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Human migration, infectious diseases, plague, global health crisis - historical evidence

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ABSTRACT

This study examines the transmission of infectious diseases through historical studies, focusing on colonialization, slave trade, religion spread, and transcontinental and island trade. Emerging diseases like leprosy, Black Death, syphilis, malaria, Spanish flu, and COVID-19 have become significant contributors to global health crises. The study uses four stages: heuristics, critique, interpretation, and historiography. It focuses on migration, pandemics, and global health crises, using relevant literature. The findings suggest that many diseases have reached pandemic proportions due to their rapid dissemination and the influence of migration caused by historical factors such as ancient travel culture, colonialism, and modern times. The evolution of contemporary language also facilitates international mobility. The research examines the issue of disease distribution resulting from the long-standing global migration process, focusing on how migration has played a significant role in the occurrence of pandemics, outbreaks, and global health crises throughout history. The migration of *Homo Sapiens* from East Africa to regions outside Africa led to the development of language, culture, and disease transmission. The domestication of animals resulted in the emergence and transmission of disease mutations, leading to the worldwide dissemination of infectious diseases like leprosy, Black Death, syphilis, malaria, and COVID-19.

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Introduction

Since ancient times, migrants have played an important role in the transmission of infectious diseases (Inhorn & Brown, 2013). Egyptian Plague 1279-1213 BC (Lotfy, 2015), the introduction of smallpox into Mexico 1520 (Agostoni, 2016), influenza pandemic 1918 (Beach et al., 2022), AIDS pandemic 1981 (Beyrer, 2021), severe acute respiratory syndrome (SARS) 2002 (Tsang et al., 2003), the 2009 Hajj-associated meningococcal meningitis outbreak (Mohammed et al., 2017), Middle East respiratory syndrome (MERS-CoV) 2012. (Matsuyama et al., 2016), and coronavirus disease 2019 (SARS-CoV-2) (Wu et al., 2020). Emerging infectious diseases are described as “infections that are newly emerging in a population or have been present but are rapidly increasing in incidence or geographic range” (Morse, 1996). Along with the introduction of smallpox and measles to Pacific island countries and the global spread of HIV, migrant populations have contributed to changes in the incidence of infections in populations as well as the potential for local transmission of diseases such as hepatitis A and tuberculosis (TB) (Reis et al., 2022).

Infections that offer little risk to the local population but expand the geographic area where these infectious diseases can be encountered by medical personnel unfamiliar with them include *leishmaniasis* (Mann et al., 2021), Chagas disease (Irish et al., 2022), and malaria in North America (Williams & Drennan, 2022). Infections such as seizures and *neurocysticercosis* (Steyn et al., 2023), heart disease and

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Chagas infection (Saraiva et al., 2021), hepatocellular cancer and hepatitis B infection (Kanda et al., 2019), create diagnostic challenges and over time also change the emergence of chronic diseases in society. The possibility of spreading new infections in North America, such as dengue and *chikungunya* in places where mosquito vectors are present, may also increase due to population mobility (Findlater & Bogoch, 2018). As immigrants often interact with people in their home countries, they can serve as conduits for the spread of infectious diseases to new locations (Greenaway & Gushulak, 2017).

This study begins with the history of migration. Migration was already practiced in prehistoric times (Bellwood, 2017; Hoerder, 2002; Lamb, 2017; Lucassen et al., 2010; Manning, 2006, 2013; Manning & Trimmer, 2020). The development and spread of migration in prehistoric times occurred around 40,000-50,000 BP, 60,000 BP (Hoerder, 2002), and 100,000-50,000 BP (Bellwood, 2017). However, according to studies, human migration with the potential to carry diseases is estimated to have occurred at 100,000 BP (Monot et al., 2005). Migration not only causes the mixing of cultures and languages, but also spreads diseases. The spread of these diseases began with advances in maritime technology that helped humans successfully circumnavigate the globe around 1,400-1,700 BP (Manning & Trimmer, 2020; Patrick, 2005). These advances in maritime technology led to the development of explorers, colonizers, traders, missionaries, and family migration (Howe, 2023).

The spread of infectious diseases began with leprosy, which occurred in 50,000- 60,000 BP (MacPherson, 2007). Leprosy is caused by *Mycobacterium leprae* (Cardona-Castro et al., 2022). The disease originated in East Africa and began to spread along with human migration (Monot et al., 2005). It was followed by *Helicobacter pylori* (Hp) a chronic gastric pathogen in humans that occurred at 12,000 BP (Kim, 2019). Hp became pandemic across the continents of Africa, Central Asia, East Asia, and Europe through migration (Falush et al., 2003). The previous studies illustrate that disease transmission by migrant groups is caused, firstly, by their behavior (Willem et al., 2017). When a person decides to migrate, he/she will encounter other cultures, which will have an impact on behavioral changes such as sexual behavior. This sexual behavior will create global transmission and prevalence of STDs and HIV/AIDS (Herdt, 1997). In addition, Hepatitis B Virus (HBV) disease studies describe asylum seekers coming from 44 countries to Western Europe. The 44 countries showed that migration had a large impact on the number of chronic HBV carriers in the receiving countries (Thijssen et al., 2019). For example, in Sweden HBV-infected migrants can transmit to the population of the receiving country.

Second, by zoonosis, which is a virus originating from an animal that mutates into humans (Filippitzi et al., 2017), as stated in the study of *Campylobacter jejuni* (*C. jejuni*) a zoonotic pathogen was found in meat and poultry consumed by migrant groups in the United States (Wilson et al., 2008). Studies show that the trade of live pigs for breeding sows to reproduce genetic improvements in pigs globally greatly influenced the spread of the 2009 influenza A virus, better known as H1N1 (Nelson et al., 2015). The virus originated in Europe and North America and, since 1970, has spread to Asian countries such as China, Japan, South Korea, Thailand, and Vietnam (Rahman et al., 2020). China has the largest pig population in the world (Lander et al., 2020), but is not a major exporter of live pigs so it was not a source of the global spread of the 2009 H1N1 virus (Vincent et al., 2014). The size of a country's pig population was not a determining factor in the rate of spread of the 2009 H1N1 virus to other countries (Zhao et al., 2022). Thus, the spread of this influenza A virus through global migration started when there was a trade in live pigs (Ren et al., 2016).

Other zoonoses are such as the bite of the female *Anopheles* mosquito in the spread of malaria (Beay et al., 2017), and rats or monkeys in the spread of measles (Beay, 2018). Furthermore, Severe Acute Respiratory Syndrome (SARS) originated from a bat virus in China in 2003 (Yang et al., 2016). Middle East Respiratory Syndrome (MERS) originated from a camel virus in the Middle East in 2012 (Wernery et al., 2017), and malaria, *schistosomiasis*, West Nile, dengue, *chikungunya*, or tuberculosis were caused by poultry, turkeys, pigs, rats, cats, worms, mosquitoes, and dogs or other wild animals (Vignier & Bouchaud, 2018), finally, COVID-19 originated from a bat virus in China in 2019 (Araujo & Naimi, 2020; Ji et al., 2020; Randhawa et al., 2020; Schnirring, 2020; Tabassum et al., 2024; Zhou et al., 2020). Global disease transmission is caused by migration and mobility using modern means of transport. After examining human migration and disease spread, the following study is about the spread of diseases caused by migrant workers.

ILO (2015) states that migrant workers are the population most vulnerable to disease transmission (Acke et al., 2022; Tjitrawati & Romadhona, 2023). Therefore, migrant workers must be protected from

disease transmission as codified in The International Convention on the Protection of the Rights of All Migrant Workers and Members of their Families commonly referred to as the Migrant Workers' Convention (MWC) (Tjitrawati et al., 2023; Wahyudi et al., 2024; Wiratama et al., 2023). The Zika virus has infected migrant workers in the manufacturing and construction industries in Singapore (Tam et al., 2016), and Myanmar migrant workers who migrated to Thailand contracted malaria (Kitvatanachai & Rhongbutsri, 2012). Ethiopian migrant workers in Lebanon have contracted tuberculosis (Fernandez, 2018), migrant workers from Indonesia and the Philippines are infected with venereal diseases (Lasimbang et al., 2016), migrant workers from China, Vietnam, the Philippines, Thailand, and Indonesia have HIV infection susceptibility in Korea (Lee, 2008), migrant workers from China, Bangladesh, India, Malaysia, Philippines, Myanmar, and Thailand in Singapore are susceptible to contracting malaria, hepatitis A and E, and tuberculosis (Sadarangani et al., 2017), Latino migrant workers in South Florida are at risk of contracting venereal diseases (Sánchez, 2015), and Mexican, African, and Hispanic (from Spain) migrant workers are susceptible to HIV/AIDS (Albarrán & Nyamathi, 2011; Organista et al., 2004; Shehadeh & McCoy, 2014). These studies illustrate that migrant workers are highly vulnerable to disease transmission in the host country.

In early 2020, COVID-19, which originated in Wuhan City, Hubei Province, China, spread globally.

Based on this explanation, this research examines the problem of disease distribution due to the global migration process that has been going on for thousands of years and thus the research has a focus on the migration process having a significant impact on the occurrence of pandemics or outbreaks and global health crises in a historical perspective.

Methodology

This research uses the historical method (Bentley, 2005). Historical research goes through four stages, which include heuristics, criticism, interpretation and historiography. The heuristic stage is a process of searching and finding historical sources. Criticism is a process of testing historical sources so that they are suitable for historical reconstruction. Interpretation is analyzing and synthesizing historical sources that have been criticized and historiography is a process of writing the results of historical research (Bentley, 2005). History is a discipline that examines alterations over time, using historical methodology to collect, assess, and interpret evidence of past events. Historians aim to offer insights into these transformations, although they do not follow the scientific method. However, the historical method requires investigation, critical assessment, and logical reasoning. The interpretation of the past is influenced by individual subjective bias, leading to potential varying interpretations of historical events, even when many narratives are based on the same data. Furthermore, historical evidence is tangible or documented information related to a specific event, individual, or era in the past. Historians gather a variety of evidence to enhance their understanding of the subject. They must differentiate between primary sources, which are directly witnessed events, and secondary sources, which are obtained through intermediaries. Primary sources involve individuals who were integral participants in the actual historical occurrence, while secondary sources are obtained through intermediaries. The sources of this research include various relevant literatures examining the issues of migration, pandemics, and the global health crisis. The methods used identified the impact of international migration on global health crisis from ancient to modern time.

Results and discussion

Tracing the history of migration from the perspectives of history, anthropology, , and epidemiology, previous studies on migration were often spatial and temporal, separating the four perspectives, whereas human migration is determined by previous periods such as the development of language, culture, agricultural expansion, animal domestication, and disease transmission. Furthermore, examining international labor migration in the postcolonial period in the form of a global economy in the name of nation building, was estimated to occur at the end of the 20th century (Manning & Trimmer, 2020; Patrick, 2005). At the end of this study, the data obtained are brought together holistically from the perspectives of history, anthropology, archaeology, language, and epidemiology with international labor migration.

Historical pandemics and migration: from ancient times to modern outbreaks

Infectious diseases have a long history, dating back to prehistoric times when humans migrated and domesticated pigs, Polynesian or Pacific rats, dogs and chickens (Cockburn, 1971). It was then that animal-to-human disease mutation and human-to-human disease transmission occurred, causing pandemics around the world (Parvez & Parveen, 2017). The following studies outline migration and infectious diseases over the course of history (Table 1).

In historical studies, there are three pandemic outbreaks that have a significant impact on the quantity of infected and dead victims: Justinian's plague pandemic (6th and 7th centuries) (Sarris, 2022), the Black Death plague (14th century) (Spyrou et al., 2016), and the third pandemic outbreak, or in other words, the bubonic plague pandemic (1855-1959) (Lotfy, 2015). The study of the Black Death plague had a major impact on mainland Europe as it killed at least one- third to two-thirds of the European population (Belich, 2016). In historical records, the Black Death plague is said to be a multiregional pandemic, this situation evidenced by the Black Death also occurring in most of Asia and the Middle East (Carmichael, 2006). As a result of the Black Death pandemic situation in the 1700s, there were several outbreaks in most parts of Europe (Cohn, 2008), namely the great plague of Milan (1629-1631) (Vicentini et al., 2020), the great plague of London (1665-1666) (Zell & Davies, 2022), the great plague of Vienna (1679) (Laifle, 1937), and the great plague of Marseille (1720-1723) (Devaux, 2013).

The global spread and evolution of leprosy

Leprosy is the oldest disease, known as Hansen's disease and named after a Norwegian man named Dr Gerhard Armauer Hansen (Trautman, 1984). Hansen first discovered and identified the bacteria causing leprosy on 28 February, 1873 (Trautman, 1984). The *Mycobacterium leprae* (M.leprae) is a bacterium that develops and causes damage to the skin, eyes, bones and nerves. Leprosy is a contagious disease through interaction with someone who has been infected by M. leprae (Aufderheide, 1998; Rees & Young, 1994). Leprosy once affected approximately 200,000 people (Schuenemann et al., 2018), and up to 250,000 people worldwide (Robbins et al., 2009). Leprosy is derived from the Sanskrit kushtha in the Atharva Veda, which refers to a plant used to cure leprosy (Zysk, 1992). The Atharva Veda shows that there is a connection between leprosy and medicine. The Atharva Veda, written in 1400 BC, is the earliest

Table 1. Development of infectious diseases in the world.

Pandemic/Epidemic	Years	Location	Infected	Deaths	Information
COVID-19 (9)	2019-2021	Global	171.5m	3.69m	Coronavirus (SARS-CoV2)
Seasonal Flu	2017-2018	USA	?	46-95k	Influenza A (H3N2)
Ebola	2013-2016	West Africa	28,600	11,325	Ebola
Swine Flu	2009-2010	Global	1400m	150k - 600k	Influenza A (H1N1)
HIV - AIDS (4)	1981 on going	Global	+40m	35m	? Sexually transmitted
Russian Flu	1977-1979	Global	?	700k	Influenza A (H1N1)
Hong Kong Flu (12)	1968-1970	Global	?	1-4m	Influenza A (H3N2)
Asian Flu (11)	1957-1958	Global	?	1-4m	Influenza A (H2N2)
Russian Typhus (10)	1918-1922	Russia	?	2-3m	Typhus
Spanish Flu (2)	1918-1920	Global	500m	17-100m	Influenza A (H1N1)
Russian Flu (19)	1889-1890	Global	?	1m	Influenza
Third Cholera (17)	1846-1860	Global	?	+1m	Cholera
Persian Plague (15)	1772-1773	Persia	?	2m	Bubonic Plague
Marseille Plague	1720-1723	France	?	100k	Bubonic Plague - 30% of population died
London Plague	1665-1666	UK	?	100k	Bubonic Plague
Naples Plague (16)	1656-1658	Italy	?	1.25m	Bubonic Plague
Italian Plague (18)	1629-1631	Italy	?	1m	Bubonic Plague
Cocoliztli (13)	1576-1580	Mexico	?	2-2.5m	Smallpox
Cocoliztli (6)	1545-1548	Mexico	?	5-15m	Smallpox
Mexico Smallpox (8)	1519-1520	Mexico, America	?	5-8m	Smallpox brought in by Spanish explorers
Black Death (1)	1346-1353	Europe, Asia and Africa	?	75-200m	Bubonic Plague (Yersinia pestis)
Japanese Smallpox (14)	735-737	Japan	?	2m	Smallpox
Plague of Justinian (3)	541-549	Europe and West Asia	?	15-100m	Bubonic Plague
Antonine Plague (7)	165-180	Roman Empire	?	5-10m	Smallpox or Measles
Plague of Athens	430 BC		?	100,000	Typhus Fever

historical reference to leprosy (Bloomfield, 1897; Buikstra, 2019). The spread of this disease was through two strains that have been standardized by several experts, including Robbins et al. (2009). The first strain, leprosy, is thought to have originated in East Africa (Mendum et al., 2014), and the second strain from South Asia, namely India (Wu et al., 2022). Subsequently, the disease spread throughout the world through migration by colonization, the slave trade, the spread of religion, and intercontinental and island trade (Rogers & Muir, 1925). According to early studies, the spread of leprosy started from migration, which already occurred at 50,000-60,000BP (Monot et al., 2005). This study used the technique of Single-Nucleotide Polymorphisms (SNPs), then classified into four types, namely types 1 to 4 (Hamblin et al., 2007). These types are related to the leprosy distribution model, as there is a correlation between the geographical origin of leprosy patients and the type of SNPs (Reibel et al., 2015). Type 1 SNPs are more predominant in Asia, the Pacific, and East Africa (Taylor et al., 2009). These type 2 SNPs are rarest and are present in Ethiopia, Malawi, India, and New Caledonia (Das et al., 2016). Type 3 SNPs are found in Europe, North Africa, and the Americas (Avanzi et al., 2020). Meanwhile, type 4 SNPs are found in West Africa and the Caribbean region near South America (Cardona-Castro et al., 2015). This leprosy disease is caused by zoonosis (Walsh et al., 1981), i.e. aquatic insect bites may be associated with the initial migration of infection to humans (Ganasegeran & Abdulrahman, 2021).

Figure 1 shows that leprosy spreads through three routes: east, west and south. From the east leprosy first evolved in East Africa before 40,000 BC (Robbins et al., 2009). From East Africa (SNPs type 1), it migrated to India, Ethiopia, Malawi and New Caledonia (SNPs type 2) (Cole & Singh, 2022). From the west, the spread of leprosy started from East Africa (SNPs type 1) migrating toward Europe and North Africa (SNPs type 3) (Taylor et al., 2009). Later, leprosy expanded to West Africa (SNP type 4) brought by explorers, traders or colonizers of European and North African descent rather than by migrants from East Africa because SNP type 4 is closer to SNP type 3 than SNP type 1. Leprosy from East Africa extended to West Africa distributed by the slave trade in the 18th century to the Caribbean Islands, Brazil, and other parts of South America, as type 4 SNPs are the same in West Africa. American type 3 SNPs is the same type SNPs as Europe and North Africa brought through colonialism in the 18th and 19th centuries.

Leprosy entered Europe with one of the earliest known cases in England as a skeleton was found from the Great Chesterford cemetery dating to 415-545 AD (Schuenemann et al., 2018). England became a key region in the early spread of leprosy in Europe through the trade in red squirrel fur. From the south, leprosy from East Africa (SNPs type 1) migrated through the Middle East, India, Sri Lanka, Thailand, and into Indonesia. This statement is supported by the results of Tayles and Buckley (2004) who found human skeletons infected with leprosy in the Mun River valley, a tributary of the Mekong River in the Khorat Plateau in northeastern Thailand at 2,500-1,700BP (Tayles & Buckley, 2004). In addition, an ancient skeleton was found in India in 2,000 BC infected with leprosy and a burial at Balathal where a person infected with *M. leprae* was buried and covered with burnt cow dung (Robbins et al., 2009), as shown in Figure 2 below.

The findings suggest that leprosy had invaded India by 2000 BC. This is evidenced by the oldest bones infected with *M. leprae*, a finding from the Vedic burial tradition of leprosy in northwest India before 1 BC. The findings are supported by translations of the Vedas as a reference for leprosy. Leprosy had evolved in Africa and then migrated to India and on to Mesopotamia (present-day Iraq), and Egypt. In Egypt, two mummies infected with leprosy in the form of finger mutilation were first discovered around the 6th century AD (Amiruddin, 2019).

Transmission of *M. leprae* took place through interaction with humans in trade networks between Mesopotamia and Egypt and the spread of religion via the Indus River during the Indus Valley Civilization between 2,800-1,800 BCE (Khan & Lemmen, 2014; Winkelmann, 2014). The items traded were beads and pottery. The trade network between Mesopotamia and Egypt and the spread of religion is known as the Middle Asian Interaction Sphere (Possehl, 2002, 2007). Interpretation of the spread of leprosy presented by studies can provide insight into the origin of the disease as evidenced by the identification of type 1 SNPs or type 2 SNPs. The *M. leprae*-infected human skeleton at Balathal marks the earliest skeletal evidence of the world's oldest infectious disease.

Leprosy entered Indonesia through the Melanesian islands probably in the 4th- 5th centuries (Prakoeswa & DSTD HIV-AIDS n.d.). Leprosy was brought by Indians and Chinese to Indonesia for trade and religious propagation (Djuanda et al., 2007). The second strain states that leprosy originated in East Africa (SNPs type 1) which had evolved from Asia (SNPs type 2) before 50,000 and 60,000 BC through massive Asian

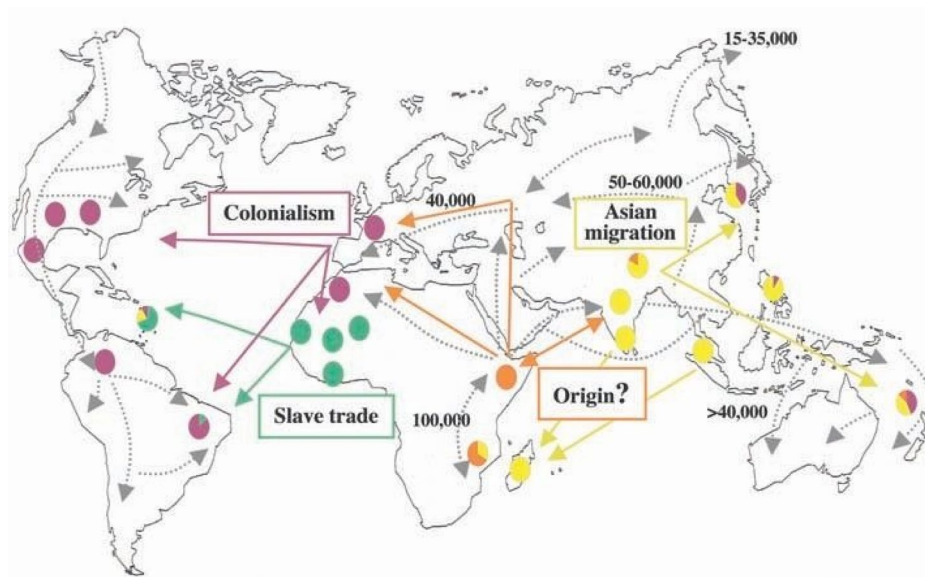


Figure 1. Leprosy disease distribution and migration. Source: Monot et al. (2005).



Figure 2. Excavation of human skeleton infected with *M. leprae* in Balathal. Source: Robbins et al. (2009).

migrations (Monot et al., 2005). With colonization estimated 40,000 years ago, leprosy spread further, with the arrival of Greek soldiers to Europe and North Africa (SNPs type 3). Subsequently, leprosy spread to West Africa and the Caribbean region of South America through the slave trade followed by the transmission of SNP type 4 leprosy in the last 500 years.

Two evolutionary strains make a lot of sense (Robbins et al., 2009). Firstly, type 2 SNPs from South Asia, i.e. India, preceded those from East Africa (type 1 SNPs), which migrated eastwards to form type 3 SNPs, and spread westwards to form type 4 SNPs. Secondly, SNP type 1 is the ancestor of SNP type 2, SNP type 3 and SNP type 4. Thus, the disease originated in East Africa or South Asia, specifically India, and spread with human migration to Europe and North Africa introducing leprosy to West Africa to the Americas. The disease began to spread along with human migration.

Maritime trade and the spread of Black Death

Entering 3,000 BC to 500 AD, this period began to be called the era of maritime trade. Maritime trade began in the Mediterranean and Indian Ocean regions (Green, 2020). The word maritime comes from the English maritime 'navigation, nautical or maritime' and refers to all shipping and trade activities related to the sea (Hamid, 2013). Thus, maritime trade is all activities related to buying and selling goods carried out at sea, and is called the sea trade route.

The most ancient maritime trade was the silk trade in the first and second centuries A.D (Kamalova, 2022). The new silk trade was opened by China around 202 BC as the most important route in distributing silk from China with Central Asia, South Asia, West Asia, and Europe and Africa (McLaughlin, 2016). Therefore, it is called the Silk Road or better known as the silk route. The Silk Road is an intermediary that brings together economic and cultural exchanges (Liu, 2010). The term silk road was first introduced by Ferdinand von Richthofen, a German geographer, around the beginning of the 19th century (Chin, 2013; Mertens, 2019; Waugh, 2007). The Silk Road had an economic impact in expanding trade as a superior commodity (Schwarz, 2014). and was a Chinese trade route with an estimated distance of 7,000 km connecting to Europe, through Central Asia, India, the Persian Empire, to Ancient Rome (Podberezkin & Podberezkina, 2015). In this maritime trade, the commodities were not only ancient Chinese silk and glass, but also spices, fragrant oils, wood, and camphor (Gan, 2016).

The Silk Road developed and successfully travelled through Central Asia, South Asia, West Asia, as well as Europe and Africa from around 1400-1700 AD (Guan, 2016). The Silk Road not only transacted goods, but also included diseases along their travelling routes, known as the black plague or Black Death (Huremović, 2019). Black death is bubonic plague, in which the skin of a sick person turns black due to sub-dermal hemorrhage (clots on the surface of the brain). Black death was spread through germs in rats hiding on ships in the silk trade (Benedictow, 2004; Noymer, 2007; Wade, 2010; Zapotoczny, 2006).

According to a plague ecologist for WHO, the silk trade route that led to the spread of Black Death originated in Central Asia, specifically at Lake Issyk-Kul in Kyrgyzstan (Pollitzer, 1951). This is based on an archaeological report in 1951 that the first Black Death was found at Lake Issyk-Kul in Kyrgyzstan in 1338-1339 with ten inscriptions. Lake Issyk-Kul as the main accessible route from China and the Caspian Sea in the silk trade route (Leroy & Giralt, 2021). China's territory, precisely in West China's Gansu province, namely Dunhuang, was the center of the main stop of the silk trade (Agnew et al., 2016) and traders from several ethnicities around the world met in silk trading transactions. Experts agree that the Black Death was caused by China as a result of the silk trade around the 1330s (Slavin, 2019). Furthermore, the distribution of silk, which had an impact on the spread of Black Death, had two routes, namely sea and land routes (Benedictow, 2013).

According to Figure 3, the first route is by sea. The spread of the Black Death is thought to be as early as 1320 (Gottfried, 2010) and initially came from the plains of China in 1320 (Gottfried, 2010), passed through Central Asia in 1330, then hit Europe in 1347 brought by Chinese traders through China's Silk Road (Byrne, 2006). The disease travelled south to India from China through the silk trade by ship. The disease spread, not only through the silk trade route, but also pilgrims by sea from India. Black death spread to Egypt and Syria in the year of the Black Death (Pamuk, 2007), and Mecca in 1349 (Byrne, 2012; Pamuk, 2007). The second route is the silk trade route by land. Whether the disease spread from Lake Issyk-Kul to the Caspian Sea or directly from China is unknown. The latter is highly unlikely as it took eight years to reach Astrakhan and the Golden Horde's capital Sarai (Schwarz, 2014).

In the year October 1347, the Black Death epidemic spread to Europe (Ditrich, 2017; Silva, 2016; Ziegler, 2013). The first reported Black Death city was Messina, Italy (Frati, 2000). The spread of Black Death started from merchant ships coming to the Black Sea via Constantinople and the Mediterranean (Koutsouradi et al., 2022). The Black Sea was a transit trade route by sea (Özveren, 1997) with the goods traded from China being silk and porcelain (Christian, 2000; Zhu, 2014). This trade route by sea was a common main route to Europe. The Black Death extended as far as the Crimean city of Caffa toward Genoa and Venice around June 1348 (Ditrich, 2017), England (Redfern & Hefner, 2019), and France (Frati, 2000; Gensini et al., 2004). Eventually, the Black Death spread across Europe between 1347 and 1351 (Ditrich, 2017; Silva, 2016; Wade, 2010; Ziegler, 2013). Prevention of the Black Death epidemic was carried out by throwing the corpses of the victims into the sea (Byrne, 2006). Meanwhile, Africa, to be precise the northern part, began to be infected in Tunis the capital of Tunisia through merchant ships in Messina Italy in January-February 1348 (Duncan & Scott, 2005). The second wave started in 1892 in Yunnan Province, China and reached India in 1896. Then Black Death then spread to South America and subsequently Black Death to the Australian continent in 1900 (McKeough, 2019). The spread of Black Death in Australia was contained due to the tightening of health protocols (Clyne, 2017) (See Figure 4).

In Indonesia, maritime trade began in the Srivijaya Kingdom centered on Sumatra Island as the connecting route of Southeast Asia through the Sunda and Malacca Straits around the 7th to 13th

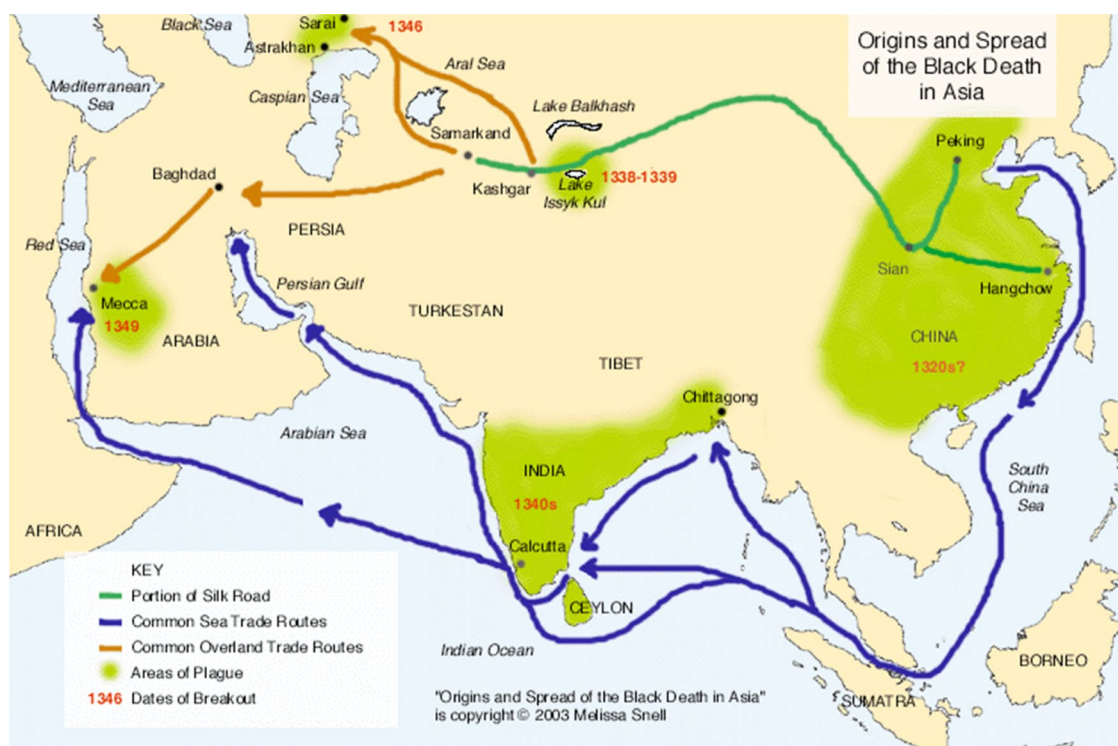


Figure 3. Distribution of Black Death in the world. Source: Gottfried, (2010).

centuries (Lockard, 2009; Manning, 2015a, 2015b; Sholeh, 2017). Srivijaya has a very strategic location so that it became a transit point for ships from China in the maritime trade route (Wolters, 1986). The ships from China had paved the way for Srivijaya's prosperity, so Srivijaya became a maritime kingdom as well as a well-known and very rich trading centre in Southeast Asia (Wolters & Sembodo, 2011). This maritime trade with China continued into the Majapahit Kingdom (Manggala, 2013). In this silk road, there were transactions both to buy and exchange between commodities from the Sriwijaya Kingdom and traders from China. The commodities from Sriwijaya Kingdom were cloves, nutmeg, cardamom, sandalwood, camphor, ivory, tin, turtle, silver, and gold (Supriyono et al., 2020) which were then bought or exchanged with Chinese traders in the form of silk cloth and ancient Chinese glass, so that the economic relationship between Sriwijaya and China was harmoniously built. These transactions were not always carried out in the Sriwijaya Kingdom, but instead the Sriwijaya Kingdom also sailed to China (Kartodirdjo et al., 1977). The maritime trade routes in Asia that were always travelled were from China to the South China Sea, Malacca Strait, Sriwijaya Kingdom, India, Oman, to Arabia, and vice versa (Soeroso, 1988).

Maritime trade routes in the Asian region other than the Srivijaya Empire were Banten Harbor (Kanumoyoso, 2018), an international port as a transit area from China, Siam, Bengal, Mecca, Denmark, and England (Bulbeck et al., 1998). The role of Banten Harbor was as a silk trade route between these countries (Adeng, n.d.; Leirissa, 1995). China's relationship with Banten Prefecture was very harmonious, as evidenced by the construction of a temple in Banten Harbor in 1687. However, the population in Banten Prefecture in 1879 was reduced due to the Black Death, which is better known in Indonesia as the bubonic plague (Kanumoyoso, 2018). In Java, the spread of the bubonic plague began with the import of rice from Rangoon, Burma, by the Dutch government to overcome the crop failure that occurred in Surabaya due to pest attacks on rice plants and drought (Candee, 1927). The rice was shipped through Tanjung Perak Surabaya on 3 October, 1910. Inadvertently, rats infected with bubonic plague were carried by the ship carrying the rice imported from Rangoon (Kur'anania, 2019).

After arriving in Surabaya on 5 November, 1910, the rice was distributed by train from Surabaya to Turen in southern Malang. The distribution of this rice apparently spread the bubonic plague. In March 1911, after Turen, the bubonic plague spread to Karanglo, Malang. Thus, Malang was the first district to

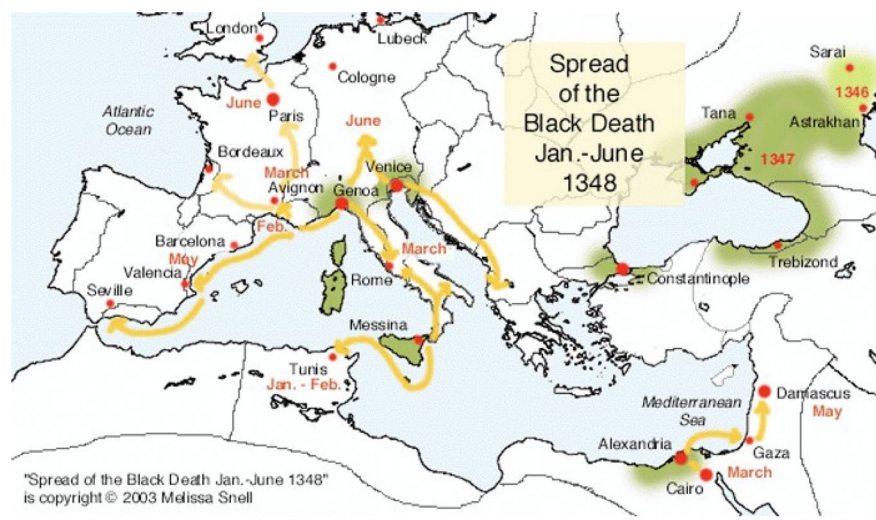


Figure 4. The Spread of the black death in Europe and Africa. Source: Benedictow, (2004).

be affected by the bubonic plague until 1916 (Gunawan, [n.d.](#); Luwis, 2020). Then, the bubonic plague spread to Kediri from 1911 to 1933 (Kur'anania dan Shinta Devi Santhi Rahayu, 2019).

The Columbian exchange – a brief of malaria, syphilis and transatlantic disease spread

The Columbian Exchange describes the exchange of malaria from the Old World, the European Continent, to the New World, the Americas. Vice versa, syphilis from the New World spread to the Old World (Boivin et al., 2012; Crosby, 2003b; Guerra, 1993; Nunn & Qian, 2010). It is called Columbian because a European sailor named Christopher Columbus and his crew explored until they found a new continent called the New World, namely the American Continent. Exploration from the European Continent to the American Continent across the Atlantic Ocean was carried out in 1492 (Crosby, 2003b; Farhi & Dupin, 2010).

The beginning of The Columbian Exchange was when, in 1492, Spain and Portugal (Horgan & Netchev, 2022) were the first European countries to make a voyage to the Americas with the aim of introducing new calorie-rich crops to the European Continent, namely potatoes, sweet potatoes, corn, and cassava, which could be expected to thrive in the climate of the European Continent. In contrast, the sugar and coffee crops of the European continent well-suited to the climate of the Americas (Crosby, 2003b; Mann, 2011; Pilcher, 2012). At the same time in the Americas, there were more than twelve million Africans as slaves. These people migrated to the Americas on demand for labor in America to work on plantations, which lasted during the transatlantic slave trade until the 19th century (Lovejoy, 2011; Manning, 1990; Nunn, 2008). Slaves from Africa became labor on American plantations because America needed them at very low wages. America was very dependent on African slaves (Wood, 2005). When these Europeans came to the Americas, the Lah Africans were the first to contract malaria from the infected Europeans, as they lived in squalid conditions. However, these African slaves were more resistant to malaria than Americans. Because of this, the disease increasingly became an epidemic in the Americas (Mann, 2011). The spread of malaria in the Americas evolved and expanded due to the interaction between people from Africa, America, and Europe. Medically, there are three genomes in the malaria mutation in the Columbian Exchange (Rishishwar et al., 2015).

In addition to malaria from Europe becoming an epidemic in the Americas, syphilis from the Americas also became an epidemic in Europe. Before the arrival of Europeans, there were no records of malaria in the Americas, only *frambusia* and syphilis (Guerra, 1993). This *frambusia* is a bacterium that can cause syphilis (Mitjå et al., 2013). However, when the Americas discovered in 1492 by Columbus, Europeans were contaminated *frambusia* and syphilis resulted in the spread of these diseases to Europe. The exchange of diseases between the Americas and Europe involved the African slave trade. The exchange of malaria and syphilis between the two continents led to disease outbreaks on the trajectory of human history in the following centuries (Boivin et al., 2012; Crosby, 2003b; Nunn & Qian, 2010).

Malaria's – from Sub-Sahara Africa to global epidemics

The word malaria is made up of two syllables, *mal* and *aria* (MacArthur, 1946). The word is of Italian origin, meaning 'bad weather' (MacArthur, 1946). In those days, Italians thought malaria was caused by bad weather. However, medically, malaria is caused by a parasite called *Plasmodium* (Yuda et al., 2001). The disease is transmitted by the bite of anopheles mosquitoes and these mosquitoes live in the tropics. The disease is transmitted by the bite of an infected mosquito (Hempelmann & Krafts, 2013; Packard, 2021). Malaria is thought to have originated in sub-Saharan Africa in the tropical forest region. Plasmodium infected non-human primates, namely gorillas and chimpanzees, and then mutated into humans. At that time, those infected by Plasmodium were animal hunters in the tropical forest (Hayakawa et al., 2009; Liu et al., 2014). The onset of malaria is estimated to have been 6,000 years ago or 8,000 to 10,000 years ago (Packard, 2021).

Malaria spread when out of Africa (Packard, 2021; Yalcindag et al., 2012). From sub-Saharan Africa it travelled north into the Italian countryside of Europe along with the influx of slaves from Africa. They entered Europe from Carthage in North Africa to Sardinia in Italy. In addition, malaria spread further with the Carthaginian wars between Carthage and Rome around the 3rd century BC (Yalcindag et al., 2012). The Carthaginian war was the largest war from 264 to 146 BC (Goldsworthy, 2019). Subsequently, malaria spread through the Nile valley to the Mediterranean coast and Mesopotamia, to Asia, namely in the Indian Peninsula and China in the 4th century, and to Greece, southeastern Europe in the 5th century BC (Bruce-Chwatt, 1985). After reaching the Indian Peninsula and China to Southeast Asia, the disease invaded Indonesia (then called the Dutch East Indies) with the first case in Cirebon in 1852 and continued to plague until 1854. Malaria reached Indonesia through the Port of Batavia in Jakarta (Arsin, 2012), and spread to all parts of Indonesia because irrigation during the Dutch East Indies government was not maintained (Marbun & Zein, 2020).

In England, the disease became endemic through the African slave trade across the Atlantic Ocean in the 16th century and was known as marsh fever or ague. Malaria was endemic in the coastal marshes of the River Medway (a tributary of the Thames estuary) in rural England from 1564 to the 1730s, causing deaths. The movement of mosquitoes from tropical to cooler climates was a cause and at the time England was having a cold winter called the Little Ice Age (Dobson, 1989, 1994; Kottnerus, 2002; Reiter, 2000). Anopheles mosquitoes adapted to colder climates and evolved into northern European regions as far as Spain, Portugal and France (Bruce-Chwatt, 1985; Kottnerus, 2002). The spread of anopheles mosquitoes from northern Europe to central Europe, specifically in Germany and Scandinavia, was via rivers and swamps due to a storm surge in 1020.

The spread of malaria to the Americas, especially North America, was through Columbus' voyages of exploration to the New World around the 16th and 17th centuries. Malaria had already spread to the North American continent during the civil war in the United States 1861-1865 with the blocking of irrigation channels. This blocking of irrigation resulted in the development of anopheles mosquitoes so that malaria spread in the Americas, among both African slaves and Americans (De Castro & Singer, 2005). According to some opinions, such as Andrews (1948) Faust (1951) and De Castro and Singer (2005), malaria was not present in the New World before it spread in the Old World (Andrews, 1948; Faust, 1951). This is reinforced by the absence of case records before Columbus entered the New World.

Syphilis: Historical perspectives and global impact

Syphilis is a sexually transmitted disease caused by the bacterium *Treponema pallidum* (T. pallidum) that affects the skin, bones, gastrointestinal tract, central nervous system, and heart (Tampa et al., 2014). In 1530, the word syphilis was first used by an Italian physician and poet named Girolamo Fracastoro (Ferreira et al., 2017). Fracastoro wrote a poem in Latin with the title "*Syphilis sive morbus gallicus*," meaning 'syphilis or French disease,' (Lederberg, 2000) which describes the disease of syphilis in Italy. The poem tells the story of a shepherd boy named *Syphilus* who lived in Haiti during the time of King Acithous. Once, *Syphilus* lost his sheep and blamed the Sun God, but worshipped King Acithous. The Sun God was angry and cursed a plague on the people of Haiti with *Syphilus* as the first person to suffer from syphilis (Franzen, 2008; Meyer et al., 2002).

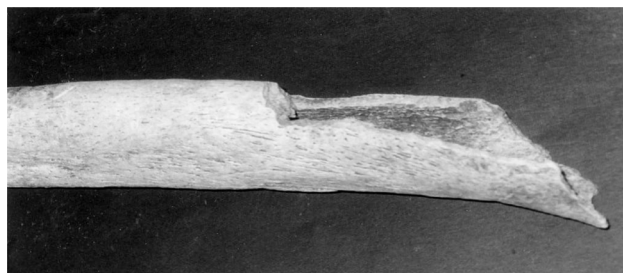


Figure 5. Syphilitic skeletal remains from a site in the Dominican Republic after contact with Colombia. Source: Rothschild et al. (2000).

The beginning of the spread of syphilis has two opinions. The first opinion, known as the Columbian and the second opinion known as the Pre-Columbian. This first opinion explains not finding a single case of syphilis in Europe before Columbus explored America in 1492 (Harper et al., 2011). When Columbus explored the Americas, he crossed the Atlantic and stopped in the Dominican Republic in the Caribbean Sea of Central America. During his stopover, syphilis spread and the first case of syphilis was found in the Dominican Republic (Rothschild et al., 2000). This is supported by evidence of 538 syphilitic skeletons at Dominican Republic region sites, indicating a route of transmission to Europe with evidence of skeletal remains from El Soco, Juan Dolio, La Caleta, Atajadizo Site, and Cueva Cabrera (Rothschild et al., 2000).

Figure 5 shows that the skeletal evidence of syphilis shows Columbus landing in the Dominican Republic, Central America. This place became the starting point for the spread of syphilis in Europe. The crew of the Columbus carried syphilis from the Central American continent on the voyage back to Europe around 1493. The first case of widespread syphilis in Europe was found in the city of Naples in Italy in 1495. The city of Naples was the location of Columbus' ship, so Columbus is considered to be the carrier of the syphilis bacteria to Europe. This disease was not known three years earlier and the spread of syphilis was a consequence of the discovery of the New World by Columbus (Ackerman, 1991; Quetel, 1990). When the Italian city of Naples was infected with syphilis, there was also an attack by French troops on the city. These French troops consisted of Swiss, Italian and Spanish soldiers. After the war ended, the disease spread to Europe through these soldiers returning to their home countries. At this time, many poets, painters, philosophers, and musicians and composers fell victim to syphilis. This disease is referred to as *Morbillus gallicus* or French disease because the French troops spread it, or it is also called *great pox* (Dayan & Ooi, 2005; Knell, 2004; Mayer & Lewis, 2020). Within a few years syphilis spread around the world in the late 15th and early 16th centuries (Mayer & Lewis, 2020) (See Figure 6).

However, this first opinion is refuted by new findings by Gaul et al. (2015) stating that congenital syphilis already existed in pre-Columbian Central Europe, before discovering the Americas. Congenital syphilis has existed in Austria since 1320, transmitted from mother to child. This is evidenced by skeletons from Austria in the form of dental abnormalities caused by congenital syphilis as shown in Figure 7 below.

The Pre-Columbian opinion describes that the beginning of widespread syphilis disease began with migration out of Africa. From Africa it spread to the Iberian Peninsula consists of the countries of Spain, Portugal, France, Andorra, and Gibraltar. At that time, Africans were made slaves by these five countries (Bhatti, 2007; Karp et al., 2009). So, syphilis was already endemic before 1492, before Columbus came to the Americas (Holcomb, 1934). According to the Pre-Columbian opinion, syphilis became more widespread throughout Europe during the colonial period in Brazil. During this time, the Portuguese came to colonize Brazil, especially the city of Rio de Janeiro, in the 16th to 19th centuries or around 1808 (Martins & Abreu, 2001). The spread of syphilis was also accompanied by a labor force that was mostly made up of African slaves (Guedes et al., 2018). In the 19th century, in the United States and Europe, one of the most common diseases was syphilis, especially in urban areas. At that time, about 8-14% of the entire population in the United States and Europe was infected with *T. pallidum* (Tramont, 1995).

Spanish flu to modern influenza – the evolution and global reach of the 1918 pandemic

Countries around the world have faced four influenza pandemics in the 20th century, which occurred in 1918, 1957, 1968, and 2009 (Kilbourne, 2006; Krause et al., 2012; Qi et al., 2011; Taubenberger & Morens,



Figure 6. Spread of syphilis around the world. *Source:* C. Meyer et al. (2002).



Figure 7. Ancient grave located about 40 miles west of Vienna, in St. Pölten's Dome Square, Austria showing congenital syphilis from a pre-Columbus center in Central Europe. *Source:* Gaul et al. (2015).

2020). The influenza pandemic that had a huge impact was Influenza 1918 or better known as the Spanish flu. Spanish flu belongs to type A subtype H1N1. The Spanish flu that occurred in 1957 (H2N2), 1968 (H3N2), and 2009 (H1N1pdm) are descendants of the 1918 virus (Morens et al., 2009; Tsoucalas et al., 2016). Taubenberger and Morens (2006) even mentioned the 1918 virus as the mother of all pandemics. Each of the H2N2, H3N2, and H1N1pdm viruses contain gene segments inherited from H1N1-1918. Some of these gene segments moved over time and were eventually “repaired” through genetic *reassortment* by H1N1-1918 influenza virus genes derived from wild waterfowl that mutated into humans (Taubenberger et al., 2006). As with the H2N2 virus, it has been shown that new viruses arise from previous viruses. Likewise, the H1N1 pdm virus was inherited from the H1N1-1918 gene segment that had mutated into the swine influenza virus and evolved.

Figure 8 shows that the Spanish flu pandemic of 1918 was caused by type A subtype H1N1 (García-Sastre & Whitley, 2006). Subsequent pandemics in 1957, 1968, and 2009 were inherited from descendants of the 1918 virus, which gained one or more genes through *reassortment*. Within 20 years of the H1N1 virus, the H3N2 virus circulated with the H1N1 virus from 1977 to 2009. The 1918 H1N1 virus was replaced by a new virus, the 2009 H1N1, which infected humans and pigs. Spanish flu spread in three waves two to three years apart. In the first wave, Spanish flu spread in the summer of 1918 (Mamelund, 2018), followed by the second wave in autumn 1918 (Bogaert, 2015), and the last wave, the third wave, in the spring of 1919 (Paulo et al., 2010). The second wave suffered more casualties than the first wave, which lasted from August to November 1918. The third wave began in the estimated months of January to February 1919 (Johnson & Mueller, 2002). The third wave occurred in the spring of 1919 and was a series of Spanish flu pandemics with a break in December 1918 and a resumption in January 1919 during the spring season (Erkoreka, 2009; Patterson & Pyle, 1991). Researchers have agreed that March

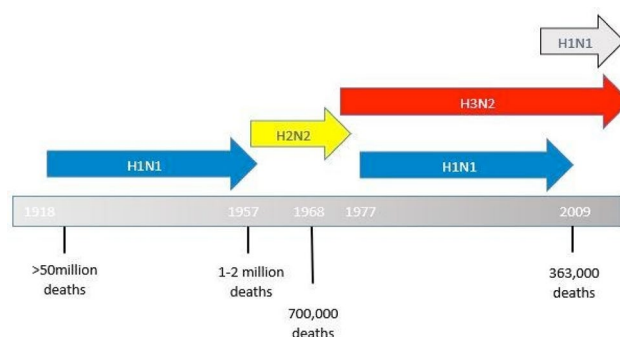


Figure 8. 1918 influenza pandemic and its derivatives. Source: Taubenberger and Morens (2020).

1918 was the beginning of the first wave of the Spanish flu (Taubenberger & Morens, 2006). The pandemic began with the participation of the United States Army in World War I by sending troops to Europe (Byerly, 2010). The 1918 Spanish Flu originated in Haskell County and travelled east across the state to Camp Funston, Kansas, USA (Adams, 2020). Camp Funston Kansas (currently known as Fort Riley) was a training ground for American soldiers. Camp Funston further spread as these American soldiers travelled in and out to Europe. This Spanish flu spread to Europe within three months causing two and a half million European deaths. By the end of July 1918, the Spanish flu had spread beyond Europe to North Africa, India, China, New Zealand, Hawaii and as far as Australia (Barry, 2020).

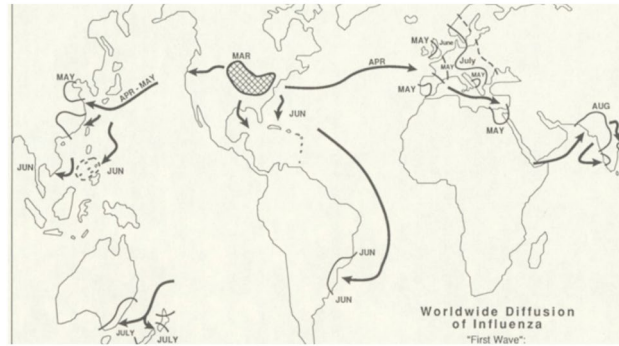
From Camp Funston Kansas in the United States, Spanish flu spread to all 50 US states such as Colorado, Georgia, New Jersey, and South Carolina (Collins et al., 1930). As a result, the Spanish flu in the first wave of the pandemic occurred (Long, 2022). The spread of the first wave of Spanish flu in several countries can be seen in Figure 9 below.

Furthermore, on Figure 9 that American soldier travelled to Europe from Camp Funston via Brest in France. Brest in France was the landing place for US soldiers in World War I. From Brest, the Spanish flu infected the allied armies of France, Russia, and Britain and all countries in Europe. By May 1918, Spanish flu had spread to Asia (including Indonesia), Africa and Australia (Pyle, 1986). From the British army, Spanish flu travelled to Scotland and Scandinavia, Italy and Greece. The Spanish flu spread to Spain is thought to have travelled through Portugal by ship (Burnet & Clark, 1942). The 1918 influenza reached Spain, during the war, a country that was not involved in World War I. Therefore, it was called the Spanish flu. Moreover, Spain had publicized the virus through the Spanish press. Since then, it has been called the Spanish flu instead of the American flu as the country that recorded the first victims of the Spanish flu, or the French flu as the country that first mapped the wide spread of the outbreak (Wibowo et al., 2009).

Although researchers have agreed that the Spanish flu originated from the US Army in Haskell County, there are two other opinions that differ from the above statement. First, the Spanish flu originated from laborers from China and Vietnam who were contracted by the French and British in World War I (Emmer & Lucassen, 2019; Wever & Van Bergen, 2014). The cause of the Spanish flu virus came from birds and pigs that mutated into Chinese and Vietnamese labor (Walters & Walters, 2014). These housed by France and the UK next to where the two animals lived. It was this Chinese labor force that spread the Spanish flu as it travelled in and out of Europe via the Trans-Siberian railway line (Barry, 2004; Collier, 1974; Weinstein, 1976).

Secondly, the Spanish flu is argued to have originated in Russia, given that the influenza of 1889–1890 originated in Russia (Berche, 2022). Russians are also highly mobile, so the Spanish flu travelled to other countries. Russians call this flu the Spanish Influenza or Spanish Lady (Bollet & Jay, 2004; Garmaroudi, 2007). The second wave began in late August to November 1918. Spanish flu quickly spread around the world. This was due to the rapid distribution of the Spanish flu by the American army through three ports, namely the Port of Freetown-Sierra Leone in West Africa, Brest in France, and Boston-Massachusetts in the United States (Athukorala & Athukorala, 2022). These three ports served as stopover points for American troops, by which the virus then spread to North and South America, Africa, Asia, Australia and the Pacific. The spread of Spanish flu in North and South America occurred

The First Wave of Spanish Flu Transmission



The Second Wave of Spanish Flu Transmission

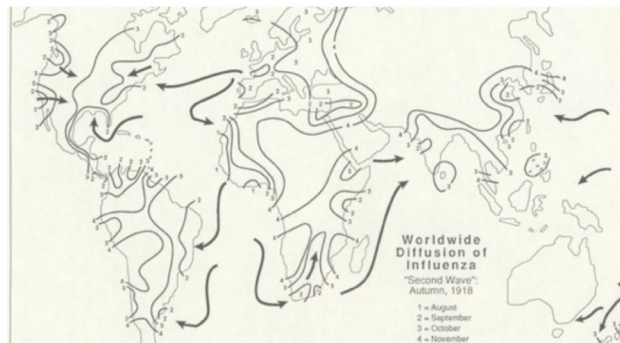


Figure 9. Second waves of Spanish flu spread. Source: Patterson and Pyle (1991).

from October 1918 to March 1919 (Chowell et al., 2014). Jamaica, located in the Caribbean Islands, was the first island to discover Spanish flu and it then spread to Guyana (South America) and Belize (Central America) (Killingray, 2003). According to Rhodes (2013), from mid-September to mid-December 1918, 500 million Americans (27% of the global population) were infected with Spanish flu (Arnold, 2018).

Spanish flu also occurred in Africa. It spread in August 1918, through ports and railways (Phillips, 2014). Countries on the African continent that experienced the Spanish flu pandemic were Senegal, Tanzania, Zambia, Katanga, Zimbabwe and South Africa (Schoenbaum, 2001). In Australia, the Spanish flu pandemic began in early 1919 during the winter season (Basco et al., 2022) after reaching New Zealand in November 1918 (Rice, 2020). The disease caused the deaths of over 12,000 people with most deaths in the military and navy (Dennis Shanks et al., 2010). Transmission occurred within Australia's borders through transport networks such as ships transiting harbors and army barracks (Curson & McCracken, 2006). In the Pacific region, the Spanish flu pandemic lasted for three years, from November 1918 in New Zealand to July 1921 in New Caledonia. The countries that experienced Spanish flu outbreaks were Tasmania to Western Samoa, including the islands of Niue, Rotuma, Jaliut, and Yule. The virus was spread through harbors and army posts (McLeod et al., 2008; Shanks et al., 2018; Shanks & Brundage, 2013).

Spanish flu spread to Asia such as Japan, China, India, Sri Lanka including Indonesia (Harper & Amrith, 2014). When the Spanish flu pandemic began to spread to Asia, China was the first country to contract the disease (Overby et al., 2004). The disease first spread in the winter around November 1918 during the First World War. The first province where Spanish flu was found was Canton (now called Guangzhou) (Shortridge, 1999). The Spanish flu spread through Hong Kong Harbor (Iijima, 2003) as China's maritime transport gateway and shipping transit with other countries such as the UK, Europe and America. Internationally, Hong Kong Port is not only a center of economic transactions and cultural exchanges, but also a source of disease transmission from several countries (Cheng & Leung, 2007; Humphries, 2014).

India was the second most severely affected country in Asia after Indonesia to experience the Spanish flu pandemic with deaths estimated at 12.5-20 million (Chandra & Kassens-Noor, 2014). The virus entered India in September 1918, and then spread to northern and southern India, as far as Sri Lanka. The spread

was via the railway (Chandra & Kassens-Noor, 2014; Reyes et al., 2018; Spreeuwenberg et al., 2018) [302, 303, 304]. Spanish flu reached Japan in two waves. The first wave from October 1918 to May 1919 affected Okinawa City. The second wave from December 1919 to May 1920 affected Tokyo, Chiba, Shizuoka, and Yamanashi. The spread of Spanish flu occurred during World War I (Rice & Palmer, 1993; Richard et al., 2009).

The spread of Spanish flu also occurred in Sri Lanka (Ceylon). There were two waves of the Spanish flu pandemic in Sri Lanka. The first wave, in June 1918, was first discovered in the capital city of Colombo. Spanish flu in Sri Lanka is known as *Ceyloninfluenza*. The second wave was in September 1918. However, in the second wave, the death rate from Spanish flu was 91,600 people (Chandra & Sarathchandra, 2014; Langford & Storey, 1992; Liew, 2007). Spanish flu spread to Indonesia (at that time called the Dutch East Indies, during the Dutch occupation), and there two opinions as to how. The first opinion is that the Spanish flu had reached Indonesia in April 1918 through the harbor in Batavia, when ships from Hong Kong docked, after transiting Singapore (Lee et al., 2007). In July 1918, Spanish flu had already travelled to East Java through the port of Surabaya and, by the end of November 1918, it had spread to Central Java (Kohn, 2007). The worst affected areas in Central Java were South Rembang and Magelang, while in East Java it was Mojowarno. The Spanish flu spread to several areas in Java through transport routes and the meeting point was the market (Brown & O. N. G, 1987; Chandra, 2013; Hirschman & Bonaparte, 2012; Kratoska, 1989).

The second opinion is that Spanish flu travelled to Indonesia in two waves. The first wave, probably in July to September 1918, invaded the Pangkatan plantation in North Sumatra via contract labor from Singapore. Within weeks it infected Surabaya, Madura, Belitung, Kalimantan and Batavia. The second wave occurred around November to December 1918. In this second wave, not a single region of the Dutch East Indies was spared from the flu. Indonesia was one of the worst hit countries in Asia with cases of Spanish flu with an average death rate of about 30.4 per 1,000 people, or about 1.5 to 4.37 million deaths for the islands of Java and Madura alone (Brown & O. N. G, 1987).

In the second wave, the spread of Spanish flu in the world claimed more lives than in the first wave. Therefore, this second wave is called “the deadliest wave and the most violent pandemic” in human history with an estimated 50–100 million people killed. Spanish flu is more rapidly transmitted through human-to-human interactions, so mass, dense, and slum gatherings are the most effective disease transmission clusters (Siegel, 2006). The 1918-1919 influenza pandemic became one of the largest outbreaks to rival the Black Death of the 14th century. The virus killed more people in less than a year than the Black Death, which lasted four years. Likewise, the virus killed more people in 24 weeks than the 24 years of AIDS (Farndon, 2006).

In the United States, to prevent human interaction, one of the places where people gather is the army barracks. It is certain then that all soldiers in the barracks would be infected with Spanish flu. In addition, many people did not understand the preventive measures against the transmission of Spanish flu, due to the poor healthcare conditions in the colonized countries and the absence of mobility restrictions (Crosby, 2003a). The Spanish flu pandemic increased at a very high speed and spread facilitated by railways and sea and river shipping. It reached small towns and rural areas through encounters in market. The 1918 influenza pandemic was never officially declared over. The Spanish flu itself never really disappeared because a new influenza would later emerge to replace the previous ones, such as the 1918, 1957, 1968 and 2009 influenza. Apparently, the 1918 virus emerged globally in what is called a pandemic outburst.

COVID-19: Initial emergences, global dissemination, and development

Coronavirus disease 2019, abbreviated as COVID-19, comes from the Latin *corona* means *crown* (Shoib et al., 2022). COVID-19 was caused by a new type of coronavirus named SARS-CoV-2 (Gorbalenya et al., 2020). Initially, COVID-19 was symbolized by the WHO as 2019-nCoV. The letter *n* means *novel* and CoV means *coronavirus*. Thus, it is called the novel coronavirus (Romadhona, 2022). On 11 February 2020, The Coronaviridae Study Group (CSG) of the International Committee on Taxonomy of Viruses (ICTV) classified 2019-nCoV under the name severe acute respiratory syndrome coronavirus 2 (*Severe acute respiratory syndrome coronavirus 2*, abbreviated as SARS-CoV-2 which is a *strain* of the SARS-CoV species) (Ciotti et al., 2020; Gorbalenya et al., 2020). The causes of SARS-CoV-2 are hedgehogs, pangolins, bats, and snakes. However, some other studies have suggested that SARS-CoV-2 is produced from snakes, a

combination of bat and snake viruses (Callaway & Cyranoski, 2020), bat virus (Zhou et al., 2020). Analyses show that 96-100% of SARS-CoV-2 is derived from bat viruses (Randhawa et al., 2020). These wildlife viruses evolved and mutated into humans (Ji et al., 2020; Schumacher et al., 2024).

The spread of SARS-CoV-2 started from a wildlife sale in Huanan Market, Wuhan City, Hubei Province, China on 1 December, 2019, which spread to 31 provinces in China (Kang et al., 2020), and was designated as a pandemic by WHO on 11 March, 2020 by calling Coronavirus Disease as COVID-19 (heng et al., 2020). The spread of COVID-19 was exacerbated by a number of travelers, especially from the UK who were going to celebrate Chinese New Year in China (Crossley & Williams, 2020; Rodríguez-Morales et al., 2020), and coinciding with the Spring Festival Travel Season (Lin et al., 2020). The spread of COVID-19 in China was further expanded through international travel and tourism through international airports (Abbas et al., 2023; Tan et al., 2024), then expanded to the countries of South Korea, Iran, and Italy in late February 2020 and spread to the rest of the world in early March 2020 (Chakraborty & Maity, 2020; Mansourian et al., 2019; Tjitrawati & Romadhona, 2024). Since then, the COVID-19 disease has infected 219 countries in the world, as shown in Figure 10 below.

Since the COVID-19 pandemic was declared by WHO, there has been the development of new COVID-19 variants B.1.1.7 (*Alpha*), B.1.351 (*Beta*), B.1.617.2 (*Delta*), P1 (*Gamma*) and B.1.1.529 (*Omicron*) (Sahoo & Samal, 2021), as shown in Figure 11 below.

Conclusion

Migration has a long history dating back to prehistoric times, with evidence from archaeology and technology. The Austric and Niger-Congo language families, which originated in the Bismarck Archipelago in eastern New Guinea around 1350BP, migrated west along the coasts of New Guinea and southeast through the Solomon Islands to various islands. The spread of Lapita culture is linked to the Neolithic expansion of the Southeast Asian archipelago, bringing Austronesian technologies and languages. Technologies from Southeast Asia, such as sedentary agriculture, animal domestication, stone tools, and pottery making, were introduced during this period. The Neolithic era is considered the beginning of human civilization, and the Austric and Niger-Congo language families play a crucial role in the development of language and cultural practices during the 3,000 BC to 500 AD era of human civilization. Infectious diseases have a long history dating back to prehistoric times, with three major pandemic outbreaks: Justinian's plague, the Black Death plague, and the bubonic plague pandemic (1855-1959). Maritime trade, which began in the Mediterranean and Indian Ocean regions between 3,000 BC and 500 AD, was an essential part of the ancient world. The Srivijaya Kingdom in Indonesia was a significant trading center and maritime kingdom during the 7th to 13th centuries. Maritime trade routes in Asia involved China to the South China Sea, Malacca Strait, Sriwijaya Kingdom, India, Oman, and Arabia. Banten Harbour, an international port, served as a silk trade route between China, Siam, Bengal, Mecca, Denmark, and England. China's relationship with Banten Prefecture was harmonious, but the population in Banten Prefecture was reduced in 1879 due to the bubonic plague. The Columbian Exchange is a historical event that describes the exchange of malaria from the Old World to the New World, specifically the Americas. It began in 1492 when Spain and Portugal were the first European countries to voyage to the Americas to introduce new crops. Over twelve million African slaves migrated to the Americas, and the Lah Africans were the first to contract malaria from the infected Europeans. However, these African slaves were more resistant to malaria than Americans, making the disease increasingly an epidemic in the Americas. Malaria originated in sub-Saharan Africa, where Plasmodium infected non-human primates and mutated into humans. The disease spread from sub-Saharan Africa to the Italian countryside of Europe when the influx of slaves from Africa entered Europe. The disease spread further with the Carthaginian wars between Carthage and Rome around the 3rd century BC. Malaria invaded Indonesia (then called the Dutch East Indies) in 1852 and continued to plague until 1854. Anopheles mosquitoes adapted to colder climates and evolved into northern European regions as far as Spain, Portugal, and France. The Spanish flu pandemic of 1918 was caused by the type A subtype H1N1, which was inherited from descendants of the 1918 virus. Subsequent pandemics in 1957, 1968, and 2009 were inherited from descendants of the 1918 virus, which gained one or more genes through reassortment.

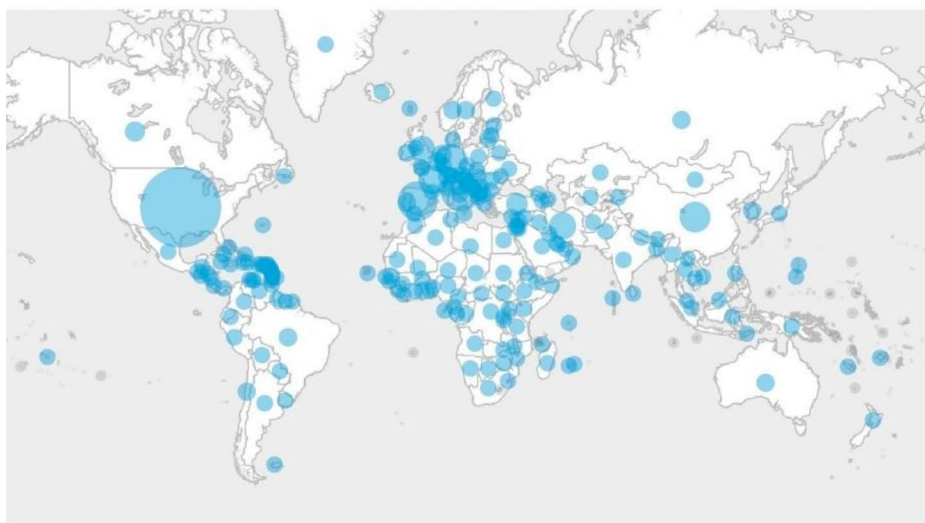


Figure 10. Distribution of COVID-19 spread in various countries. *Source:* WHO (2020b).



Figure 11. Development of COVID-19 variants. *Source:* Sahoo and Samal (2021).

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