Zaki, A.M., van Boheemen, S., Bestebroer, T.M., Osterhaus, A.D., Fouchier, R.A., 2012. Isolation of a novel coronavirus from a man with pneumonia in Saudi Arabia. *N. Engl. J. Med.* 367, 1814–1820.
- Aiumlamai, S., Alenius, S., Nithichai, K., 1992. Prevalence of antibodies to various bovine viruses in bulk tank milk samples from dairy herds in Muaklek area. *Thai J Vet Med* 22, 112–119.
- Almeida, J.D., Tyrrell, D.A., 1967. The morphology of three previously uncharacterized human respiratory viruses that grow in organ culture. *J. Gen. Virol.* 1, 175–178.
- Anon, 2019. Thailand migration report 2019. In: Thailand, United Nations Thematic Working Group on Migration in Thailand. Bangkok, Thailand. Accessed 1st August 2020. [https://thailand.iom.int/sites/default/files/document/publications/Thailand%20Report%202019\\_22012019\\_HiRes.pdf](https://thailand.iom.int/sites/default/files/document/publications/Thailand%20Report%202019_22012019_HiRes.pdf).
- Anon, 2020a. Information on covid-19: Thailand's ungowned and unsung heroes play significant roles in battling covid-19. Department of Protocol, Ministry of Foreign Affairs of the Kingdom of Thailand, Bangkok, Thailand. Thailand's-Ungowned-and-Ungown-Heroes-Play-Si.html (Accessed 1<sup>st</sup> August 2020). <http://www.mfa.go.th/protocol/en/news/4853/119261>.
- Anon, 2020b. International Tourists Arrivals to Thailand 2019 (Jan - Dec). Ministry of Tourism and Sports, Bangkok, Thailand. Accessed 1st August 2020. [https://www.mots.go.th/more\\_news\\_new.php?cid=527](https://www.mots.go.th/more_news_new.php?cid=527).
- Anon, 2020c. Thailand in brief. Thailand Board of Investment, Bangkok, Thailand. Accessed 1st August 2020. <https://www.boi.go.th/index.php?page=demographic>.
- Antarasena, C., Sahapong, S., Aowcharoen, B., Choe-ngern, N., Kongkanunt, R., 1990. Avian infectious bronchitis in the Southern part of Thailand. *Songklanakarin J. Sci. Technol.* 12, 273–279.
- Anthony, S.J., Epstein, J.H., Murray, K.A., Navarrete-Macias, I., Zambrana-Torrel, C. M., Solovoyov, A., Ojeda-Flores, R., Arrigo, N.C., Islam, A., Ali Khan, S., Hosseini, P., Bogich, T.L., Olival, K.J., Sanchez-Leon, M.D., Karesh, W.B., Goldstein, T., Luby, S.P., Morse, S.S., Mazet, J.A., Daszak, P., Lipkin, W.I., 2013. A strategy to estimate unknown viral diversity in mammals. *mBio* 4, e00598–13.
- Aungkulanon, S., McCarron, M., Lertindumrong, J., Olsen, S.J., Bundhamcharoen, K., 2012. Infectious disease mortality rates, Thailand, 1958–2009. *Emerg. Infect. Dis.* 18, 1794–1801.
- Bande, F., Arshad, S.S., Omar, A.R., Bejo, M.H., Abubakar, M.S., Abba, Y., 2016. Pathogenesis and diagnostic approaches of avian infectious bronchitis. *Adv. Virol.* 2016, 4621659.
- Beaudette, F.R., Hudson, C.B., 1937. Cultivation of the virus of infectious bronchitis. *J. Am. Vet. Med. Assoc.* 90, 51–60.
- Birmingham, A., Chand, M.A., Brown, C.S., Aarons, E., Tong, C., Langrish, C., Hoshler, K., Brown, K., Galiano, M., Myers, R., Pebody, R.G., Green, H.K., Boddington, N.L., Gopal, R., Price, N., Newsholme, W., Drosten, C., Fouchier, R.A., Zambon, M., 2012. Severe respiratory illness caused by a novel coronavirus, in a patient transferred to the United Kingdom from the Middle East, September 2012. *Euro Surveill.* 17, 20290.
- Binn, L.N., Lazar, E.C., Keenan, K.P., Huxsoll, D.L., Marchwicki, R.H., Strano, A.J., 1974. Recovery and characterization of a coronavirus from military dogs with diarrhea. *Proc. Annu. Meet. U. S. Anim. Health Assoc.* 359–366.
- Boni, M.F., Lemey, P., Jiang, X., Lam, T.T., Perry, B.W., Castoe, T.A., Rambaut, A., Robertson, D.L., 2020. Evolutionary origins of the SARS-CoV-2 sarbecovirus lineage responsible for the COVID-19 pandemic. *Nat. Microbiol.* 5, 1408–1417.
- Booth, C.M., Matukas, L.M., Tomlinson, G.A., Rachlis, A.R., Rose, D.B., Dwosh, H.A., Walmsley, S.L., Mazzulli, T., Avendano, M., Derkach, P., Ephantimos, I.E., Kitai, I., Mederski, B.D., Shadowitz, S.B., Gold, W.L., Hawrylyck, L.A., Rea, E., Chenkin, J.S., Cescon, D.W., Poutanen, S.M., Detsky, A.S., 2003. Clinical features and short-term outcomes of 144 patients with SARS in the greater Toronto area. *JAMA* 289, 2801–2809.
- Bukhari, K., Mulley, G., Gulyaeva, A.A., Zhao, L., Shu, G., Jiang, J., Neuman, B.W., 2018. Description and initial characterization of metatranscriptomic nidovirus-like genomes from the proposed new family Abyssoviridae, and from a sister group to the Coronavirinae, the proposed genus Alphaletovirus. *Virology* 524, 160–171.
- Cavanagh, D., 2007. Coronavirus avian infectious bronchitis virus. *Vet. Res.* 38, 281–297.
- Chaovavanich, A., Wongsawat, J., Dowell, S.F., Inthong, Y., Sangsajja, C., Sanguanwongse, N., Martin, M.T., Limpakarnjanarat, K., Sirirat, L., Waicharoen, S., Chittaganpitch, M., Thawatsupha, P., Auwanit, W., Sawanpanyalert, P., Melgaard, B., 2004. Early containment of severe acute respiratory syndrome (SARS); experience from Bamrasnaradura Institute. *Thailand. J. Med. Assoc. Thai* 87, 1182–1187.
- Cheever, F.S., Daniels, J.B., et al., 1949. A murine virus (JHM) causing disseminated encephalomyelitis with extensive destruction of myelin. *J. Exp. Med.* 90, 181–210.
- Chen, L., Liu, B., Yang, J., Jin, Q., 2014. DBatVir: the database of bat-associated viruses. *Database (Oxford)*, 2014, bau021.
- Chen, B., Tian, E.K., He, B., Tian, L., Han, R., Wang, S., Xiang, Q., Zhang, S., El Arnaout, T., Cheng, W., 2020. Overview of lethal human coronaviruses. *Signal Transduct. Target. Ther.* 5, 89.
- Chindavanig, P., 1962. Studies on the attenuation of infectious bronchitis virus. *J. Thai Vet. Med. Assoc.* 12, 1–7.
- Corman, V.M., Muth, D., Niemeyer, D., Drosten, C., 2018. Hosts and sources of endemic human coronaviruses. *Adv. Virus Res.* 100, 163–188.

- Coronaviridae Study Group of the International Committee on Taxonomy, 2020. The species Severe acute respiratory syndrome-related coronavirus: classifying 2019-nCoV and naming it SARS-CoV-2. *Nat. Microbiol.* 5, 536–544.
- Dare, R.K., Fry, A.M., Chittaganpitch, M., Sawanpanyaler, P., Olsen, S.J., Erdman, D.D., 2007. Human coronavirus infections in rural Thailand: a comprehensive study using real-time reverse-transcription polymerase chain reaction assays. *J. Infect. Dis.* 196, 1321–1328.
- Decaro, N., Buonavoglia, C., 2008. An update on canine coronaviruses: viral evolution and pathobiology. *Vet. Microbiol.* 132, 221–234.
- Dong, N., Fang, L., Zeng, S., Sun, Q., Chen, H., Xiao, S., 2015. Porcine deltacoronavirus in Mainland China. *Emerg. Infect. Dis.* 21, 2254–2255.
- Elfadil, A.A., Ahmed, A.G., Abdalla, M.O., Gumaa, E., Osman, O.H., Younis, A.E., Abu-Obeida, A., Al-Hafufi, A.N., Saif, L.J., Zaki, A., Al-Rumaihi, A., Al-Harbi, N., Kasem, S., Al-Brahim, R.H., Al-Sahhaf, A., Bayoumi, F.E., Al-Dowairij, A., Qasim, I. A., 2018. Epidemiological study of Middle East respiratory syndrome coronavirus infection in dromedary camels in Saudi Arabia, April–May 2015. *Rev. Sci. Tech.* 37, 985–997.
- Ellis, J., 2019. What is the evidence that bovine coronavirus is a biologically significant respiratory pathogen in cattle? *Can. Vet. J.* 60, 147–152.
- Erls, K., Toomey, C., Brooks, H.W., Brownlie, J., 2003. Detection of a group 2 coronavirus in dogs with canine infectious respiratory disease. *Virology* 310, 216–223.
- Fouchier, R.A., Hartwig, N.G., Bestebroer, T.M., Niemeyer, B., de Jong, J.C., Simon, J.H., Osterhaus, A.D., 2004. A previously undescribed coronavirus associated with respiratory disease in humans. *Proc. Natl. Acad. Sci. U. S. A.* 101, 6212–6216.
- Fuller, J., Hanley, K., Schultz, R., Lewis, M., Freed, N.E., Ellis, M., Ngaury, V., Stoebner, R., Ryan, M., Russell, K., 2006. Surveillance for febrile respiratory infections during Cobra Gold 2003. *Mil. Med.* 171, 357–359.
- Gledhill, A.W., Andrewes, C.H., 1951. A hepatitis virus of mice. *Br. J. Exp. Pathol.* 32, 559–568.
- Goldstein, S.A., Weiss, S.R., 2017. Origins and pathogenesis of Middle East respiratory syndrome-associated coronavirus: recent advances. *F1000Res* 6, 1628.
- Gorbunova, V., Seluanov, A., Kennedy, B.K., 2020. The world goes bats: living longer and tolerating viruses. *Cell Metab.* 32, 31–43.
- Guarner, J., 2020. Three emerging coronaviruses in two decades. *Am. J. Clin. Pathol.* 153, 420–421.
- Hamre, D., Procknow, J.J., 1966. A new virus isolated from the human respiratory tract. *Proc. Soc. Exp. Biol. Med.* 121, 190–193.
- Hodnik, J.J., Jezek, J., Staric, J., 2020. Coronaviruses in cattle. *Trop. Anim. Health Prod.*
- Holmes, K.V., 1999. Coronaviruses (*Coronaviridae*). In: Granoff, A.W., R.G. (Eds.), *Encyclopedia of Virology* (Second Edition). Academic Press, Cambridge, MA, pp. 291–298.
- Holzworth, J., 1963. Some important disorders of cats. *Cornell Vet.* 53, 157–160.
- Horthongkham, N., Athipanyasilp, N., Sirijatuphat, R., Assanasen, S., Sutthent, R., 2014. Prevalence and molecular characterization of human metapneumovirus in influenza a negative sample in Thailand. *J. Clin. Lab. Anal.* 28, 398–404.
- Hsu, L.Y., Lee, C.C., Green, J.A., Ang, B., Paton, N.I., Lee, L., Villacian, J.S., Lim, P.L., Earnest, A., Leo, Y.S., 2003. Severe acute respiratory syndrome (SARS) in Singapore: clinical features of index patient and initial contacts. *Emerg. Infect. Dis.* 9, 713–717.
- Huang, C., Wang, Y., Li, X., Ren, L., Zhao, J., Hu, Y., Zhang, L., Fan, G., Xu, J., Gu, X., Cheng, Z., Yu, T., Xia, J., Wei, Y., Wu, W., Xie, X., Yin, W., Li, H., Liu, M., Xiao, Y., Gao, H., Guo, L., Xie, J., Wang, G., Jiang, R., Gao, Z., Jin, Q., Wang, J., Cao, B., 2020. Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. *Lancet* 395, 497–506.
- Hui, D.S., Chan, P.K., 2010. Severe acute respiratory syndrome and coronavirus. *Infect. Dis. Clin. North Am.* 24, 619–638.
- Janetanakit, T., Lumyai, M., Bunpapong, N., Boonyapisitsopa, S., Chaiyawong, S., Nonthabenjawan, N., Kesdaengsakonwut, S., Amonsin, A., 2016. Porcine Deltacoronavirus, Thailand, 2015. *Emerg. Infect. Dis.* 22, 757–759.
- Jordan, B., 2017. Vaccination against infectious bronchitis virus: a continuous challenge. *Vet. Microbiol.* 206, 137–143.
- Joyjinda, Y., Rodpan, A., Chartpituck, P., Suthum, K., Yaemsakul, S., Cheun-Arom, T., Bunprakob, S., Olival, K.J., Stokes, M.M., Hemachudha, T., Wacharapluesadee, S., 2019. First complete genome sequence of human coronavirus HKU1 from a nonill bat guano miner in Thailand. *Microbiol. Resour. Announc.* 8, e01457-18.
- Kauffman, K.S., Myers, D.H., 1997. The changing role of village health volunteers in northeast Thailand: an ethnographic field study. *Int. J. Nurs. Stud.* 34, 249–255.
- Kendall, E.J., Bynoe, M.L., Tyrrell, D.A., 1962. Virus isolations from common colds occurring in a residential school. *Br. Med. J.* 2, 82–86.
- Lau, S.K., Woo, P.C., Li, K.S., Huang, Y., Tsoi, H.W., Wong, B.H., Wong, S.S., Leung, S.Y., Chan, K.H., Yuen, K.Y., 2005. Severe acute respiratory syndrome coronavirus-like virus in Chinese horseshoe bats. *Proc. Natl. Acad. Sci. U. S. A.* 102, 14040–14045.
- Lee, S., Lee, C., 2014. Complete genome characterization of Korean porcine deltacoronavirus strain KOR/KNU14-04/2014. *Genome Announc.* 2, e01191-14.
- Lee, N., Hui, D., Wu, A., Chan, P., Cameron, P., Joynt, G.M., Ahuja, A., Yung, M.Y., Leung, C.B., To, K.F., Lui, S.F., Szeto, C.C., Chung, S., Sung, J.J., 2003. A major outbreak of severe acute respiratory syndrome in Hong Kong. *N. Engl. J. Med.* 348, 1986–1994.
- Leroy, E.M., Kumulungui, B., Pourrut, X., Rouquet, P., Hassanin, A., Yaba, P., Delicat, A., Paweska, J.T., Gonzalez, J.P., Swanepoel, R., 2005. Fruit bats as reservoirs of Ebola virus. *Nature* 438, 575–576.
- Levy, J.W., Bhoombonchoo, P., Simasathien, S., Salje, H., Huang, A., Rangsin, R., Jarman, R.G., Fernandez, S., Klungthong, C., Hussem, K., Gibbons, R.V., Yoon, I.K., 2015. Elevated transmission of upper respiratory illness among new recruits in military barracks in Thailand. *Influenza Other Respir. Viruses* 9, 308–314.
- Li, W., Shi, Z., Yu, M., Ren, W., Smith, C., Epstein, J.H., Wang, H., Crameri, G., Hu, Z., Zhang, H., Zhang, J., McEachern, J., Field, H., Daszak, P., Eaton, B.T., Zhang, S., Wang, L.F., 2005. Bats are natural reservoirs of SARS-like coronaviruses. *Science* 310, 676–679.
- Licitra, B.N., Millet, J.K., Regan, A.D., Hamilton, B.S., Rinaldi, V.D., Duhamel, G.E., Whittaker, G.R., 2013. Mutation in spike protein cleavage site and pathogenesis of feline coronavirus. *Emerg. Infect. Dis.* 19, 1066–1073.
- Liebing, J., Volker, I., Curland, N., Wohlsein, P., Baumgartner, W., Braune, S., Runge, M., Moss, A., Rautenschlein, S., Jung, A., Ryll, M., Raue, K., Strube, C., Schulz, J., Heffels-Redmann, U., Fischer, L., Gethoffer, F., Voigt, U., Lierz, M., Siebert, U., 2020. Health status of free-ranging ring-necked pheasant chicks (*Phasianus colchicus*) in North-Western Germany. *PLoS One* 15, e0234044.
- Lillie, P.J., Samson, A., Li, A., Adams, K., Capstick, R., Barlow, G.D., Easom, N., Hamilton, E., Moss, P.J., Evans, A., Ivan, M., Phe Incident, T., Taha, Y., Duncan, C.J. A., Schmid, M.L., The Airborne Hcid, N., 2020. Novel coronavirus disease (Covid-19): the first two patients in the UK with person to person transmission. *J. Infect.* 80, 578–606.
- Lorsirigool, A., Saeng-Chuto, K., Madapong, A., Temeeyasen, G., Tripipat, T., Kaewprommal, P., Tantituvanont, A., Piriyaopongsa, J., Nilubol, D., 2017. The genetic diversity and complete genome analysis of two novel porcine deltacoronavirus isolates in Thailand in 2015. *Virus Genes* 53, 240–248.
- Manasateinkij, W., Nilkumhang, P., Jaroensong, T., Noosud, J., Lekcharoensuk, C., Lekcharoensuk, P., 2009. Occurrence of feline coronavirus and feline infectious peritonitis virus in Thailand. *Kasetsart J. Soc. Sci.* 43, 720–726.
- McIntosh, K., Peiris, J.S.M., 2009. Coronaviruses. *J. Clin. Virol.* 1155–1171.
- McIntosh, K., Becker, W.B., Chanock, R.M., 1967a. Growth in suckling-mouse brain of "IBV-like" viruses from patients with upper respiratory tract disease. *Proc. Natl. Acad. Sci. U. S. A.* 58, 2268–2273.
- McIntosh, K., Dees, J.H., Becker, W.B., Kapikian, A.Z., Chanock, R.M., 1967b. Recovery in tracheal organ cultures of novel viruses from patients with respiratory disease. *Proc. Natl. Acad. Sci. U. S. A.* 57, 933–940.
- Mebus, C.A., White, R.G., Stair, E.L., Rhodes, M.B., Twiehaus, M.J., 1972. Neonatal calf diarrhea: results of a field trial using a reo-like virus vaccine. *Vet. Med. Small Anim. Clin.* 67, 173–174 passim.
- Mebus, C.A., Stair, E.L., Rhodes, M.B., Twiehaus, M.J., 1973a. Neonatal calf diarrhea: propagation, attenuation, and characteristics of a coronavirus-like agent. *Am. J. Vet. Res.* 34, 145–150.
- Mebus, C.A., Stair, E.L., Rhodes, M.B., Twiehaus, M.J., 1973b. Pathology of neonatal calf diarrhea induced by a coronavirus-like agent. *Vet. Pathol.* 10, 45–64.
- Munyahongse, S., Pohuang, T., Nonthabenjawan, N., Sasipreeyajan, J., Thontiravong, A., 2020. Genetic characterization of infectious bronchitis viruses in Thailand, 2014–2016: identification of a novel recombinant variant. *Poult. Sci.* 99, 1888–1895.
- Nishiyama, A., Wakasugi, N., Kirikae, T., Quy, T., Ha le, D., Ban, V.V., Long, H.T., Keicho, N., Sasazuki, T., Kuratsui, T., 2008. Risk factors for SARS infection within hospitals in Hanoi, Vietnam. *Jpn. J. Infect. Dis.* 61, 388–390.
- O'Reilly, K.J., Fishman, B., Hitchcock, L.M., 1979. Feline infectious peritonitis: isolation of a coronavirus. *Vet. Rec.* 104, 348.
- Pawan, J.L., 1948. Fruit-eating bats and paralytic rabies in Trinidad. *Ann. Trop. Med. Parasitol.* 42, 173–177.
- Payne, S., 2017. Family *Coronaviridae*. *Viruses* 2017, 149–158.
- Pensaert, M.B., de Bouck, P., 1978. A new coronavirus-like particle associated with diarrhea in swine. *Arch. Virol.* 58, 243–247.
- Piewbang, C., Rungsipipat, A., Poovorawan, Y., Techangamsuwan, S., 2017. Development and application of multiplex PCR assays for detection of virus-induced respiratory disease complex in dogs. *J. Vet. Med. Sci.* 78, 1847–1854.
- Plipat, T., Buathong, R., Wacharapluesadee, S., Siriariyapong, P., Pittayawonganon, C., Sangsajja, C., Kaewpom, T., Petcharap, S., Pongpint, J., Jumpasri, J., Joyjinda, Y., Rodpan, A., Ghai, S., Jitmittraphat, A., Khongwichtit, S., Smith, D.R., Corman, V.M., Drosten, C., Hemachudha, T., 2017. Imported case of Middle East respiratory syndrome coronavirus (MERS-CoV) infection from Oman to Thailand, June 2015. *Euro Surveill.* 22, 30598.
- Pohuang, T., Chansiripornchai, N., Tawatsin, A., Sasipreeyajan, J., 2009. Detection and molecular characterization of infectious bronchitis virus isolated from recent outbreaks in broiler flocks in Thailand. *J. Vet. Sci.* 10, 219–223.
- Pohuang, T., Chansiripornchai, N., Tawatsin, A., Sasipreeyajan, J., 2011. Sequence analysis of S1 genes of infectious bronchitis virus isolated in Thailand during 2008–2009: identification of natural recombination in the field isolates. *Virus Genes* 43, 254–260.
- Pratheepamornkull, T., Ratanakorn, W., Samransamruajkit, R., Poovorawan, Y., 2015. Causative agents of severe community acquired viral pneumonia among children in Eastern Thailand. *Southeast Asian J. Trop. Med. Public Health* 46, 650–656.
- Priestnall, S.L., Brownlie, J., Dubovi, E.J., Erls, K., 2006. Serological prevalence of canine respiratory coronavirus. *Vet. Microbiol.* 115, 43–53.
- ProMed-Mail, 2003. SARS - Worldwide (166): Cases (Archive Number 20030817.2061), International Society for Infectious Diseases.
- Promkuntod, N., Thongmee, S., Yoidam, S., 2015. Analysis of the S1 gene of the avian infectious bronchitis virus (IBV) reveals changes in the IBV genetic groups circulating in southern Thailand. *Res. Vet. Sci.* 100, 299–302.
- Puranaveja, S., Poolperm, P., Lertwatcharasarakul, P., Kesdaengsakonwut, S., Boonsongnern, A., Urairong, K., Kitikoon, P., Choojai, P., Kedkovid, R., Teankum, K., Thanawongnuwech, R., 2009. Chinese-like strain of porcine epidemic diarrhea virus. *Thai. Emerg. Infect. Dis.* 15, 1112–1115.
- Saeng-Chuto, K., Lorsirigool, A., Temeeyasen, G., Vui, D.T., Stott, C.J., Madapong, A., Tripipat, T., Wegner, M., Intrakamhaeng, M., Chongcharoen, W., Tantituvanont, A., Kaewprommal, P., Piriyaopongsa, J., Nilubol, D., 2017a. Different lineage of porcine

- deltacoronavirus in Thailand, Vietnam and lao PDR in 2015. *Transbound. Emerg. Dis.* 64, 3–10.
- Saeng-Chuto, K., Stott, C.J., Wegner, M., Senasuthum, R., Tantituvanont, A., Nilubol, D., 2017b. Retrospective investigation and evolutionary analysis of a novel porcine deltacoronavirus strain detected in Thailand from 2008 to 2015. *Arch. Virol.* 162, 2103–2108.
- Sakulwira, K., Vanapongtipagorn, P., Theamboonlers, A., Oraveerakul, K., Poovorawan, Y., 2003. Prevalence of canine coronavirus and parvovirus infections in dogs with gastroenteritis in Thailand. *Vet. Med. – Czech.* 48, 163–167.
- Salem, E., Dhanasekaran, V., Cassard, H., Hause, B., Maman, S., Meyer, G., Ducatez, M.F., 2020. Global transmission, spatial segregation, and recombination determine the long-term evolution and epidemiology of bovine coronaviruses. *Viruses* 12, 534.
- Schalk, A.F., Hawn, M.C., 1931. An apparently new respiratory disease of baby chicks. *J. Am. Vet. Assoc.* 78, 413–420.
- Shaw, K., 2006. The 2003 SARS outbreak and its impact on infection control practices. *Public Health* 120, 8–14.
- Singasa, K., Songserm, T., Lertwatcharasarakul, P., Arunvipas, P., 2017. Molecular and phylogenetic characterization of bovine coronavirus virus isolated from dairy cattle in Central Region, Thailand. *Trop. Anim. Health Prod.* 49, 1523–1529.
- Song, D., Zhou, X., Peng, Q., Chen, Y., Zhang, F., Huang, T., Zhang, T., Li, A., Huang, D., Wu, Q., He, H., Tang, Y., 2015. Newly emerged porcine deltacoronavirus associated with diarrhoea in swine in China: identification, prevalence and full-length genome sequence analysis. *Transbound. Emerg. Dis.* 62, 575–580.
- Srinuntapunt, S., Trongwongsa, L., Antarasena, C., Sangsuwan, W., Prommuang, P., 1995. Porcine epidemic diarrhoea in Trang province. *J. Thai Vet. Med. Assoc.* 46, 11–19.
- Stair, E.L., Rhodes, M.B., White, R.G., Mebus, C.A., 1972. Neonatal calf diarrhoea: purification and electron microscopy of a coronavirus-like agent. *Am. J. Vet. Res.* 33, 1147–1156.
- Stott, C.J., Temeeyasen, G., Tripipat, T., Kaewprommal, P., Tantituvanont, A., Piriyaopongsa, J., Nilubol, D., 2017. Evolutionary and epidemiological analyses based on spike genes of porcine epidemic diarrhoea virus circulating in Thailand in 2008–2015. *Infect. Genet. Evol.* 50, 70–76.
- Suttha, P., Sangsajja, C., Wiboonchutikul, S., Chitwarakorn, N., Ritsumrage, P., Jeamsak, U., Uttayamakul, S., Manosuthi, W., 2018. Epidemiology and clinical characteristics of patients under investigation for middle east respiratory syndrome coronavirus infection in Thailand. *J. Infect. Dis. Antimicrob. Agents* 35, 151–159.
- Suwannakarn, K., Chieochansin, T., Vichiwattana, P., Korkong, S., Theamboonlers, A., Poovorawan, Y., 2014. Prevalence and genetic characterization of human coronaviruses in southern Thailand from July 2009 to January 2011. *Southeast Asian J. Trop. Med. Public Health* 45, 326–336.
- Suwantarat, N., Apisarnthanarak, A., 2015. Risks to healthcare workers with emerging diseases: lessons from MERS-CoV, Ebola, SARS, and avian flu. *Curr. Opin. Infect. Dis.* 28, 349–361.
- Taylor, S., Lopez, P., Weckx, L., Borja-Tabora, C., Ulloa-Gutierrez, R., Lazzano-Ponce, E., Kerdpnich, A., Angel Rodriguez Weber, M., Mascarenas de Los Santos, A., Tinoco, J. C., Safadi, M.A., Lim, F.S., Hernandez-de Mezerville, M., Faingezicht, I., Cruz-Valdez, A., Feng, Y., Li, P., Durvieux, S., Haars, G., Roy-Ghanta, S., Vaughn, D.W., Nolan, T., 2017. Respiratory viruses and influenza-like illness: epidemiology and outcomes in children aged 6 months to 10 years in a multi-country population sample. *J. Infect.* 74, 29–41.
- Techangamsuwan, S., Radtanakattikanon, A., Purnaveja, S., 2012. Molecular detection and genotype differentiation of feline coronavirus isolates from clinical specimens in Thailand. *Thai J. Vet. Med.* 42, 413–422.
- Techangamsuwan, S., Radtanakattikanon, A., Thanawongnuwech, R., 2013. Development and application of reverse transcription loop-mediated isothermal amplification (RT-LAMP) for feline coronavirus detection. *Thai J. Vet. Med.* 43, 229–233.
- Tekes, G., Thiel, H.J., 2016. Feline coronaviruses: pathogenesis of feline infectious peritonitis. *Adv. Virus Res.* 96, 193–218.
- Temeeyasen, G., Srijangwad, A., Tripipat, T., Tipsombatboon, P., Piriyaopongsa, J., Phoolcharoen, W., Chuanasa, T., Tantituvanont, A., Nilubol, D., 2014. Genetic diversity of ORF3 and spike genes of porcine epidemic diarrhoea virus in Thailand. *Infect. Genet. Evol.* 21, 205–213.
- Theamboonlers, A., Samransamruajkit, R., Thongme, C., Amonsin, A., Chongsrisawat, V., Poovorawan, Y., 2007. Human coronavirus infection among children with acute lower respiratory tract infection in Thailand. *Intervirology* 50, 71–77.
- Tingpalapong, M., Whitmire, R.E., Watts, D.M., Burke, D.S., Binn, L.N., Tesaprateep, T., Laungtongkum, S., Marchwicki, R.H., 1982. Epizootic of viral enteritis in dogs in Thailand. *Am. J. Vet. Res.* 43, 1687–1690.
- Tuanthap, S., Vongpunsawad, S., Phupolphan, C., Duang-In, A., Wattanaphansak, S., Assavacheep, P., Theamboonlers, A., Luengyosluetchakul, S., Amonsin, A., Poovorawan, Y., 2019. Analysis of the spike, ORF3, and nucleocapsid genes of porcine epidemic diarrhoea virus circulating on Thai swine farms, 2011–2016. *PeerJ* 7, e6843.
- Tyrell, D.A., Bynoe, M.L., 1965. Cultivation of a novel type of common-cold virus in organ cultures. *Br. Med. J.* 1, 1467–1470.
- Upatoom, N., Jirathanawat, V., Srihakim, S., Leesirikul, N., Chirawatanapong, W., Bunyahotra, R., Siriwan, P., Likitdecharoj, B., 1983. Infectious bronchitis (nephritis-nephrosis) in broilers. *Thai J. Vet. Med.* 13, 36–43.
- van der Hoek, L., Pyrc, K., Jebbink, M.F., Vermeulen-Oost, W., Berkhout, R.J., Wolthers, K.C., Wertheim-van Dillen, P.M., Kaandorp, J., Spaargaren, J., Berkhout, B., 2004. Identification of a new human coronavirus. *Nat. Med.* 10, 368–373.
- Wacharapluesadee, S., Sintunawa, C., Kaewpom, T., Khongnomnan, K., Olival, K.J., Epstein, J.H., Rodpan, A., Sangsri, P., Intarut, N., Chindamporn, A., Suksawa, K., Hemachudha, T., 2013. Group C betacoronavirus in bat guano fertilizer. *Thail. Emerg. Infect. Dis.* 19, 1349–1351.
- Wacharapluesadee, S., Duengkae, P., Rodpan, A., Kaewpom, T., Maneeorn, P., Kanchanasaka, B., Yingsakmongkon, S., Sittidetboripat, N., Chareesaen, C., Khlangsap, N., Pidthong, A., Leadprathom, K., Ghai, S., Epstein, J.H., Daszak, P., Olival, K.J., Blair, P.J., Callahan, M.V., Hemachudha, T., 2015. Diversity of coronavirus in bats from Eastern Thailand. *Virol. J.* 12, 57.
- Wacharapluesadee, S., Duengkae, P., Chaives, A., Kaewpom, T., Rodpan, A., Yingsakmongkon, S., Petcharat, S., Phengsakul, P., Maneeorn, P., Hemachudha, T., 2018. Longitudinal study of age-specific pattern of coronavirus infection in Lyle's flying fox (*Pteropus lylei*) in Thailand. *Virol. J.* 15, 38.
- Walker, P.J., Siddell, S.G., Lefkowitz, E.J., Mushegian, A.R., Dempsey, D.M., Dutilh, B.E., Harrach, B., Harrison, R.L., Hendrickson, R.C., Junglen, S., Knowles, N.J., Kropinski, A.M., Krupovic, M., Kuhn, J.H., Nibert, M., Rubino, L., Sabanadzovic, S., Simmonds, P., Varsani, A., Zerbini, F.M., Davison, A.J., 2019. Changes to virus taxonomy and the international code of virus classification and nomenclature ratified by the international committee on taxonomy of viruses (2019). *Arch. Virol.* 164, 2417–2429.
- Wang, L.F., Eaton, B.T., 2007. Bats, civets and the emergence of SARS. *Curr. Top. Microbiol. Immunol.* 315, 325–344.
- Wang, L., Byrum, B., Zhang, Y., 2014. Detection and genetic characterization of deltacoronavirus in pigs, Ohio, USA, 2014. *Emerg. Infect. Dis.* 20, 1227–1230.
- Wertheim, H.F.L., Nadjm, B., Thomas, S., Agustiningih, Malik, S., Nguyen, D.N.T., Vu, D.V.T., Van Nguyen, K., Van Nguyen, C.V., Nguyen, L.T., Tran, S.T., Phung, T.B.T., Nguyen, T.V., Hien, T.T., Nguyen, U.H., Taylor, W., Truong, K.H., Ha, T.M., Chokephaibulkit, K., Farrar, J., Wolbers, M., de Jong, M.D., van Doorn, H.R., Puthavathana, P., 2015. Viral and atypical bacterial aetiologies of infection in hospitalised patients admitted with clinical suspicion of influenza in Thailand, Vietnam and Indonesia. *Influenza Other Respir. Viruses* 9, 315–322.
- WHO, 2020a. Coronavirus Disease (COVID-19) Situation Report – 194. World Health Organization, Geneva, Switzerland.
- WHO, 2020b. MERS Situation Update, January 2020, Geneva, Switzerland.
- WHO, 2020c. Novel Coronavirus – Thailand (ex-China). World Health Organization, Geneva, Switzerland.
- Wong, A.C.P., Li, X., Lau, S.K.P., Woo, P.C.Y., 2019. Global epidemiology of bat coronaviruses. *Viruses* 11, 174.
- Woo, P.C., Lau, S.K., Chu, C.M., Chan, K.H., Tsoi, H.W., Huang, Y., Wong, B.H., Poon, R.W., Cai, J.J., Luk, W.K., Poon, L.L., Wong, S.S., Guan, Y., Peiris, J.S., Yuen, K.Y., 2005. Characterization and complete genome sequence of a novel coronavirus, coronavirus HKU1, from patients with pneumonia. *J. Virol.* 79, 884–895.
- Woo, P.C., Lau, S.K., Lam, C.S., Lau, C.C., Tsang, A.K., Lau, J.H., Bai, R., Teng, J.L., Tsang, C.C., Wang, M., Zheng, B.J., Chan, K.H., Yuen, K.Y., 2012. Discovery of seven novel mammalian and avian coronaviruses in the genus deltacoronavirus supports bat coronaviruses as the gene source of alphacoronavirus and betacoronavirus and avian coronaviruses as the gene source of gammacoronavirus and deltacoronavirus. *J. Virol.* 86, 3995–4008.
- Xu, R.H., He, J.F., Evans, M.R., Peng, G.W., Field, H.E., Yu, D.W., Lee, C.K., Luo, H.M., Lin, W.S., Lin, P., Li, L.H., Liang, W.J., Lin, J.Y., Schnur, A., 2004. Epidemiologic clues to SARS origin in China. *Emerg. Infect. Dis.* 10, 1030–1037.
- Yob, J.M., Field, H., Rashdi, A.M., Morrissey, C., van der Heide, B., Rota, P., bin Adzhar, A., White, J., Daniels, P., Jamaluddin, A., Ksiazek, T., 2001. Nipah virus infection in bats (order Chiroptera) in peninsular Malaysia. *Emerg. Infect. Dis.* 7, 439–441.