







[17]. According to this idea, diseases were caused and transmitted by the presence of toxic vapor (miasma) in the air, which contained particles of decaying matter and had a characteristic odor [18].

**Table 2.** Overview of the main zoo noses in human history.

Disease	Originator	Source	Known from
Rabies	Lyssavirus	Birds, Bats, Wild / Domestic Animals	~ 10,000 BC
Malaria	Parasite (Plasmodium)	Chimpanzees	~ 8000 BC
Measles	Virus	Sheep, Goats	~ 6000 BC
Smallpox	Virus	Rodents	~ 2000 BC
Tuberculosis, Leprosy	Mycobacteria	Rodents	~ 1000 BC
Typhus	Rickettsie	Rodents	430 BC
Malleus	Bacteria	Solipeds	~ 400 BC (description 1783)
Leishmaniasis (Kala-Azar, Dum-Dum Fever)	Protozoa (Leishmania)	Rodents, Dogs	~ 100 AD (identification of the originator 1903)
Plague	Bacteria	Rodents	541 AD
Dengue Fever	Virus	Monkey	~ 1000 AD
Yellow Fever	Arbovirus	Monkey	1141 AD
Leptospirosis	Bacteria	Rodents	1886 (identification of originator 1907)
Trypanosomiasis (Sleeping Sickness)	Protozoa (Trypanosomes)	Wild Animals, Cattle	Since ancient times (identification of the originator 1901)
'Spanish' Flu	Virus	Birds, Pigs	1918
AIDS / HIV-1, -2	Virus	Monkeys, Chimpanzees	20 <sup>th</sup> century
Borreliosis	Bacteria	Small Mammals, Wildlife, Reptiles, Domestic Animals	1975 (identification of the originator 1982)
Bleeding (Hemorrhagic) Fever Ebola	Filovirus Ebola (5 Strains)	Waterfowl, Monkey, Antelope, Pigs?	1976
Balamutium Amoebic Encephalitis	Protozoa (Amoebas)	Monkey	1986
MERS-CoV	Coronavirus	Camel, Bat	2012

This idea was later challenged by the 'disease theory' proposed by Girolamo Fracastoro in 1546, which considered germs to be chemical rather than living organisms, and revealed three different modes of disease transmission: direct contact with a sick person, indirect contact through

objects and clothing belonging to the sick and remote transmission by air [19,20]).

At the beginning of the 19<sup>th</sup> century, both the theory of 'miasma' and the principle of 'contagion' began to be replaced by the 'germ theory' postulated by Louis Pasteur

and supported by the evidence presented by Robert Koch [9,10]. However, under pressure from shipowners in 1818, the British Parliament voted that the plague was not contagious, and when a local epidemic of yellow fever broke out in Barcelona in 1821, French doctors explained its cause by miasma theory. In 1828 the French House ruled that yellow fever was not a contagious disease, and in that context, Nicolas Chervin was awarded the Grand Prize for Medicine by the Academy.

When a cholera epidemic broke out in Europe a year later (1829), believers of the germ theory of contagious disease were considered to be completely ignorant. This was another half a century before Robert Koch definitively confirmed, in 1876, Louis Pasteur's germline theory of infectivity [21]. Epidemics have always triggered feelings of guilt and repentance (flagellation). Even the English historian E. Gibbon (1737-1794) interpreted the causes of the disintegration and demise of the Western Roman Empire as a punishment for softened and immoral life [16-18]. Almost at the same time, the English economist TR Malthus (1766-1834) published his population theory [19], which had a significant impact on demography, sociology and economics. He was the first to explain the causes of epidemics sociologically: uncontrollable population growth, associated with scarce food and other resources, resulted in poverty, hunger, social storms, and ultimately the outbreak of an epidemic as a natural brake on overpopulation.

Misinterpretations of the causes of epidemic outbreaks have arisen, on one hand, from the limited knowledge we had at the time, but also from clinging to earlier, seemingly proven evidences and facts. As an example, in the recent past, gastroduodenal ulcers were thought to be the result of so-called civilization stress, but their presumed etiological agent is *Helicobacter pylori* (discovered in 1982) [21].

#### **NEW FOCUSES ON DISEASES AND THE WAYS OF THEIR SPREAD**

As in the past, outbreaks of disease are still emerging in overcrowded urban agglomerations. Mass migration from rural regions brings specific infections to cities where newcomers live in primitive unhygienic conditions, without sanitation, electricity or affordable healthcare. The nutritional habits, social and sexual behaviors of the population are changing.

As far as the transmission of diseases directly between people is concerned, tourism and intercontinental air transport of people constitute a serious threat. The populations travel more and more often, especially between climatically diverse localities with a different history of infections. Migration represents the greatest cause of infections spreading. Populations from different ethnicities and religions, political and war conflicts all contributed to an increased traffic between different parts of the world. There is no shortage of examples from the past. Already at the time

of the migration of nations, infections such as the plague, the typhoid fever, the smallpox and measles, were spreading, decimating America's original population within decades of their discovery. However, it is not just about human migration. The transport of livestock's, through which pathogens enter new areas, plays an important role in the emergence and spread of infections.

The relocation of critically endangered plants and animals also plays a role here as part of rescue programs organized by, for example, the International Fund for Animal Welfare (IFAW) and a number of other organizations. In the last few decades alone, there have been several hundred relocations of livestock and wildlife worldwide without recording their health status or systematically monitoring their morbidity. To this can be added harvested timber as well as agricultural and food products international mass transport. Another vector spreading infectious diseases are the dozens of species of microorganisms (viruses, bacteria, protozoa) and multicellular parasites that contaminate wastewater. Therefore, some of the most serious infections are spread, especially in third world countries. Their incidence and number of victims are quantified in millions and are constantly changing. Up-to-date information can be obtained from the relevant WHO references [22]. Another potential risk is bioterrorism, the misuse of highly virulent pathogenic microorganisms capable of causing difficult-to-manage epidemics. Potentially, these are mainly viral (hemorrhagic fevers) and bacterial (plague and anthrax) infections [8,9].

#### **COMMUNICATIONS DISEASES AFFECTING THE CURRENT GENERATION**

##### **'Old' infectious diseases**

These include, in particular, tuberculosis, which still affects a large part of the world's population, regional leprosy and cholera. This latter is an indicator of the social and hygienic conditions that millions of refugees and migrants find themselves in (see above) remaining therefore a global threat. According to the WHO, it still affects 1.3 to 4 million people a year and causes 21,000 to 143,000 deaths a year. While some diseases were the causes of epidemics and pandemics that destroyed humanity more than wars, others, such as diarrheal diseases, malaria, measles and twentieth-century diseases, AIDS are also dangerous. Pertussis, cryptosporidiosis and hepatitis C and *Mycobacterium leprae*, which are still surviving in leprosarium's, are also considered to be potentially threatening [23].

##### **New Infections**

Over the past fifty years, a number of previously unknown and undiagnosed infections have emerged. These mainly include AIDS, and a number of hemorrhagic fevers of viral origin, namely Ebola caused by filoviruses derived from monkeys (recorded in 1976). Between 2014 and 2016, local epidemic arose in West Africa (Guinea, Sierra Leone and Liberia), and in Congo between 2018 and 2020. Due to

strict, uncompromising anti-epidemic measures, enforced by high mortality, which ranged from 40 to 60%, the foci were eliminated before an active vaccine was developed. New viral hepatitis, new influenza diseases (caused by H5N1, H7N7, H1N1 viruses) and coronaviruses (SARS, MERS,

SARS-CoV-2) also developed (**Table 3**). Typical features of these diseases include their rapid spread and acute course. The vast majority of their agents is pathogenic, especially for humans, and begins as anthrozooses.

**Table 3.** The most important causes of new diseases since 1950.

Year identification	Originator	Disease
1951	Hantavirus Soul ( <i>Bunyaviridae</i> )	Korean hemorrhagic fever
1953	Arenavirus Junin ( <i>Arenaviridae</i> )	Argentine hemorrhagic fever
1953	Fengivirus Dengu ( <i>Flaviviridae</i> )	Hemorrhagic fever
1957	<i>Babesia microti</i> , <i>B. divergens</i> (protozoa)	Febrile illness with symptoms of muscle pain, tremor and fatigue
1959	Alfavirus O'nyong-nyong ( <i>Togaviridae</i> )	Hemorrhagic fever
1967	Filovirus Marburg ( <i>Filoviridae</i> )	Hemorrhagic fever
1969	Arenavirus Lassa ( <i>Arenaviridae</i> )	Hemorrhagic fever
1973	Various rotaviruses ( <i>Reoviridae</i> )	Diarrhea
1973	Hepatitis A virus (HBA) ( <i>Picornaviridae</i> )	Acute hepatitis
1973	Hepatitis B virus (HBV) ( <i>Hepadnaviridae</i> )	Chronic hepatitis
1976	Filovirus Ebola ( <i>Filoviridae</i> )	Hemorrhagic fever
1976	<i>Cryptosporidium parvum</i> (element)	Enterocolitis
1977	<i>Legionella pneumophila</i> (bacteria)	Legionnaires' disease
1977	Hepatitis D deltavirus (HBD) (HBV satellite virus)	Hepatitis
1977	Hantaan hantavirus ( <i>Bunyaviridae</i> )	Hemorrhagic fever, renal syndrome (HFRS)
1982	<i>Borrelia burgdorferi</i> (bacteria)	Lyme disease
1982	<i>Escherichia coli</i> O157: H7 (bacteria)	Bleeding enteritis
1983	HIV1, HIV2 ( <i>Lentiviridae</i> )	AIDS
1983	<i>Helicobacter pylori</i> (bacteria)	Gastrointestinal ulcer disease
1988	Hepatitis C virus (HBC) ( <i>Flaviviridae</i> )	Post-transfusion inflammation of the liver
1990	hepatitis E virus (HBE) (related to <i>Caliciviridae</i> )	Hepatitis
1993	hantavirus Sin nombre ( <i>Bunyaviridae</i> )	Hantavirus pulmonary syndrome (HPS)
1992	<i>Bartonella henselae</i> (bacteria)	Cat scratch disease
1994	herpesvirus 8 ( <i>Herpesviridae</i> )	Kaposi's sarcoma*
1994	Hendravirus ( <i>Paramyxoviridae</i> )	Meningoencephalitis
1996	prion BSE	Variant of Creutzfeld-Jacob syndrome
1995-96	hepatitis G virus (HBG) (related to <i>Flaviviridae</i> )	Coincidence with AIDS
1999	Nipah virus ( <i>Paramyxoviridae</i> )	Meningoencephalitis
2001	Metapneumovirus ( <i>Paramyxoviridae</i> )	Bronchiolitis
2002-03	coronavirus SARS ( <i>Coronaviridae</i> )	Acute respiratory distress syndrome with severe pneumonia
2008	Merkel polyomavirus (MCV)	Merkel cell carcinoma of the skin
2012	MERS-CoV ( <i>Coronaviridae</i> )	Middle Eastern respiratory syndrome (MERS: Middle East Respiratory Syndrome)
2019/2020	Coronavirus SARS-CoV-2I ( <i>Coronaviridae</i> )	Severe acute respiratory syndrome (SARS: Severe Acute Respiratory Syndrome)

The disease was described as early as 1872 by the Hungarian physician M. Kaposim, rare at that time, today it mainly affects patients with impaired immunity (AIDS).

At the beginning of this century, completely new epidemic diseases appeared, caused by corona viruses (Coronaviridae). The first human coronavirus was discovered by the Scottish virologist JD Almeida (1930-2007) as early as 1964 [24]. The first epidemic of the disease occurred in 2002-2003, and because it was characterized by severe breathing difficulties, it was called Serious Acute Respiratory Syndrome (SARS). In 2012, a new coronavirus disease appeared in Saudi Arabia, which spread to 27 countries in the Mediterranean, Africa and Asia. It was referred to as MERS (Middle East Respiratory Syndrome) and manifested by an inflammation of the lungs and digestive system. As an anthroozoonosis, its original source of infection was bats and it was transmitted to humans from camels [25-27]. We are currently witnessing a completely new pandemic, which is again caused by coronaviruses. The disease broke out in 2019 and has since spread globally. In the short time taken by the disease to spread, dozens of studies, often contradictory, have been published. However, it is still too early to evaluate accurately its course or the number of infected people or deaths. Current data can again be found on the WHO portals [28].

## CONCLUSION

Despite the unmissable achievements of biomedicine, humanity will still be threatened by both recurring and emerging infectious diseases. Some diseases (namely poliomyelitis) are already approaching eradication, but others, mainly caused by viral pathogens (influenza, hepatitis and similar viruses), are not yet close to disappear. We still have to reckon the high genetic variability of viruses, antibiotic resistance of pathogenic bacteria and adaptability of multicellular parasites or their vectors. Potential problems could also arise from permafrost thawing. In the future, practicing traditional preventive measures, such as basic hygienic anti-epidemic measures or restricting the movement of people in an effort to prevent the spread of infections in the community would not be enough. The development of reliable diagnostic tests, effective and at the same time safe vaccines as well as new effective medicines is primordial. Regarding the testing and tracing of contacts, it is important especially in the initial phase of the epidemic before mass, community spread, i.e., in the phase enabling effective tracing and subsequent isolation of contacts.

Monitoring of SARS-CoV-2 in municipal wastewater using RNA polymerase reverse transcription (RT-qPCR) is now considered as a promising tool for virus surveillance and impeding epidemic prediction [29]. Within endangered, high-risk areas, adopting social programs to improve living conditions, including tolerable hygiene standards for local populations, ensuring early detection and reliable

identification of the pathogens, early initiation of the above-mentioned anti-epidemic measures and clear identification of the population at risk of infection, are desirable steps. The occurrence of the current SARS CoV-2 pandemic is considered positive in the sense that it is a 'wake-up call' for a situation in which an epidemic such as a virus with mortality at the Ebola level develops. In this context, criminally enforceable rules could be voted to palliate the often indiscipline of part of the population.

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## REFERENCES

1. Stewart WH (1968) Symposium on circumpolar health related problems, July 23-28, 1967. Opening remarks. Arch Environ Health 17(4): 460-461.
2. Mahler H (1977) Worldwide smallpox eradication: 1977. Nord Med 92(10): 236-240.
3. Fenner F, Henderson DA, Arita I, Jezek Z, Ladnyi ID (1988) Smallpox and its eradication. Geneva: World Health Organization. Available online at: <https://apps.who.int/iris/handle/10665/39485>
4. Boylston AW (2012) Defying Providence. Smallpox and the forgotten 18<sup>th</sup> century medical revolution. Charleston, SC: CreateSpace, 2012. 282 pp: ISBN 978-1478232452.
5. WHO (1982) Archives of the smallpox eradication program, a guide and inventory. Geneva.
6. Black FL (1975) Infectious diseases in primitive societies. Science 187(4176): 515-518.
7. Sakula A (2021) Robert Koch: Centenary of the Discovery of the Tubercle Bacillus [online]. Available online at: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1790283/pdf/canvetj00269-0053.pdf>
8. Riedel S (2005) Anthrax: A continuing concern in the era of bioterrorism. Proc (Bay Univ Med Cent) 18(3): 234-243.
9. Klement C (2020) Biological weapons and bioterrorism - a permanent role for public health. Hygiene 65(1): 3-4.
10. Koch R (1876) The etiology of environmental public health, based on the developmental history of Bacillus Anthracis. Contrib Plant Biol 2: 277-310.
11. CDC (2021) History of Anthrax [online]. Available online at: <https://www.cdc.gov/anthrax/resources/history/index.html>

12. Budianski S (1997) The covenant of the wild: Why animals chose domestication. London: Phoenix.
13. Karamanou M, Panayiotakopoulos G, Tsoucalas G, Kousoulis AA, Androustos G (2012) From miasmas to germs: A historical approach to theories of infectious disease transmission. *Infez Copper* 20(1): 58-62.
14. Wikipedia (2021) Miasma theory [online]. Available online at: <http://broughttolife.sciencemuseum.org.uk>
15. Infectious diseases at the Edward Worth library (2021) Theory of Contagion [online]. Available online at: <http://infectiousdiseases.edwardworthlibrary.ie/theory-of-contagion/>
16. Oldstone MBA (2020) Viruses, plagues and history: Past present and future. New York: Oxford University Press.
17. Gibbon E (1983) The Decline and Fall of the Roman Empire: Committee. 1<sup>st</sup> ed. Prague: Odeon.
18. Karlen A (1995) Plague's progress: A social history of man and disease. London: Indigo.
19. Malthus TR (2003) An essay on the principle of population. Available online at: <http://www.esp.org/books/malthus/population/malthus.pdf>.
20. Bencko V (2011) Primary disease prevention: Current pitfalls and opportunities. (In Czech) *Prakt Lék* 91(3): 127-130.
21. Warren JR, Marshall B (1983) Unidentified curved bacilli on gastric epithelium in active chronic gastritis. *Lancet* 1(8336): 1273-1275.
22. WHO (2021) World Health Data Platform [online]. Available online at: <https://www.who.int/data>
23. White Franco-Paredes C (2015) Leprosy in the 21<sup>st</sup> century. *Clin Microbiol Rev* 28(1): 80-94.
24. Almeida DJ, Tyrrell DAJ (1967) The morphology of three previously uncharacterized human respiratory viruses that grow in organ culture. *J Gen Virol* 1(2): 175-178.
25. Šíma P (2003) Infectious diseases do not end there. *Universe* 82: 443-445.
26. Coronaviridae Study Group of the International Committee on Taxonomy of Viruses, Gorbalenya AE, Baker SC, et al (2020) The species Severe acute respiratory syndrome-related coronavirus: Classifying 2019-nCoV and naming it SARS-CoV-2. *Nat Microbiol* 5(4): 536-544.
27. WHO links: <https://www.who.int/data>
28. Mlejnková H, Sovová K, Vašíčková P, Očenášková V, Jasíková L, et al. (2020) Preliminary study of SARS-Cov-2 occurrence in wastewater in Czech Republic. *Int J Environ Res Public Health* 17: 5508.
29. Lowe N, Bencko V (2021) Using wastewater-based epidemiology as an upcoming tool for the prediction and control of COVID-19 disease outbreaks. *Am J Biomed Sci Res* 14(2): AJBSR.MS.ID.001975.