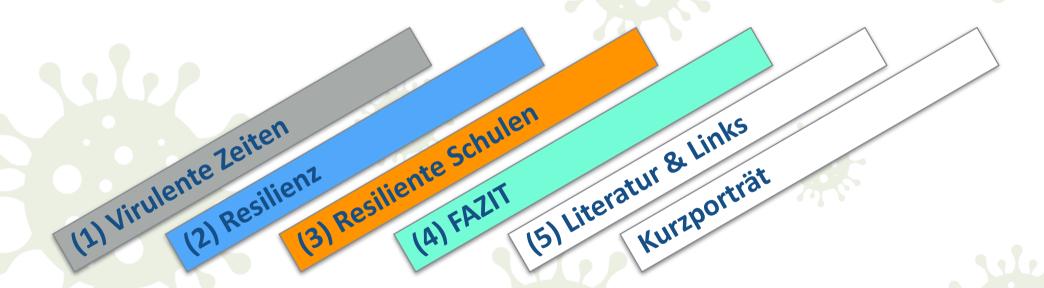


Resiliente Schulen in virulenten Zeiten

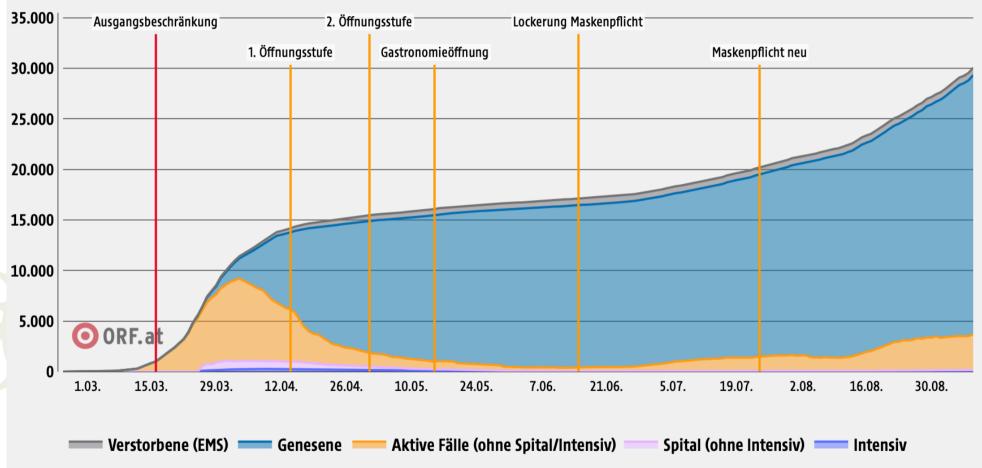
Ein neuer Fokus zukunftsweisender Schulentwicklung



Karikatur: Thomas Plaßmann (SPIEGEL Online, 8.8.2020)

(1) Virulente Zeiten

Coronavirus Österreich: Entwicklung der Fallzahlen



Grafik: ORF.at/corona

Quelle: Gesundheitsministerium/EMS, Stand: 8.9.2020, 23.00 Uhr (Aktualisierung: Täglich)

Quelle: orf.at/corona



Aktuelle gesellschaftliche Strategien gegen Covid-19:

- Herdenimmunität (aktueller Stand)
- Impfung (Stand und Perspektive)

Nachgewiesene Mehrfachinfektionen

Das doppelte Spiel des Coronavirus

Offenbar hat sich nicht nur ein Mann in Hongkong zweimal mit dem Virus angesteckt. Auch in den Niederlanden und Belgien gibt es je einen Fall von Reinfektion. Was bedeutet das für den weiteren Verlauf der Pandemie?

Von Julia Merlot

25.08.2020, 16.34 Uhr



Epidemien und Pandemien durch Zoonosen

Quelle: UN / ILRI (7 2020): Preventing the next pandemic. Zoonotic deseases and how to break the chain of transmission. Nairobi.

nce of significant diseases caused by coronaviruses and other pathogens



Avian infectious bronchitis Pathogen: Infectious bronchitis

virus (IBV)
Genus: Gammacoronavirus
Host: Chickens
Place of emergence:
North Dakota. USA

IBV causes an acute, highly contagious respiratory disease in chickens. It can also damage the reproductive tract, causing decreased egg quality and production. First documented in USA, the disease is now prevalent in all countries with an intensive poultry industry.



Porcine epidemic diarrhoea

Pathogen: Porcine epidemic diarrhoea virus (PEDV)

Genus: Alphacoronavirus Host: Pigs

Place of emergence: United Kingdom

Following the first appearance in the UK, it spread to other European countries and Asia. A highly virulent PEDV strain emerged in 2013 and caused nationwide outbreaks in the US, and rapidly spread to North, Central and South American countries. The virus is not zoonotic and poses no risk to humans, or food safety.

1940



Severe acute respiratory syndrome (SARS)

Pathogen: SARS coronavirus (SARS-CoV)

Genus: Betacoronavirus

Natural reservoir: Horseshoe bats Intermediate host: Masked civet cats Place of emergence: Guangdong, China

This pneumonia-like infection spread from Guangdong, China, to more than 26 countries in Asia, Europe, North America and South America before it was contained. SARS-like coronavirus has been found in horseshoe bats, suggesting that bats are natural reservoirs

1970



Middle East respiratory syndrome (MERS)

Pathogen: MERS coronavirus (MERS-CoV)

Genus: Betacoronavirus Natural reservoir: Probably bats Intermediate host: Dromedary camels Place of emergence: Saudi Arabia

First reported in Saudi Arabia, MERS has spread to 27 countries with a large outbreak in Korea in 2015. A study in 2018 shows high prevalence of MERS-CoV strains in local camels in Saudi Arabia, compared to imported camels from Africa.



Swine acute diarrhoea syndrome (SADS)

Pathogen: SADS coronavirus (SADS-CoV)
Genus: Alphacoronavirus
Natural reservoir: Probably bats

Host: Pigs
Place of emergence: Guangdong, China

SADS-CoV caused severe and acute diarrhoea and vomiting in newborn piglets. The outbreak killed nearly 25,000 piglets in Guangdong. Case fatality ratio: 90% in piglets less than five days old. This coronavirus did not appear to jump to humans.

2000



Coronavirus disease 2019

Pathogen: SARS-CoV-2 Genus: Betacoronavirus Natural reservoir: Probably bats Intermediate host: Unknown Place of emergence: Wuhan, China

SARS-CoV-2 appears to be a recent mix, or genetic recombination, of two coronaviruses. Genome sequencing suggests that SARS-CoV-2 is 96% identical to a coronavirus in horseshoe bats.

2010

1920 1930



1920s

Human Immunodeficiency Virus (HIV) infection Pathogen: HIV

Genus: Lentivirus Natural reservoir: Chimpanzee for HIV type 1, and Sooty Mangabey for HIV type 2

Place of emergence: Kinshasa, Democratic Republic of Congo

Based on genetic sequencing and historical records, the emergence of HIV is traced back to 1920s in Kinshasa, DRC. It is thought that simian immunodeficiency viruses (SIVs) in primates crossed over to humans at the time, presumably as a result of hunting and meat consumption. SIVs then adapted to the new human host to become HIV.

For references see page 61.



West Nile fever

Pathogen: West Nile virus Genus: Flavivirus Host: Birds Place of emergence: West Nile district, Uganda

Mosquitoes serve as disease vectors carrying the virus from infected birds to people and some mammals. Humans are usually incidental and dead-end hosts for the virus. The first recognized outbreak occurred in Israel in 1951, then Egypt. The virus re-emerged in Romania in 1996, and has established itself in the US since 1999. West Nile virus belongs to the same genus as dengue virus and yellow fever virus.



1947

Zika virus disease

Pathogen: Zika virus (ZIKV) Genus: Flavivirus Natural reservoir: Primates including humans Place of emergence: The Zika forest, Uganda

ZIKV was first discovered in a febrile sentinel rhesus monkey from the Zika forest, and in the Aedes africanus mosquito from the same forest a year later. The first human cases were detected in Uganda and Tanzania in 1952. An outbreak occurred in the Yap Islands, Federated State of Micronesia in 2007, followed by a major epidemic in the Americas in 2015-16.



1950

Ebola virus disease

Pathogen: Ebola virus Genus: Ebolavirus Natural reservoir: Unconfirmed but likely to be African fruit bats of the Pteropodidae family Intermediate host: Apes and monkeys

Place of emergence: Two simultaneous outbreaks in Democratic Republic of Congo (DRC) and South Sudan

The largest outbreak in history occurred primarily in Guinea, Liberia and Sierra Leone from 2014 to 2016, killing 11,323 people. The virus also recently re-emerged in eastern DRC from 2018 to 2019. Case fatality ratio of Ebola varied from 25% to 90%.



1986

1980

Bovine spongiform encephalopathy or mad cow disease

Agent: Pathogenic prions Host: Cattle Place of emergence: United Kingdom

Mad cow disease is a progressive, fatal neurological disorder in cattle. The human form of the mad cow disease known as variant Creutzfeldt-Jakob disease is linked to consumption of beef from cattle infected with the disease.



1994

1990

Hendra virus infection Pathogen: Hendra virus Genus: Henipavirus

Natural reservoir: Large fruit bats (Pteropus spp.) or flying fox Host: Horses Place of emergence: Hendra, Australia

Sporadic outbreaks have occurred in Australia over the years since its initial appearance in 1994. So far, no cases have been reported outside Australia. Case fatality ratio is 75% in horses, and 50% in humans. Hendra virus belongs to the same genus as Nipah virus.



1996

Highly pathogenic avian influenza (HPAI) or bird flu Pathogen: HPAI virus subtype

Pathogen: HPAI virus subtype H5N1

Genus: Alphainfluenzavirus Natural reservoir: Wild waterfowl Host: Poultry Place of emergence: Guangdong, China

First human cases found in Hong Kong in 1997 were traced back to wild and domestic waterfowl in Guangdong in 1996. Re-emerging in Hong Kong in 2002, the virus spread rapidly to South East Asian countries. Over 100 million domesticated chickens and ducks either died of the disease or were culled to stop the outbreak in Asia.



2020

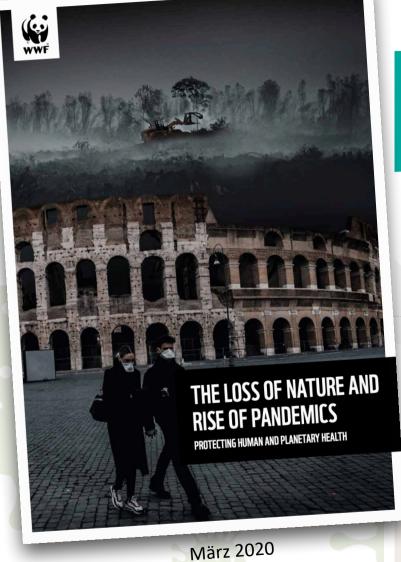
Nipah virus infection

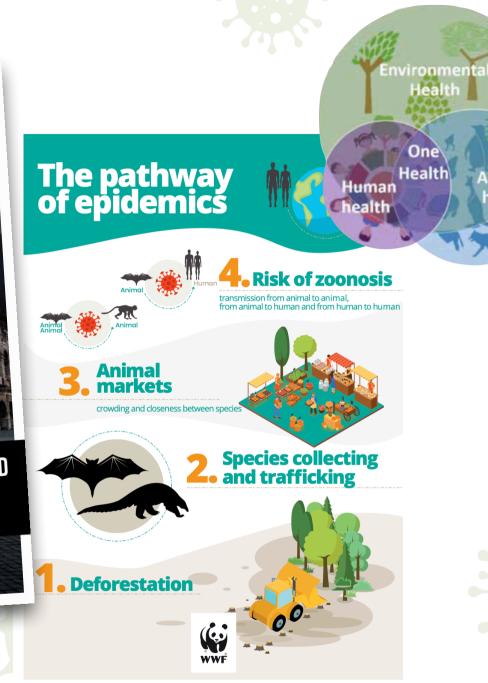
Pathogen: Paramyxovirus Genus: Henipavirus Natural reservoir: Large fruit bats (Pteropus spp.) or

flying fox Host: Pigs Place of emergence: Sungai Nipah village, Ipoh, Malaysia

Nipah virus emerged as a respiratory and neurologic disease in pigs, and then spread to humans. A large outbreak in Malaysia from 1998 to 1999 was followed by five outbreaks in Bangladesh from 2001 to 2005. To control the outbreak in Malaysia, at least one million pigs were culled.

(1) Virulente Zeiten





Anima

health









PREVENTING THE NEXT PANDEMIC

Zoonotic diseases and how to break the chain of transmission



A Scientific Assessment with Key Messages for Policy-Makers A Special Volume of UNEP's Frontiers Report Series

Uno-Bericht

Die nächste Pandemie kommt bestimmt

Das Coronavirus hat seinen Ursprung im Tierreich - kein Einzelfall, zeigt nun ein Bericht der Uno. Solche Zoonosen werden sich auch in Zukunft ausbreiten. Schuld daran ist der

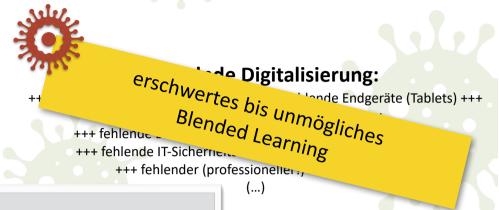
06.07.2020, 18.31 Uhr

Virologen gehen davon aus, dass es derzeit weltweit 40 Viren mit Pandemiepotenzial gibt.

Juli 2020

(1) Virulente Zeiten

erschwerte bis unmögliche Umsetzung ++ fehlende Klassenzime von Hygienekonzepten --- mangelhafter Putzservice +++



Schule als Risikopatient mit schweren (chronischen) Vorerkrankungen

Lehrermangel: (Stand 1 2020)

his 2025 fehlen in D ca. 12.400 LKs in GS (lt. KMK)

labile bis mangelnde Lehrer:innen-Versorgung (ca. 5-10% gehören aktuell selbst zur Risikogruppe)

Grund: steigende Geburtenzahlen seit 201

und falsche Annahmen zur Entwicklung der Schüler:innen-Zahlen durch uie ... Quelle: https://karriere.unicum.de/berufsorientierung/branchencheck/lehrermangel-2020

verstärkt die Bildungsungleichheit durch abnehmende Chancengerechtigkeit LPS und SLs +++



1. ZwischenFAZIT:

- Covid-19 ist eine Pandemie mit Ansage.
- Wir müssen aktuell mit Covid-19 leben und davon ausgehen, dass wir zukünftig mit weiteren Viren-Epidemien/-Pandemien zu leben haben werden.
- Schulen erweisen sich als "Risikopatienten mit schweren Vorerkrankungen".
- Wir brauchen gesündere Schulen.

